

QY 366 GGCACCCAGCAGCGGATCGGCTGCCCTGCGAGCGGCTGGGGGCGCCCGCTGGG 425
Db 61 GGCACCCAGCAGCGATCGGCTGCCCTGCGAGCGGCTGGGGGCGCCCGCTGGG 120
QY 426 CTGGGCTGCCCGGAGACGACGAGACGACGAGCCGAGAGCCCGCGGAGGGGAGCTTT 485
Db 121 CTGGGCTGCCCGGAGACGACGAGACGACGAGCCGAGAGCCCGCGGAGGGGAGCTTT 180
QY 486 GTGGAGATGGTGGAACCTGAGGGCAAGTGGGGGAGGCTACTAGCTGGAGATGACC 545
Db 181 GTGGAGATGGTGGAACCTGAGGGCAAGTGGGGGAGGCTACTAGCTGGAGATGACC 240
QY 546 GTGGGACGCCCCCGCAGACGCTCAACATCTCTGGTGATACAGGACGAGTAACCTTTGCA 605
Db 241 GTGGGACGCCCCCGCAGACGCTCAACATCTCTGGTGATACAGGACGAGTAACCTTTGCA 300
QY 606 GTGGGTGCTGCCCGCCACCCCTTCTGATGCTACTACAGAGGAGGCTGTCACGACA 665
Db 301 GTGGGTGCTGCCCGCCACCCCTTCTGATGCTACTACAGAGGAGGCTGTCACGACA 360
QY 666 TACCGGAGACCTCCGGAAGGCTGTATGTCCCTACACCCAGGCAAGTGGGAAGGGAG 725
Db 361 TACCGGAGACCTCCGGAAGGCTGTATGTCCCTACACCCAGGCAAGTGGGAAGGGAG 420
QY 726 CTGGGACCGGACCTGGTAAGCATCCCCCATGGCCCCAACCTCACTGCTGCCAACATTT 785
Db 421 CTGGGACCGGACCTGGTAAGCATCCCCCATGGCCCCAACCTCACTGCTGCCAACATTT 480
QY 786 GCTGCATCACTGAATCAGACGAATTTCTTCATCAACGGCTCCCACTGGGAAGGCAATCCTG 845
Db 481 GCTGCATCACTGAATCAGACGAATTTCTTCATCAACGGCTCCCACTGGGAAGGCAATCCTG 540
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QY 906 CTGTGTAAGCAGACCCACCTTCCCAACCTCTTCTCCCTGACGCTTTGTGGTCTGGCTTC 965
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QY 966 CCCCTCAACCACTGTAAGTGTGGGCTCTGTGGAGGGAGCATGATCATTTGGAGGTATTC 1025
Db 661 CCCCTCAACCACTGTAAGTGTGGGCTCTGTGGAGGGAGCATGATCATTTGGAGGTATTC 720
QY 1026 GACCACTCGCTTACACAGGCACTCTCTGTGTATACACCCATCCCGCGGAGTGGTATTAT 1085
Db 721 GACCACTCGCTTACACAGGCACTCTCTGTGTATACACCCATCCCGCGGAGTGGTATTAT 780
QY 1086 GAGGTGATCATTTGGGGTGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 1145
Db 781 GAGGTGATCATTTGGGGTGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
QY 1146 TACAACTATGACAAGAGCATTTGGGAGTGGGACGACCAACCACTTCGTTTCCCAAGAAA 1205
Db 841 TACAACTATGACAAGAGCATTTGGGAGTGGGACGACCAACCACTTCGTTTCCCAAGAAA 900
QY 1206 GTGTTTGAAGCTGCACTCAAAATCCATCAAGGAGGCTTCTCCAGGAGAAATTCCTGTAT 1265
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QY 1266 GGTTCCTGGCTAGGAGAGAGCTGGTGTGTGCAAGCAGGACCAACCCCTTTGGAAACATTT 1325
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QY 1326 TTCCAGTCATCTCACTTACCTAATGGGTGAGGTTACCAACCACTTCCTTCGGCATCACC 1385
Db 1021 TTCCAGTCATCTCACTTACCTAATGGGTGAGGTTACCAACCACTTCCTTCGGCATCACC 1080
QY 1386 ATCCCTTCGCGACCAATACCTCGCGCCAGTGGAGATGTGGCCAGCTTCCCAAGACGACTGT 1445
Db 1081 ATCCCTTCGCGACCAATACCTCGCGCCAGTGGAGATGTGGCCAGCTTCCCAAGACGACTGT 1140
QY 1446 TACAAGTTTGGCATCTCAGAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1505

Db 1141 TACAAGTTTGGCATCTCAGATCATCCACGGGCACTGTTATGGAGCTGTTATCATGACAG 1200
QY 1506 GGCCTTACGTTGCTTTCATCGGGCCGAAACGAATTCGCTTTCGCTCAGCCCTTGC 1565
Db 1201 GGCCTTACGTTGCTTTCATCGGGCCGAAACGAATTCGCTTTCGCTCAGCCCTTGC 1260
QY 1566 CATGTGCAGATGAGTTTCAAGGCGCAGCGGTGGAAGCCCTTTTGTCAACCTTGGACATG 1625
Db 1261 CATGTGCAGATGAGTTTCAAGGCGCAGCGGTGGAAGCCCTTTTGTCAACCTTGGACATG 1320
QY 1626 GAAGACTTGGCTTACAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1685
Db 1321 GAAGACTTGGCTTACAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1380
QY 1686 GTCATGGCTGCCATCTGCCCTCTTTCATGCTGCCACTCTGCCCTCATGGTGTGTCAGTGG 1745
Db 1381 GTCATGGCTGCCATCTGCCCTCTTTCATGCTGCCACTCTGCCCTCATGGTGTGTCAGTGG 1440
QY 1746 CGCTGCCCTCCGCTGCCCTGCCAGCAGCATGATGACTTTTGTGATGACATCTCCCTGCTG 1805
Db 1441 CGCTGCCCTCCGCTGCCCTGCCAGCAGCATGATGACTTTTGTGATGACATCTCCCTGCTG 1500
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Db 1501 AAGTGAGAGGCGCCATGGGCGAAGATYAGAGATTCGCCCTGGACACACCTCCGTTGGTTCA 1560
QY 1866 CTTTGGTGCACAGTAGGAGACACAGATGGCACCTGTGGCAGAGCAGCCTCAGACCCCTCC 1925
Db 1561 CTTTGGTGCACAGTAGGAGACACAGATGGCACCTGTGGCAGAGCAGCCTCAGGACCCCTCC 1620
QY 1926 CCACCCACCAATGCTCTGCCCTTGTATGGAGAAGAAAGGCTGGCAAGTGGTTCAG 1985
Db 1621 CCACCCACCAATGCTCTGCCCTTGTATGGAGAAGAAAGGCTGGCAAGTGGTTCAG 1680
QY 1986 GGACTGTACCTGTAGAAACAGAAAGAGAAAGAGCACTCTGCTGGCGGGAATACT 2045
Db 1681 GGACTGTACCTGTAGAAACAGAAAGAGAAAGAGCACTCTGCTGGCGGGAATACT 1740
QY 2046 CTTGCTACCTCAAAATTTAAGTCGGGAAATTCGCTCTGCTGAAACTTCAGCCCTCAACCT 2105
Db 1741 CTTGCTACCTCAAAATTTAAGTCGGGAAATTCGCTCTGCTGAAACTTCAGCCCTCAACCT 1800
QY 2106 TTGTCCACCAATTCCTTAAATTCCTCAACCAAGATATCTCTTCTTCTTCTTCTTCTTCTTCT 2165
Db 1801 TTGTCCACCAATTCCTTAAATTCCTCAACCAAGATATCTCTTCTTCTTCTTCTTCTTCTTCT 1860
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QY 2226 AGACCAAGCTTCTTCCCTGCTGGCCAAAGTTCAGTAGGAGAGATGACAGTTCGTATTT 2285
Db 1921 AGACCAAGCTTCTTCCCTGCTGGCCAAAGTTCAGTAGGAGAGATGACAGTTCGTATTT 1980
QY 2286 TGCTTTAGACAGGAGCTGTATAAACCAACCCCTTAACATTTGCTGCAAGATTCGCTCTTCA 2345
Db 1981 TGCTTTAGACAGGAGCTGTATAAACCAACCCCTTAACATTTGCTGCAAGATTCGCTCTTCA 2040
QY 2346 ATT 2348
Db 2041 ATT 2043

RESULT 2
US-09-795-847-3
; Sequence 3, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Helinikson, Robert L.
; APPLICANT: Parodi, Luis A.

APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-847-3

Query Match 86.9%; Score 2039.8; DB 10; Length 2070;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	966	CCCTCAACAGTCTGAAGTGGCTGCTGCGGAGGAGCATGATCATTTGGAGGTATC	1025
DB	661	CCCTCAACAGTCTGAAGTGGCTGCTGCGGAGGAGCATGATCATTTGGAGGTATC	720
QY	1026	GACCACTCGCTGTACACAGGCACTCTCTGGTATACACCATCGGCGGAGTGGTATTAT	1085
DB	721	GACCACTCGCTGTACACAGGCACTCTCTGGTATACACCATCGGCGGAGTGGTATTAT	780
QY	1086	GAGGTGATCATTTGTGCGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG	1145
DB	781	GAGGTGATCATTTGTGCGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG	840
QY	1146	TACAACTATGACAAGAGCATTTGTGGACAGTGGACACCAACCTCTGTTTGGCCCAAGAA	1205
DB	841	TACAACTATGACAAGAGCATTTGTGGACAGTGGACACCAACCTCTGTTTGGCCCAAGAA	900
QY	1206	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGAGGCTCTCCACGGAGAGTTCCCTGAT	1265
DB	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGAGGCTCTCCACGGAGAGTTCCCTGAT	960
QY	1266	GGTTTCTGGCTAGGAGAGCAGCTGGTGTCTGGCAAGCAGGACACCCCTTTGGAACATT	1325
DB	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTCTGGCAAGCAGGACACCCCTTTGGAACATT	1020
QY	1326	TTCCAGTCTCATCTACCTTAATGGTGGAGTTTACCAACAGTCTCTCCGCATCACC	1385
DB	1021	TTCCAGTCTCATCTACCTTAATGGTGGAGTTTACCAACAGTCTCTCCGCATCACC	1080
QY	1386	ATCTCTTCCGACGATACCTGCGGCGAGTGGAGATGTGGCCACGTCCTCAAGACGACTGT	1445
DB	1081	ATCTCTTCCGACGATACCTGCGGCGAGTGGAGATGTGGCCACGTCCTCAAGACGACTGT	1140
QY	1446	TACAAGTTTGGCATCTCAGTCACTACGTCATCCAGGCACTGTTATGGAGCTGTTATCATGGAG	1505
DB	1141	TACAAGTTTGGCATCTCAGTCACTACGTCATCCAGGCACTGTTATGGAGCTGTTATCATGGAG	1200
QY	1506	GGCTTCTACGTTGTCTTTGATCGGGCCGAAACAACTTGGCTTTGCTGTCAGCGCTTGC	1565
DB	1201	GGCTTCTACGTTGTCTTTGATCGGGCCGAAACAACTTGGCTTTGCTGTCAGCGCTTGC	1260
QY	1566	CATGTGCAGCATGAGTTTCAAGGAGGCGGAGTGGAGAGGCGCTTTTGTCACTTTGGACATG	1625
DB	1261	CATGTGCAGCATGAGTTTCAAGGAGGCGGAGTGGAGAGGCGCTTTTGTCACTTTGGACATG	1320
QY	1626	GAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT	1685
DB	1321	GAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT	1380
QY	1686	GTATGGCTGCCATCTGCGCCCTTCTTCATGCTGCCACTCTGCCATCATGGTGTGTCAGTGG	1745
DB	1381	GTATGGCTGCCATCTGCGCCCTTCTTCATGCTGCCACTCTGCCATCATGGTGTGTCAGTGG	1440
QY	1746	CGCTGCCCTCGCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1805
DB	1441	CGCTGCCCTCGCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
QY	1806	AAGTAGGAGGCGCCATGGGCAAGATAGAGATTCCTCCCTGGACACACCTCCCTGGTGTCA	1865
DB	1501	AAGTAGGAGGCGCCATGGGCAAGATAGAGATTCCTCCCTGGACACACCTCCCTGGTGTCA	1560
QY	1866	CTTTGGTCAAAAGTAGGAGACAGATGGACCTGTGGCCAGAGCAGCCTCAGGACCTCC	1925
DB	1561	CTTTGGTCAAAAGTAGGAGACAGATGGACCTGTGGCCAGAGCAGCCTCAGGACCTCC	1620
QY	1926	CCACCCACCAATGCTGCTGCTTGTATGAGAGGAGAAAGGCTGGCAAGGTGGGTTCAG	1985
DB	1621	CCACCCACCAATGCTGCTGCTTGTATGAGAGGAGAAAGGCTGGCAAGGTGGGTTCAG	1680
QY	1986	GGACTGTACCTGTAGAAACAGAAAGAGAAAGAAAGCACTCTGCTGGCGGAACTACT	2045
DB	1681	GGACTGTACCTGTAGAAACAGAAAGAGAAAGAAAGCACTCTGCTGGCGGAACTACT	1740
QY	2046	CTTGGTCACTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTTTCAGCCTGAACCT	2105

QY	306	ATFGCCCAAGCCCTCGCTGGCTCTGCTGTGGATGGGCGGGAGTGTGCTGCCAC	365
DB	1	ATFGCCCAAGCCCTCGCTGGCTCTGCTGTGGATGGGCGGGAGTGTGCTGCCAC	60
QY	366	GGCAGCCAGCAGGATCGGCTGCCCTGCCAGCGGCTGGGGCGCCCTGGGG	425
DB	61	GGCAGCCAGCAGGATCGGCTGCCCTGCCAGCGGCTGGGGCGCCCTGGGG	120
QY	426	CTGCGGCTGCCCGGAGACCCGACGAGCCGAGGCGCGGCGGAGGGGCGAGCTTT	485
DB	121	CTGCGGCTGCCCGGAGACCCGACGAGCCGAGGCGCGGCGGAGGGGCGAGCTTT	180
QY	486	GTGGAGATGGTGACAACTGAGGGGCAAGTGGGCGAGGCTACTACGTGAGATGACC	545
DB	181	GTGGAGATGGTGACAACTGAGGGGCAAGTGGGCGAGGCTACTACGTGAGATGACC	240
QY	546	GTGGCAGCCCCCGCAGACGCTCAACATCTCTGGTGATACAGGAGCAGTAACTTGA	605
DB	241	GTGGCAGCCCCCGCAGACGCTCAACATCTCTGGTGATACAGGAGCAGTAACTTGA	300
QY	606	GTGGGTGCTGCCCGCCACCCCTTCTGTCATCGCTACTACAGAGGAGCTGTCCAGACA	665
DB	301	GTGGGTGCTGCCCGCCACCCCTTCTGTCATCGCTACTACAGAGGAGCTGTCCAGACA	360
QY	666	TACCGGAGCTCCGGAAGGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG	725
DB	361	TACCGGAGCTCCGGAAGGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG	420
QY	726	CTGGCAGCCGACCTGTAAGCATCCCCATGGCCCAAGCTCAGTCTGCTGCCACATT	785
DB	421	CTGGCAGCCGACCTGTAAGCATCCCCATGGCCCAAGCTCAGTCTGCTGCCACATT	480
QY	786	GCTGCATCACTGAATCAGACAAGTTCTTTCATCAACGGCTCCAACCTGGGAAGGATCTTG	845
DB	481	GCTGCATCACTGAATCAGACAAGTTCTTTCATCAACGGCTCCAACCTGGGAAGGATCTTG	540
QY	846	GGGTGGCTATGCTGAGATGCCAGGCTGACGACTCCCTGGAGCTTTTCTTGTACTCT	905
DB	541	GGGTGGCTATGCTGAGATGCCAGGCTGACGACTCCCTGGAGCTTTTCTTGTACTCT	600
QY	906	CTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGCAGCTTTGCTGGCTTC	965
DB	601	CTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGCAGCTTTGCTGGCTTC	660

QY 1566 CATGTGCAGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCTACCTTGGACATG 1625
Db 1261 CATGTGCAGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCTACCTTGGACATG 1320
QY 1626 GAAGACTGTGGCTACAACTTCCACAGACAGATGAGTCAACCTCATGACCATAGCTTAT 1685
Db 1321 GAAGACTGTGGCTACAACTTCCACAGACAGATGAGTCAACCTCATGACCATAGCTTAT 1380
QY 1686 GTCTGGCTGCCATCTGCCCTCTTTCATGCTGCCACTCTGGCTCATGTGTGTCAAGTGG 1745
Db 1381 GTCTGGCTGCCATCTGCCCTCTTTCATGCTGCCACTCTGGCTCATGTGTGTCAAGTGG 1440
QY 1746 CGCTGCTCCGCTGCGTGGCCAGCAGCATGATGACTTTGTGTGATGACATCTCCCTGCTG 1805
Db 1441 CGCTGCTCCGCTGCGTGGCCAGCAGCATGATGACTTTGTGTGATGACATCTCCCTGCTG 1500
QY 1806 AAGTCAGGAGCCCATGGGCAGAAGATACAGATTCCCTTGGACCACACCTCCGTGTTTCA 1865
Db 1501 AAGTCAGGAGCCCATGGGCAGAAGATAGAGATTCCCTTGGACCACACCTCCGTGTTTCA 1560
QY 1866 TTCTGTCTACAACTAGGAGACACAGATGACCTGTGGCCAGAGCACCTCAGGACCTCC 1925
Db 1561 TTCTGTCTACAACTAGGAGACACAGATGACCTGTGGCCAGAGCACCTCAGGACCTCC 1620
QY 1926 CCACCCACCAATGCTCTGCTTGTATGAGAGAGAAAGGCTGGCAAGTGGGTTTCCAG 1985
Db 1621 CCACCCACCAATGCTCTGCTTGTATGAGAGAGAAAGGCTGGCAAGTGGGTTTCCAG 1680
QY 1986 GGACTGTACTGTAGGAACAGAAAGAGAGAAAGAGCACTCTGCTGGCGGGAATACT 2045
Db 1681 GGACTGTACTGTAGGAACAGAAAGAGAGAAAGAGCACTCTGCTGGCGGGAATACT 1740
QY 2046 TTCTGTCTACCAATTTAAGTCGGGAAATCTGTGCTTGAACCTTCAGCCCTGAACCT 2105
Db 1741 TTCTGTCTACCAATTTAAGTCGGGAAATCTGTGCTTGAACCTTCAGCCCTGAACCT 1800
QY 2106 TTGTCCACCATCTTTAAATTTCCAAACCCAAAGTATTTCTTTCTTTTAGTTTCAGAA 2165
Db 1801 TTGTCCACCATCTTTAAATTTCCAAACCCAAAGTATTTCTTTCTTTTAGTTTCAGAA 1860
QY 2166 GTACTGGCATCACGCGAGTTACCTTGGCGTGTGCTTGGTACCTTGGCAGAGAAG 2225
Db 1861 GTACTGGCATCACGCGAGTTACCTTGGCGTGTGCTTGGTACCTTGGCAGAGAAG 1920
QY 2226 AGACCAAGCTTGTTCCTTGGTGGCCAAAGTCAGTAGGAGGATGCACAGTTTGTATT 2285
Db 1921 AGACCAAGCTTGTTCCTTGGTGGCCAAAGTCAGTAGGAGGATGCACAGTTTGTATT 1980
QY 2286 TGCCTTTAGACAGGAGCTGTATAACAAAGCCTTAACATTGGTGCAAGATTTGCTTTGA 2345
Db 1981 TGCCTTTAGACAGGAGCTGTATAACAAAGCCTTAACATTGGTGCAAGATTTGCTTTGA 2040
QY 2346 ATT 2348
Db 2041 ATT 2043

RESULT 4

US-09-794-748-3
; Sequence 3, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-748-3

Query Match 86.9%; Score 2039.8; DB 10; Length 2070;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 306 ATGGCCCAAGCCCTGCCCTGGCTCTCTGTGTGATGGGCGGGAGTGTGCTGCCCCAC 365
Db 1 ATGGCCCAAGCCCTGCCCTGGCTCTCTGTGTGATGGGCGGGAGTGTGCTGCCCCAC 60
QY 366 GGCACCCAGCAGCGCATCCGGCTGCCCTCGCAGCGGCTGGGGGCGGCCCTGGGG 425
Db 61 GGCACCCAGCAGCGCATCCGGCTGCCCTCGCAGCGGCTGGGGGCGGCCCTGGGG 120
QY 426 CTGCGCTGCTCCCGGGAGACCGAGAGCCCGAGAGCCCGCGGAGGCGGCGGCGGCTTT 485
Db 121 CTGCGCTGCTCCCGGGAGACCGAGAGCCCGAGAGCCCGCGGAGGCGGCGGCGGCTTT 180
QY 486 GTGGAGATGGTGACAACTGAGGGCAAGTCCGGGAGGGCTACTACGTGGAGATGACC 545
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QY 1146 TACAACATATGACAAGAGCATTTGGACAGTGGCAGCACCAACCTTGGTTGGCCCAAGAAA 1205
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QY 1326 TTCCAGTCAATCTACATCTACCTAATGGGTGAGGTTACCAACAGTCTTTCCGCATCAAC 1385
Db 1021 TTCCAGTCAATCTACATCTACCTAATGGGTGAGGTTACCAACAGTCTTTCCGCATCAAC 1080
QY 1386 ATCCCTTCGGCAGCAATACCTGCGGCCAGTGGAAAGATGTGGCCACGTCCTCAAGACGACTGT 1445
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QY 1446 TACAAGTTTGGCCATCTCACAGTCTATCCACGGCAGCTGTATGGGAGCTGTATCATGGAG 1505
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Db 1201 GGTTCCTAGCTTGTCTTTGATCGGGCCGGAACCAAGTGGCTTGGCTGTCAGCGCTTGC 1260
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Db 1261 CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTTGGACATG 1320
QY 1626 GAAGACTGTGGCTTACAACTTCCACAGACATGATGATCAACCTCATGACCATAGCCTAT 1685
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QY 1686 GTCATGGCTGCCATCTCGCCCTCTTCTATGCTGCACATCTGCTCATGCTGTGTCAGTGG 1745
Db 1381 GTCATGGCTGCCATCTCGCCCTCTTCTATGCTGCACATCTGCTCATGCTGTGTCAGTGG 1440
QY 1746 CGCTGCTCGCTCGCTCGCCAGCAGCATGATGATCTTGTGATGACATCTCCCTGCTG 1805
Db 1441 CGCTGCTCGCTCGCTCGCCAGCAGCATGATGATCTTGTGATGACATCTCCCTGCTG 1500
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Db 1501 AAGTGAGGAGGCCATGGGAGAGATAGAGATTCCCTTGGACACACCTTCCCTGGTTCA 1560
QY 1866 CTTTGTGCACAACTAGGAGACAGATGGCACCCTGTGGCCAGACACCTCAGGACCCCTCC 1925
Db 1561 CTTTGTGCACAACTAGGAGACAGATGGCACCCTGTGGCCAGACACCTCAGGACCCCTCC 1620
QY 1926 CCACCCACCAAAATGCTTGTGATGGAGAGGAAAGGCTGGCAAGTGGGTTCACG 1985
Db 1621 CCACCCACCAAAATGCTTGTGATGGAGAGGAAAGGCTGGCAAGTGGGTTCACG 1680
QY 1986 GGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGAGACTCTGCTGGCGGGAATACT 2045
Db 1681 GGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGAGACTCTGCTGGCGGGAATACT 1740
QY 2046 CTTTGTCACTCAAAATTAAGTCGGGAAATTTCTGCTGTGAACTTTCAGCCCTGAACCT 2105
Db 1741 CTTTGTCACTCAAAATTAAGTCGGGAAATTTCTGCTGTGAACTTTCAGCCCTGAACCT 1800
QY 2106 TTGTCCACCAATTCCTTTAAATTTCTCCAAACCAAAAGTATTTCTTTTCTTTAGTTTCAGAA 2165
Db 1801 TTGTCCACCAATTCCTTTAAATTTCTCCAAACCAAAAGTATTTCTTTTCTTTAGTTTCAGAA 1860

RESULT 5

US-09-794-925-3
; Sequence 3, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
; FILE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280H1
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-925-3

Query Match 86.9%; Score 2039.8; DB 10; Length 2070;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 306 ATGGCCCAAGCCCTGCCCCCTGGCTCTGCTGTGGATGGGCGGGAGTGTGCTTGGCCAC 365
Db 1 ATGGCCCAAGCCCTGCCCCCTGGCTCTGCTGTGGATGGGCGGGAGTGTGCTTGGCCAC 60
QY 366 GGCACCCAGCAGCGCATCCCGCTGCCCTTGGCAGCGGCTGGGGGGCGCCCTGGG 425
Db 61 GGCACCCAGCAGCGCATCCCGCTGCCCTTGGCAGCGGCTGGGGGGCGCCCTGGG 120
QY 426 CTGCGGCTGCCCCGGGAGACCGAGAGCCGAGAGCCCGAGAGCCCGCCGGAGGGGAGCTTT 485
Db 121 CTGCGGCTGCCCCGGGAGACCGAGAGCCGAGAGCCCGAGAGCCCGCCGGAGGGGAGCTTT 180
QY 486 GTGGAGATGTGGACAACCTGAGGGGCAAGTCTGGGGCAGGGTCTACTGCTGGAGATCACC 545
Db 181 GTGGAGATGTGGACAACCTGAGGGGCAAGTCTGGGGCAGGGTCTACTGCTGGAGATCACC 240
QY 546 GTGGGAGCCCCCGGAGACGCTCAACATCTGCTGGATACAGGACGACGTAACCTTTGCA 605
Db 241 GTGGGAGCCCCCGGAGACGCTCAACATCTGCTGGATACAGGACGACGTAACCTTTGCA 300

QY 606 GTGGGTGCTGCCCCACCCCTTCTTCATCGCTACTACAGAGGAGCTGTCCAGCACA 665
DB 301 GTGGGTGCTGCCCCACCCCTTCTTCATCGCTACTACAGAGGAGCTGTCCAGCACA 360
QY 666 TACCGGAGCTCCGGGAAGGCTGTATGTATGCTCCCTACACCCAGGCGAAGTGGGAAGGGAG 725
DB 361 TACCGGAGCTCCGGGAAGGCTGTATGTATGCTCCCTACACCCAGGCGAAGTGGGAAGGGAG 420
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DB 421 CTGGGACCCAGCTGTATAGCATCCCCCATGGCCCAAGCTCACTGTGGTGCACACATT 480
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DB 481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGGTCCAACTGGGAAGGCATCCCTG 540
QY 846 GGGCTGGCTATGCTGAGATGGCAGGCTGACGACTCCCTGGAGGCTTTCTTTGACTCT 905
DB 541 GGGCTGGCTATGCTGAGATGGCAGGCTGACGACTCCCTGGAGGCTTTCTTTGACTCT 600
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DB 601 CTGGTAAGCAGACCCACCTTCCCAACCTTCTTCCTCCCTGCAGCTTTGTGGTGGCTTC 660
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DB 661 CCCTCAACGAGCTCTGAAGTGTGGCTCTGTTCGGAGGAGCATGATCATTTGGAGGTATC 720
QY 1026 GACCACTCGCTGACAGGAGCTCTCTGTATACACCCATCGGGGGAGTGGTATTAT 1085
DB 721 GACCACTCGCTGACAGGAGCTCTCTGTATACACCCATCGGGGGAGTGGTATTAT 780
QY 1086 GAGGTATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAATGGACTGCAAGGAG 1145
DB 781 GAGGTATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAATGGACTGCAAGGAG 840
QY 1146 TACAACATATCACAAGAGCATTTGTGGACAGTGGCACCACCAACCTTCTGTTGCCCAAGAAA 1205
DB 841 TACAACATATCACAAGAGCATTTGTGGACAGTGGCACCACCAACCTTCTGTTGCCCAAGAAA 900
QY 1206 GTGTTTGAAGTGCATCAATCCATCAAGGAGCTCTCCACGAGAGTTCCTGTAT 1265
DB 901 GTGTTTGAAGTGCATCAATCCATCAAGGAGCTCTCCACGAGAGTTCCTGTAT 960
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DB 961 GGTTCCTGCTAGGAGAGCTGTGTGCTGCAAGCAGGACCAACCTTTCGGAACATT 1020
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DB 1021 TTCCCACTCATCTCACTTACCTTAATGGGTGAGGTTACCAACCACTCTTCCGCATCACC 1080
QY 1386 ATCTTTCCGAGCAATACCTCGGGCCAGTGGGAAGATGTGGCCACGTCCTCCCAAGACGACTGT 1445
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QY 1446 TACAAGTTTGGCATCTCACAGTCATCCAGGGCACTGTTATGGAGCTGTTATCATGGAG 1505
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QY 1506 GGTTCCTACGTTCTCTTGTATCGGGCCGAAAAACGAATTTGGCTTGTGTCAGCGCTTGC 1565
DB 1201 GGTTCCTACGTTCTCTTGTATCGGGCCGAAAAACGAATTTGGCTTGTGTCAGCGCTTGC 1260
QY 1566 CATGTGCAGATGAGTTTCAGGACGCGGCTGGGAAGGCCCTTTTGTACCTTTGGACATG 1625
DB 1261 CATGTGCAGATGAGTTTCAGGACGCGGCTGGGAAGGCCCTTTTGTACCTTTGGACATG 1320
QY 1626 GAAGACTGTGGCTACAAACATTTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCAT 1685
DB 1321 GAAGACTGTGGCTACAAACATTTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCAT 1380

QY 1686 GTCATGGCTGCCATCTGCGCCCTTCTTCATGCTGCCACTCTGCTCATGTGTGTGTCAGTGG 1745
DB 1381 GTCATGGCTGCCATCTGCGCCCTTCTTCATGCTGCCACTCTGCTCATGTGTGTGTCAGTGG 1440
QY 1746 CGCTGGCTCGGCTGCGCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1805
DB 1441 CGCTGGCTCGGCTGCGCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
QY 1806 AAGTGAAGGAGGCCCATTTGGGCAGAGATAGAGATTCCTCTGGACACACCTCCGTTGGTTCA 1865
DB 1501 AAGTGAAGGAGGCCCATTTGGGCAGAGATAGAGATTCCTCTGGACACACCTCCGTTGGTTCA 1560
QY 1866 CTTTGGTTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCAGCTTCAGACCCCTCC 1925
DB 1561 CTTTGGTTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCAGCTTCAGACCCCTCC 1620
QY 1926 CCACCCACCAATGCTCTGCTCTGCTTGTATGGAGAAGGAAAGCTGGCAAGTGGTTCAG 1985
DB 1621 CCACCCACCAATGCTCTGCTCTGCTTGTATGGAGAAGGAAAGCTGGCAAGTGGTTCAG 1680
QY 1986 GGACTGTACCTGTAGGAAACAGAAAGAGAAAGAACGACTCTGCTGGCAGAAATACT 2045
DB 1681 GGACTGTACCTGTAGGAAACAGAAAGAGAAAGAACGACTCTGCTGGGGAATACT 1740
QY 2046 CTTTGGTCAACCTCAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 2105
DB 1741 CTTTGGTCAACCTCAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 1800
QY 2106 TTTGTCACCATTCCTTTTAAATTTCTCAACCCAAAGATTTCTTCTTTTAGTTTCAGAA 2165
DB 1801 TTTGTCACCATTCCTTTTAAATTTCTCAACCCAAAGATTTCTTCTTTTAGTTTCAGAA 1860
QY 2166 GTACTGSCATCACACGAGGTTACCTTTGGCGTGTGTCCCTGTGTACCCCTGGCAGAGAAG 2225
DB 1861 GTACTGSCATCACACGAGGTTACCTTTGGCGTGTGTCCCTGTGTACCCCTGGCAGAGAAG 1920
QY 2226 AGACCAAGCTTGTTCCTGCTGCGCCAAAGTCAGTAGGAGGATGCACAGTTTGTCTATT 2285
DB 1921 AGACCAAGCTTGTTCCTGCTGCGCCAAAGTCAGTAGGAGGATGCACAGTTTGTCTATT 1980
QY 2286 TGTCTTAGACAGAGGAGCTGTATTAACCAAGCCTTAACATTTGGTGGAAAGATTGCTCTTGA 2345
DB 1981 TGTCTTAGACAGAGGAGCTGTATTAACCAAGCCTTAACATTTGGTGGAAAGATTGCTCTTGA 2040
QY 2346 ATT 2348
DB 2041 ATT 2043

RESULT 6
US-09-681-442-3
; Sequence 3, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594

Qy	306	ATGGCCCAAGCCCTGCCCTGGCTCTCTGTGTGATGGCGGGGAGTGTCTGCTCTGCCAC	365
Db	1	ATGGCCCAAGCCCTGCCCTGGCTCTCTGTGTGATGGCGGGGAGTGTCTGCTCTGCCAC	60
Qy	366	GGCACCAGACGGATCCGGCTGCCCTTCGCGAGCGGCTTGGGGGGGCCCCCTGGGG	425
Db	61	GGCACCAGACGGATCCGGCTTCGCGAGCGGCTTGGGGGGGCCCCCTGGGG	120
Qy	426	CTGCGGCTGCCCCGGGAGACCGACGAAGACCCGAGGAGCCGCCCGGAGGGGACGCTTT	485
Db	121	CTGCGGCTGCCCCGGGAGACCGACGAAGACCCGAGGAGCCGCCCGGAGGGGACGCTTT	180
Qy	486	CTGGAGATGGTGACAACTGAGGGGCAAGTCGGGGCAGGCGTACTAGTGGAGATGACC	545
Db	181	CTGGAGATGGTGACAACTGAGGGGCAAGTCGGGGCAGGCGTACTAGTGGAGATGACC	240
Qy	546	GTGGCAGCCCCCGCAGACGCTCAACATCTCGTGGATACAGCAGCAGTAACCTTTGCA	605
Db	241	GTGGCAGCCCCCGCAGACGCTCAACATCTCGTGGATACAGCAGCAGTAACCTTTGCA	300
Qy	606	GTGGGTGCTGCCCCCAGCCCTTCTTGATCTCGTACTACAGAGGCAGCTGTCCAGCACA	665
Db	301	GTGGGTGCTGCCCCCAGCCCTTCTTGATCTCGTACTACAGAGGCAGCTGTCCAGCACA	360
Qy	666	TACCGGGACCTCCGGAAGGGTGTATGTGCCCCCTACACCCAGGGCAAGTGGGAAGGGGAG	725
Db	361	TACCGGGACCTCCGGAAGGGTGTATGTGCCCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	726	CTGGGCACCGACCTGGTAAGCATGCCCATGGCCCCAACGTCATCTGCGTGCCAACTTT	785
Db	421	CTGGGCACCGACCTGGTAAGCATGCCCATGGCCCCAACGTCATCTGCGTGCCAACTTT	480
Qy	786	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGATCCCTG	845
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGATCCCTG	540
Qy	846	GGGTGGGCTATGCTGAGATTGCCAGGCGCTGACGACTCCCTGGAGCCTTCTCTTTGACTCT	905
Db	541	GGGTGGGCTATGCTGAGATTGCCAGGCGCTGACGACTCCCTGGAGCCTTCTCTTTGACTCT	600
Qy	906	CTGTTAAAGCAGACCCACGTTCCCAACCTTCTCTCCTCGAGCTTTGTGGTGGCTGGCTTC	965
Db	601	CTGTTAAAGCAGACCCACGTTCCCAACCTTCTCTCCTCGAGCTTTGTGGTGGCTGGCTTC	660
Qy	966	CCCTCAACCACTCTGAAGTGTGGGCTCTGTGGGAGGAGCATGATCATTTGGAGGTATC	1025
Db	661	CCCTCAACCACTCTGAAGTGTGGGCTCTGTGGGAGGAGCATGATCATTTGGAGGTATC	720
Qy	1026	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCCGGGGGAGTGGTATTAT	1085
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCCGGGGGAGTGGTATTAT	780
Qy	1086	GAGGTGATCATTTGTCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	1145
Db	781	GAGGTGATCATTTGTCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	1146	TACAACTATGACAAGAGCATTTGGGAGGTGGCACCACCAACCTTCGTTTGGCCCAAGAAA	1205
Db	841	TACAACTATGACAAGAGCATTTGGGAGGTGGCACCACCAACCTTCGTTTGGCCCAAGAAA	900

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Db 1981 TGCTTTAGACAGCAGGAGTGTATATAACAGCCTTAACATTGGTGCAAGATTGGCTCTCTGA 2040
QY 2346 ATT 2348
Db 2041 ATT 2043

RESULT 7
US-09-969-671A-1
: Sequence 1, Application US/09969671A
: Publication No. US20030036112A1
: GENERAL INFORMATION:
: APPLICANT: CHAPMAN, CONRAD G.
: APPLICANT: MURPHY, KAY
: APPLICANT: POWELL, DAVID J.
: APPLICANT: SMITH, TRUDI S.
: TITLE OF INVENTION: ASP2
: FILE REFERENCE: GH-70368-D1
: CURRENT APPLICATION NUMBER: US/09/969,671A
: CURRENT FILING DATE: 2001-10-03
: PRIOR APPLICATION NUMBER: UK 9701684.4
: PRIOR FILING DATE: 1997-01-28
: PRIOR APPLICATION NUMBER: 09/009,191
: PRIOR FILING DATE: 1998-01-20
: PRIOR APPLICATION NUMBER: 09/694,200
: PRIOR FILING DATE: 2000-10-23
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 2541
: TYPE: DNA
: ORGANISM: Homo sapiens.
: FEATURE:
: NAME/KEY: unknown
: LOCATION: (2455)(2456)(2463)(2478)(2480)(2497)(2507)(2509)(2512)(2516)
: LOCATION: (2520)(2522)(2525)(2529)(2539)(2540)
: OTHER INFORMATION: Wherein n can be represented by a, c, t, or g
US-09-969-671A-1

Query Match 86.2%; Score 2024; DB 9; Length 2541;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2038; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Db 1 ATGGCCCAAGCCCTCGCTCGCTGCTGCTGATGGCGGGGAGTGCCTGGCCAC 60
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Db 61 GGCACCCAGCAGCGCATCCCGCTGCCCTGCGCAGCGGCTGGGGGCGCCCGCTGGG 120
QY 426 CTGCGGCTGCCCGGAGACCGACGAAGACGCCGAGAGCCCGCGGAGCGGCGGAGGCTTT 485
Db 121 CTGCGGCTGCCCGGAGACCGACGAAGACGCCGAGAGCCCGCGGAGCGGCGGAGGCTTT 180
QY 486 GTGAGATGTGTGACAACTTGGGGCACTGCGGGCAGGCGTACTACGTGGAGATCAC 545
Db 181 GTGAGATGTGTGACAACTTGGGGCACTGCGGGCAGGCGTACTACGTGGAGATCAC 240
QY 546 GTGGGAGCCCCCGCAGACGCTCAACATCTGTGTGATACAGCAGCAGTAACTTTGCA 605
Db 241 GTGGGAGCCCCCGCAGACGCTCAACATCTGTGTGATACAGCAGCAGTAACTTTGCA 300
QY 606 GTGGGTGCTGCCCGCCACCCCTTCTGTCATCGTCTACTACAGAGGCGAGTGTCCAGACA 665
Db 301 GTGGGTGCTGCCCGCCACCCCTTCTGTCATCGTCTACTACAGAGGCGAGTGTCCAGACA 360
QY 666 TACCGGACCTCCGGAAGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG 725
Db 361 TACCGGACCTCCGGAAGGTGTGTATGTAGCCCTTACACCCAGGCAAGTGGGAAGGGAG 420
QY 726 CTGGGCACCACTGGTGAAGCATCCCCCATGGCCCAACGCTCACTGTGCGTGCCAACATT 785
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Db 421 CTGGGCACCACTGGTGAAGCATCCCCCATGGCCCCAACGTCACCTGTCGCGTGCACAACATT 480
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Db 481 GCTGGCATCACTGAATCAGACAAGTTCTTTCATCAACGGCTCCCACTCGGAAGGATCCTG 540
QY 846 GGGCTGGCCTATGCTGAGATTGGCAGGCCTGACGACTCCCTGGAGCCCTTTCTTTGACTCT 905
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QY 966 CCCCTCAACCACTGCTGAAGTGTCTGGGCTCTGTGGAGGGAGCATGATCATTTGGAGTATC 1025
Db 661 CCCCTCAACCACTGCTGAAGTGTCTGGGCTCTGTGGAGGGAGCATGATCATTTGGAGTATC 720
QY 1026 GACCACTCGCTTACACAGCAGTCTCTGGTATACACCCCATCCCGCGGAGTGTGATTAT 1085
Db 721 GACCACTCGCTTACACAGCAGTCTCTGGTATACACCCCATCCCGCGGAGTGTGATTAT 780
QY 1086 GAGGTGATCATTTGTGCGGTTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 1145
Db 781 GAGGTGATCATTTGTGCGGTTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
QY 1146 TACAACATGACACAGACATTTGGACAGTGGCAGCAGCAACCTTCGTTGCCCAAGAAA 1205
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QY 1266 GTTTCCTGCTAGGAGACAGTGTGTGCTGCGAAGCAGCAGCACCACCCCTTGAACATT 1325
Db 961 GTTTCCTGCTAGGAGACAGTGTGTGCTGCGAAGCAGCAGCACCACCCCTTGAACATT 1020
QY 1326 TTCCAGCTCATCTCACHCTACCTAATGGGTGAGGTACCAACCAAGTCTTCCCGATCAC 1385
Db 1021 TTCCAGCTCATCTCACHCTACCTAATGGGTGAGGTACCAACCAAGTCTTCCCGATCAC 1080
QY 1386 ATCTCTCCGAGCAATACCTCGGCCAGTGGGAAGATGTGGCAGCTGCCAAGACAGCTGT 1445
Db 1081 ATCTCTCCGAGCAATACCTCGGCCAGTGGGAAGATGTGGCAGCTGCCAAGACAGCTGT 1140
QY 1446 TACAAGTTTGGCACTCACAGTCAATCCACGGGCACTGTTATGGAGCTGTTATCATGGAG 1505
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Db 1201 GGCTTCTACGTTGTCTTTGATCGGGGCGGAAAACGAATTTGGCTTGTGTCAGGCGTTGC 1260
QY 1566 CATGTGCACATGATGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTGTACCTTGGACATG 1625
Db 1261 CATGTGCACATGATGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTGTACCTTGGACATG 1320
QY 1626 GAAGACTGTGGCTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1685
Db 1321 GAAGACTGTGGCTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1380
QY 1686 GTCATGGCTGCCATCTGGGCCCTCTTTCATGCTGCCACTCTGCCCTCATGCTGTGTCAGTGG 1745
Db 1381 GTCATGGCTGCCATCTGGGCCCTCTTTCATGCTGCCACTCTGCCCTCATGCTGTGTCAGTGG 1440
QY 1746 CGCTGCCCTCGCTCGCTGGCCAGCAGCATGATGACTTTGCTGTGATGACATCTCCCTGCTG 1805
Db 1441 CGCTGCCCTCGCTCGCTGGCCAGCAGCATGATGACTTTGCTGTGATGACATCTCCCTGCTG 1500
QY 1806 AAGTGAGGAGGCCCATGGCGAAGATAGAGATTCCCTT -GGACACACCTCCGCTGGTTC 1864
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Db 1501 AAGTGAGAGGCCCATGGAGAGAAAGATAGAGATTCCCTGGGACCAACACCTCCGTGGTTC 1560
QY 1865 ACTTTGGTCAACAAGTAGGAGACACAGATGGCACTGTGGCGAGAGCACTCAGGACCCCTC 1924
Db 1561 ACTTTGGTCAACAAGTAGGAGACACAGATGGCACTGTGGCGAGAGCACTCAGGACCCCTC 1620
QY 1925 CCCACCCACCAATGCTCTGCTTTGATGGAGAGAAAGGCTGGCAAGGTGGTTCCTCA 1984
Db 1621 CCCACCCACCAATGCTCTGCTTTGATGGAGAGAAAGGCTGGCAAGGTGGTTCCTCA 1680
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Db 1681 GGGACTGTACCTGTAGGAACACAGAAAGAGAAAGCACTCTGCTGGCGGGAATAC 1740
QY 2045 TCTTGGTCACTCAAAATTAAGTCGGGAAATCTGCTGTGAAACTTCAGCCCTGAACC 2104
Db 1741 TCTTGGTCACTCAAAATTAAGTCGGGAAATCTGCTGTGAAACTTCAGCCCTGAACC 1800
QY 2105 TTGTGCCACCAATCTTTAAATTCCTCAACCCCAAGATATCTCTTTTCTTAGTTTCAGA 2164
Db 1801 TTGTGCCACCAATCTTTAAATTCCTCAACCCCAAGATATCTCTTTTCTTAGTTTCAGA 1860
QY 2165 AGTACTGGCATCACAGCAGGTACCTTGGCGTGTGTCCCTGGGTACCTGGCGAGAA 2224
Db 1861 AGTACTGGCATCACAGCAGGTACCTTGGCGTGTGTCCCTGGGTACCTGGCGAGAA 1920
QY 2225 GAGACCAAGCTTGTTCCTGCTGGCAAGTCAGTAGGAGAGATGCACAGTTTGTCTAT 2284
Db 1921 GAGACCAAGCTTGTTCCTGCTGGCAAGTCAGTAGGAGAGATGCACAGTTTGTCTAT 1980
QY 2285 TTGCTTTAGACAGAGGACTGTATTAACAGCCTAACATTTGGTGAAGATTTGCTCTTG 2344
Db 1981 TTGCTTTAGACAGAGGACTGTATTAACAGCCTAACATTTGGTGAAGATTTGCTCTTG 2040
QY 2345 AATT 2348
Db 2041 AATT 2044

RESULT 8
US-09-795-903A-1
; Sequence 1, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-903A-1

Query Match 85.3%; Score 2004; DB 9; Length 3252;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 GCGGAGTGTCTCCCTGCCACCGCACCCAGCATCCGGTTCGCCCTCCGACGCGC 404
Db 1 GCGGAGTGTCTCCCTGCCACCGCACCCAGCATCCGGTTCGCCCTCCGACGCGC 60
QY 405 CTGGGGGCGGCCCTCGGGCTGCGCGGAGAGCCGAGAGAGCCGAGGAG 464
Db 61 CTGGGGGCGGCCCTCGGGCTGCGCGGAGAGCCGAGAGAGCCGAGGAG 120
QY 465 CCGGCGGAGGCGGAGCTTTCTGGAGATGGTGACAACTGAGGGGCAAGTCGGGGCGAG 524
Db 121 CCGGCGGAGGCGGAGCTTTCTGGAGATGGTGACAACTGAGGGGCAAGTCGGGGCGAG 180
QY 525 GGCTACTACGTGGAGATGACCGTGGGCGAGCCCGCGAGAGCGCTCAACATCTCTGTGTGAT 584
Db 181 GGCTACTACGTGGAGATGACCGTGGGCGAGCCCGCGAGAGCGCTCAACATCTCTGTGTGAT 240
QY 585 ACAGGACGAGTAACCTTTGCGAGTGGTGTGCGCCCGCGAGAGCGCTTCTGTGATGCTTAC 644
Db 241 ACAGGACGAGTAACCTTTGCGAGTGGTGTGCGCCCGCGAGAGCGCTTCTGTGATGCTTAC 300
QY 645 CAGAGGAGCTGTCCAGCACATACCGGACCTCCGGAAGGTGTGTATGTGCGCTTACACC 704
Db 301 CAGAGGAGCTGTCCAGCACATACCGGACCTCCGGAAGGTGTGTATGTGCGCTTACACC 360
QY 705 CAGGCAAGTGGGAAGGAGGAGCTGGGCAACCGACTGTGTAAAGCATCCCGCCATGCCCCAAC 764
Db 361 CAGGCAAGTGGGAAGGAGGAGCTGGGCAACCGACTGTGTAAAGCATCCCGCCATGCCCCAAC 420
QY 765 GTCACTGTGCGTGCCAACTTTGTCGATCACTGAATCAGACAAGTTCTTCAATCAACGCGC 824
Db 421 GTCACTGTGCGTGCCAACTTTGTCGATCACTGAATCAGACAAGTTCTTCAATCAACGCGC 480
QY 825 TCCAACTGGGAAGGAGCTCCTGGGCTGGCTATGCTGAGATTTGCCAGGCTGACACATCC 884
Db 481 TCCAACTGGGAAGGAGCTCCTGGGCTGGCTATGCTGAGATTTGCCAGGCTGACACATCC 540
QY 885 CTGGAGCCTTTCTTTGACTCTCTGTGTAAGCAGACCCAGCTTCCCAAGCTCTTCTCCCTG 944
Db 541 CTGGAGCCTTTCTTTGACTCTCTGTGTAAGCAGACCCAGCTTCCCAAGCTCTTCTCCCTG 600
QY 945 CAGCTTTGTGCTGGCTTCCCGCTCAACAGCTGCTGAAGTGTGCGCTCTGTCGAGGCG 1004
Db 601 CAGCTTTGTGCTGGCTTCCCGCTCAACAGCTGCTGAAGTGTGCGCTCTGTCGAGGCG 660
QY 1005 AGCATGATCAATTGGAGGTATCGACCACTGCTGTACACAGGAGCTCTCTGGTATACACC 1064
Db 661 AGCATGATCAATTGGAGGTATCGACCACTGCTGTACACAGGAGCTCTCTGGTATACACC 720
QY 1065 ATCCGCGGGAGTGGTATTTATGAGGTGATCATTGTGGGGTGGAGATCAATGGAGAGGAT 1124
Db 721 ATCCGCGGGAGTGGTATTTATGAGGTGATCATTGTGGGGTGGAGATCAATGGAGAGGAT 780
QY 1125 CTGAAATGGACTGCAAGGAGTACAATATGACAAGAGCATTTGGACAGTGGGACACCACC 1184
Db 781 CTGAAATGGACTGCAAGGAGTACAATATGACAAGAGCATTTGGACAGTGGGACACCACC 840
QY 1185 AACCTTCTCTTCCCAAGAAAGTGTGTAAGCTGCACTCAATCCATCAAGGAGGCTCC 1244
Db 841 AACCTTCTCTTCCCAAGAAAGTGTGTAAGCTGCACTCAATCCATCAAGGAGGCTCC 900
QY 1245 TCCAGGAGAAAGTTCCCTGATGGTCTGCTAGGAGAGCAGCTGCTGTGCTGGCAAGCA 1304
Db 901 TCCAGGAGAAAGTTCCCTGATGGTCTGCTAGGAGAGCAGCTGCTGTGCTGGCAAGCA 960
QY 1305 GGCACCCACCTTTGGAACATTTCCAGTCACTCTACCTTAATGGGTGAGGTACC 1364
Db 961 GGCACCCACCTTTGGAACATTTCCAGTCACTCTACCTTAATGGGTGAGGTACC 1020
QY 1365 AACGAGTCTTCCGATCACCCTCTTCCAGCAATACCTGCGGCGAGTGGAAAGATGTG 1424
Db 1021 AACGAGTCTTCCGATCACCCTCTTCCAGCAATACCTGCGGCGAGTGGAAAGATGTG 1080

QY 1425 GCCACGTCACAGACGACTGTTACAAAGTTTGGCATCTCACAGTCATCCAGCGGCACTGTT 1484
Db 1081 GCCACGTCACAGACGACTGTTACAAAGTTTGGCATCTCACAGTCATCCAGCGGCACTGTT 1140
QY 1485 ATGGGAGCTGTTATCATGAGAGGCTTCTACGTTGCTTTGATCGGGCCGAAACAAAT 1544
Db 1141 ATGGGAGCTGTTATCATGAGAGGCTTCTACGTTGCTTTGATCGGGCCGAAACAAAT 1200
QY 1545 GCGTTTGCTGCTCAGCGCTTGCATGTGCACAGTGTTCAGGACGCGCAGCGTGGAGGC 1604
Db 1201 GCGTTTGCTGCTCAGCGCTTGCATGTGCACAGTGTTCAGGACGCGCAGCGTGGAGGC 1260
QY 1605 CTTTTTGTCCACCTTGACATGGAAGACTGTGGCTACAACATCCACAGACAGATGAGTCA 1664
Db 1261 CTTTTTGTCCACCTTGACATGGAAGACTGTGGCTACAACATCCACAGACAGATGAGTCA 1320
QY 1665 ACCCTCATGACCATAGCCTATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1724
Db 1321 ACCCTCATGACCATAGCCTATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1725 TGCTCATGCTGTGTCAGTGGCGCTGCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1784
Db 1381 TGCTCATGCTGTGTCAGTGGCGCTGCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1785 GCTGATGACATCTCCCTGCTGAAGTGAAGAGGCGCCATGGGAGAGATAGAGATTCGCCCT 1844
Db 1441 GCTGATGACATCTCCCTGCTGAAGTGAAGAGGCGCCATGGGAGAGATAGAGATTCGCCCT 1500
QY 1845 GGACACACCTCGTGGTTCACCTTTGGTCAAGTAGGAGACACAGATGGCAGCTGTGGC 1904
Db 1501 GGACACACCTCGTGGTTCACCTTTGGTCAAGTAGGAGACACAGATGGCAGCTGTGGC 1560
QY 1905 CAGAGCACCTCAGGACCCCTCCACCCACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1964
Db 1561 CAGAGCACCTCAGGACCCCTCCACCCACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1965 GCGTGCAAGGTGGGTTCCAGGAGCTGTATCTGTAGGAACAGAAAGAGAAAGAAAG 2024
Db 1621 GCGTGCAAGGTGGGTTCCAGGAGCTGTATCTGTAGGAACAGAAAGAGAAAGAAAG 1680
QY 2025 CACTGCTGCTGGGGGAATCTTGTGTCACCTCAAAATTTAAGTCGGGAAATCTGCTGCT 2084
Db 1681 CACTGCTGCTGGGGGAATCTTGTGTCACCTCAAAATTTAAGTCGGGAAATCTGCTGCT 1740
QY 2085 TGAACCTCAGCCCTCAACCTTTGTCACCATTCCTTTAAATTCCTCAACCCAAAGTATT 2144
Db 1741 TGAACCTCAGCCCTCAACCTTTGTCACCATTCCTTTAAATTCCTCAACCCAAAGTATT 1800
QY 2145 CTTCTTTTCTTAGTTTTCAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2204
Db 1801 CTTCTTTTCTTAGTTTTCAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
QY 2205 TGTGGTACCTTGGCAGAGAGACCAAGCTTTTCCCTGCTGGCCAAAGTCAGTAGGA 2264
Db 1861 TGTGGTACCTTGGCAGAGAGACCAAGCTTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920
QY 2265 GAGGATGCAAGTTCCTATTCTGCTTTAGAGACAGGAGCTGTATAACAAAGCCCTAACATT 2324
Db 1921 GAGGATGCAAGTTCCTATTCTGCTTTAGAGACAGGAGCTGTATAACAAAGCCCTAACATT 1980
QY 2325 GGTGCAAGATTGCCCTCTTGAATT 2348
Db 1981 GGTGCAAGATTGCCCTCTTGAATT 2004

RESULT 9
US-09-796-264-1
; Sequence 1, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald

; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/796, 264
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604, 608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-264-1

Query Match 85.3%; Score 2004; DB 10; Length 3252;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 GCGGGAGTGTGCTGCCACGCGCACCCAGCAGCGGATCGCGCTGCCCTGCCAGCGGC 404
Db 1 GCGGGAGTGTGCTGCCACGCGCACCCAGCAGCGGATCGCGCTGCCCTGCCAGCGGC 60
QY 405 CTGGGGGGCGCCCTGCGGCTGCGGCTGCCCGGGAGACCGACGAGAGCCCGAGGAG 464
Db 61 CTGGGGGGCGCCCTGCGGCTGCGGCTGCCCGGGAGACCGACGAGAGCCCGAGGAG 120
QY 465 CCGCGCGGAGGGGAGCTTTGTGGAGATGGTGGACAACTGAGGGGCAAGTCGGGGCAG 524
Db 121 CCGCGCGGAGGGGAGCTTTGTGGAGATGGTGGACAACTGAGGGGCAAGTCGGGGCAG 180
QY 525 GGCTACTAGTGTGAGATGACCTGGGCGAGCGCCCGCAGAGCGCTCAACATCTCGTGGTGGAT 584
Db 181 GGCTACTAGTGTGAGATGACCTGGGCGAGCGCCCGCAGAGCGCTCAACATCTCGTGGTGGAT 240
QY 585 ACAGGAGCAGTAACCTTTGCACTGCGGCTGCGGCTGCCCGCCCGCAGAGCGCTCAACATCTCGTGGTGGAT 644
Db 241 ACAGGAGCAGTAACCTTTGCACTGCGGCTGCGGCTGCCCGCCCGCAGAGCGCTCAACATCTCGTGGTGGAT 300
QY 645 CAGAGGAGCTGTCCAGCAGCATACCGGGAGCTCCGGAGGCTCCGGAGGCTGTGTATGTGCCCTACACC 704
Db 301 CAGAGGAGCTGTCCAGCAGCATACCGGGAGCTCCGGAGGCTCCGGAGGCTGTGTATGTGCCCTACACC 360
QY 705 CAGGGCAAGTGGGAAGGGAGCTGGGCGACCGAGCTGGTAAGCATCCCGCATGGCCCAAC 764
Db 361 CAGGGCAAGTGGGAAGGGAGCTGGGCGACCGAGCTGGTAAGCATCCCGCATGGCCCAAC 420
QY 765 GTCACCTGTGGTGCCCAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
Db 421 GTCACCTGTGGTGCCCAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 825 TCCAATGGGAAGGCAATTCCTGGGGCTGGCCTATGCTGAGATGGCAGGCTGAGGAGTCC 884
Db 481 TCCAATGGGAAGGCAATTCCTGGGGCTGGCCTATGCTGAGATGGCAGGCTGAGGAGTCC 540
QY 885 CTGGAGGCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGCTTCCCAACCTCTTCTCCCTG 944
Db 541 CTGGAGGCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGCTTCCCAACCTCTTCTCCCTG 600
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QY 1005 AGCATGATCATTTGGAGGTATCGACCACTGCTGTATACAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1064


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Db 661 AGCATGATCATTTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720
QY 1065 ATCCGGCGGAGTGGTATTATGAGTGTATCATTTGTCGGGTGAGATCAATGGACAGAT 1124
Db 721 ATCCGGCGGAGTGGTATTATGAGTGTATCATTTGTCGGGTGAGATCAATGGACAGAT 780
QY 1125 CTGAAATGGACTGCAAGGAGTACAACTATGACAGAGCATTTGTGGACAGTGGCACCACC 1184
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QY 1185 AACCTTCGTTTGGCCCAAGAAAGTGTTCAGCTGACAGTCAATATCCATCAGGAGCCCTCC 1244
Db 841 AACCTTCGTTTGGCCCAAGAAAGTGTTCAGCTGACAGTCAATATCCATCAGGAGCCCTCC 900
QY 1245 TCCACGGAGAAAGTTCCTCGTATGGTTCTTCGGCTAGGAGAGCAGCTGTGTCTGGCAAGCA 1304
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Db 961 GGCACCAACCCCTTGGAAACATTTTCCAGTCACTCTCACTATCTACCTAATGGGTGAGTTACC 1020
QY 1365 AACCAAGTCTTCCGCATCACCATCTTCCGCAGCAATACCTGCGGCGAGTGGAAAGATGTG 1424
Db 1021 AACCAAGTCTTCCGCATCACCATCTTCCGCAGCAATACCTGCGGCGAGTGGAAAGATGTG 1080
QY 1425 GCCACGTCCCAAGACGAGTGTACAAAGTTTGGCATCTCACAGTCATCCACGGGCAGCTGT 1484
Db 1081 GCCACGTCCCAAGACGAGTGTACAAAGTTTGGCATCTCACAGTCATCCACGGGCAGCTGT 1140
QY 1485 ATGGGAGCTGTATCATGAGGGCTTCTACGTGTCTTTGATCGGGCCCCGAAACGAATT 1544
Db 1141 ATGGGAGCTGTATCATGAGGGCTTCTACGTGTCTTTGATCGGGCCCCGAAACGAATT 1200
QY 1545 GCGTTTGTCTGTCAGCGCTTGGCATGTGCACAGTGTAGTTCAGAGCGGCGGTGGAGGC 1604
Db 1201 GCGTTTGTCTGTCAGCGCTTGGCATGTGCACAGTGTAGTTCAGAGCGGCGGTGGAGGC 1260
QY 1605 CTTTTGTCACTTGGACATGGAAGTGTGGCTACAACTATCCACAGACAGATGAGTCA 1664
Db 1261 CTTTTGTCACTTGGACATGGAAGTGTGGCTACAACTATCCACAGACAGATGAGTCA 1320
QY 1665 ACCCTCATGACATAGCCTATGTGATGGCTGCGCATCTGCGGCGCTCTTCACTGCGCCACT 1724
Db 1321 ACCCTCATGACATAGCCTATGTGATGGCTGCGCATCTGCGGCGCTCTTCACTGCGCCACT 1380
QY 1725 TGCTCATGTGTCTCAGTGGCGCTGCTCCGCTGCTGCGCCAGCAGCATGATGACTTT 1784
Db 1381 TGCTCATGTGTCTCAGTGGCGCTGCTCCGCTGCTGCGCCAGCAGCATGATGACTTT 1440
QY 1785 GCTGATGACATCTCCCTGCTGAAGTGAAGAGGCCCATGGGCGAAGATAGAGATTCCCT 1844
Db 1441 GCTGATGACATCTCCCTGCTGAAGTGAAGAGGCCCATGGGCGAAGATAGAGATTCCCT 1500
QY 1845 GGACACACCTCCGTGGTTCACTTTGGTCAAGTAGGAGACACAGATGCGACCTGTGGC 1904
Db 1501 GGACACACCTCCGTGGTTCACTTTGGTCAAGTAGGAGACACAGATGCGACCTGTGGC 1560
QY 1905 CAGAGACCTTCAGACCTCCCGACCCACCAATGCCTGCTGCTGATGAGAGGAAAA 1964
Db 1561 CAGAGACCTTCAGACCTCCCGACCCACCAATGCCTGCTGCTGATGAGAGGAAAA 1620
QY 1965 GCGTGGCAAGGTGGTTTCCAGGAGTGTACCTGTAGGAACAGAAAAAGAAAGAAAG 2024
Db 1621 GCGTGGCAAGGTGGTTTCCAGGAGTGTACCTGTAGGAACAGAAAAAGAAAGAAAG 1680
QY 2025 CACTGTGCTGGCGGAATACCTTGGTGCACCTCAATTTAAGTCGGGAAATTTCTGCTGCT 2084
Db 1681 CACTGTGCTGGCGGAATACCTTGGTGCACCTCAATTTAAGTCGGGAAATTTCTGCTGCT 1740
QY 2085 TGAACCTTCAGCCTGAACCTTTGTCACCATTTCTTAAATCTCCACCCCAAGATT 2144
Db 1741 TGAACCTTCAGCCTGAACCTTTGTCACCATTTCTTAAATTTCTCCACCCCAAGATT 1800
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QY 2145 CTTCTTTCTTTAGTTTTCAGAACTACTGGCATCACACGACGTTACCTTTGGCGTGTGTCCC 2204
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QY 2205 TGTGGTACCCCTGGCAGAGAAGACCAAGCTTTTTCCTTGGCTGGCCAAAGTCAGTAGGA 2264
Db 1861 TGTGGTACCCCTGGCAGAGAAGACCAAGCTTTTTCCTTGGCTGGCCAAAGTCAGTAGGA 1920
QY 2265 GAGGATCACAGTTTGTCTATTTCCTTTAGAGACAGGACTGTATAAACAAGCCTTAACATT 2324
Db 1921 GAGGATCACAGTTTGTCTATTTCCTTTAGAGACAGGACTGTATAAACAAGCCTTAACATT 1980
QY 2325 GGTGCAAAAGATTGCTCTTTGAATT 2348
Db 1981 GGTGCAAAAGATTGCTCTTTGAATT 2004

RESULT 10
US-09-845-226-1
; Sequence 1, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845, 226
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603, 713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168, 060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177, 836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178, 368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210, 292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-226-1

Query Match 85.3%; Score 2004; DB 10; Length 3252;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 GCGGGAGTGTGCTGCCCGACGGCACCCAGCGGATCCGGCTGCCCTGCCGACGCGC 404
Db 1 GCGGGAGTGTGCTGCCCGACGGCACCCAGCGGATCCGGCTGCCCTGCCGACGCGC 60
QY 405 CTGGGGGCGGCGCCCTCGGGCTGCGGGCTGCCCGGAGACCGACGAAGAGCCCGAGGAG 464
Db 61 CTGGGGGCGGCGCCCTCGGGCTGCGGGCTGCCCGGAGACCGACGAAGAGCCCGAGGAG 120
QY 465 CCCGGCGGAGGGGCGAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGGAG 524
Db 121 CCCGGCGGAGGGGCGAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGGAG 180
QY 525 GGCTACTACGTGGAGATGACCGTGGGAGCGCCCCCGACGACGCTCAACATCCTGTGGT 584
Db 181 GGCTACTACGTGGAGATGACCGTGGGAGCGCCCCCGACGACGCTCAACATCCTGTGGT 240
QY 585 ACAGGCAGCAGTAACCTTTTGCAGTGGTGTGCTGCCCGCCACCCCTTCTTGCATCGCTAC 644
Db 241 ACAGGCAGCAGTAACCTTTTGCAGTGGTGTGCTGCCCGCCACCCCTTCTTGCATCGCTAC 300
QY 645 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAAGGTTGTGTATGTGCCCTTACACC 704
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Db	1381	TGCCCTCATGGTGTGTGTCAGTGGCGCTGCCCTCCGCTGCCCTGGCCGACGACCATGATGACTTTT	1444
Qy	1785	GCTGATGACATCTCCCTGCTGCTGAAGTGAGAGGCCCATGGGAGAGATAGAGATTCCCCCT	1844
Db	1441	GCTGATGACATCTCCCTGCTGCTGAAGTGAGAGGCCCATGGGAGAGATAGAGATTCCCCCT	1500
Qy	1845	GGACCACACCTTCGGTGGTTTCACTTTTGGTTCACAAGTAGAGACACAGATGGCACCTGTGGC	1904
Db	1501	GGACCACACCTTCGGTGGTTTCACTTTTGGTTCACAAGTAGAGACACAGATGGCACCTGTGGC	1560
Qy	1905	CAGAGCACCTCAGGAGCCCTCCCAACCCACCAATGCCCTTGCTTGGAGAGAGAAAA	1964
Db	1561	CAGAGCACCTCAGGAGCCCTCCCAACCCACCAATGCCCTTGCTTGGAGAGAGAAAA	1620
Qy	1965	GGCTGGCAAGTGGGTTCCAGGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGAAAG	2024
Db	1621	GGCTGGCAAGTGGGTTCCAGGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGAAAG	1680
Qy	2025	CACCTGCTGGCGGGAATACTCTTGGTCACCTCAAAATTTAAGTCGGGAAATTCCTGCTGCT	2084
Db	1681	CACCTGCTGGCGGGAATACTCTTGGTCACCTCAAAATTTAAGTCGGGAAATTCCTGCTGCT	1740
Qy	2085	TGAACACTTCACGCCCTGAACCTTTGTGCCACCATTCCTTTTAAATTTCTCCAAACCCAAAGTATT	2144
Db	1741	TGAACACTTCAGCCCTGAACCTTTGTGCCACCATTCCTTTTAAATTTCTCCAAACCCAAAGTATT	1800
Qy	2145	CTTCTTTTCTTACTTTTCAGAACTACTGGCATCAGCAGGTTACCTTTGGCGTGTGTGCC	2204
Db	1801	CTTCTTTTCTTACTTTTCAGAACTACTGGCATCAGCAGGTTACCTTTGGCGTGTGTGCC	1860
Qy	2205	TGTGGTACCTTGGCAGAGAGAGACCAAGCTTTTTCCTGCTGCCAAAGTCAGTAGGA	2264
Db	1861	TGTGGTACCTTGGCAGAGAGAGACCAAGCTTTTTCCTGCTGCCAAAGTCAGTAGGA	1920
Qy	2265	GAGGTGCACAGTTTGCATTTTGTCTTTAGACAGAGGACTGTATAAACAAGCCTAACATT	2324
Db	1921	GAGGTGCACAGTTTGCATTTTGTCTTTAGACAGAGGACTGTATAAACAAGCCTAACATT	1980
Qy	2325	GGTGCAAGATTGCCCTCTTGAATT	2348
Db	1981	GGTGCAAGATTGCCCTCTTGAATT	2004

RESULT 11
US-09-794-927-5
Sequence 5, Application US/09794927
Patent No. US20010016324A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Blenkowski, Michael J.
APPLICANT: Heinrikson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 28341/6280FG
CURRENT APPLICATION NUMBER: US/09/794,927
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 5
LENGTH: 1977

TYPE: DNA
ORGANISM: Homo sapiens
US-09-794-927-5

Query Match 80.1%; Score 1881; DB 10; Length 1977;									
Best Local Similarity 96.3%; Pred. No. 0;									
Matches 1966; Conservative 0; Mismatches 0; Indels 75; Gaps 1;									
QY	306	ATGCCCCAAGCCCTGCCCTGGCTGCTGCTGGATGGCGCGGAGTGCCTGCCCTGCCAC	365						
DB	1	ATGCCCCAAGCCCTGCCCTGGCTGCTGCTGGATGGCGCGGAGTGCCTGCCCTGCCAC	60						
QY	366	GGCACCAGCAGCGGATCCGGCTGCCCTGCGCAGCGGCTGGGGGCGCCCGCTGGGG	425						
DB	61	GGCACCAGCAGCGGATCCGGCTGCCCTGCGCAGCGGCTGGGGGCGCCCGCTGGGG	120						
QY	426	CTGGGGTGGCCCCGGGAGACCGACCAAGAGCCGAGGAGCCCGCGGGAGGGGAGCTTT	485						
DB	121	CTGGGGTGGCCCCGGGAGACCGACCAAGAGCCGAGGAGCCCGCGGGAGGGGAGCTTT	180						
QY	486	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCCGGGCGAGGGCTACTACGTGGAGATGACC	545						
DB	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCCGGGCGAGGGCTACTACGTGGAGATGACC	240						
QY	546	GTGGGCGAGCCCCCGCAGACGCTCAACATCCCTGGTGGATACAGGCGACGATTAACCTTGA	605						
DB	241	GTGGGCGAGCCCCCGCAGACGCTCAACATCCCTGGTGGATACAGGCGACGATTAACCTTGA	300						
QY	606	GTGGGTCTGCCCCCACCCTTCCTGCATCGCTACTACAGAGGCGAGCTGTCCAGCACA	665						
DB	301	GTGGGTCTGCCCCCACCCTTCCTGCATCGCTACTACAGAGGCGAGCTGTCCAGCACA	360						
QY	666	TACCGGACCTCCCGAAGGGTGTATGTGCCCTACACCCAGGCGAAGTGGGAAGGGGAG	725						
DB	361	TACCGGACCTCCCGAAGGGTGTATGTGCCCTACACCCAGGCGAAGTGGGAAGGGGAG	420						
QY	726	CTGGGCGACCGACCTGGTAAGCATCCCCCATGCGCCCAAGCTACTGTGCGTGCCCAACT	785						
DB	421	CTGGGCGACCGACCTGGTAAGCATCCCCCATGCGCCCAAGCTACTGTGCGTGCCCAACT	480						
QY	786	GCTGCCATCACTGAATCAGCAAGTCTTCATCAACGGCTCCCAACTGGGAAGGCACTCGT	845						
DB	481	GCTGCCATCACTGAATCAGCAAGTCTTCATCAACGGCTCCCAACTGGGAAGGCACTCGT	540						
QY	846	GGGTGGCCCTATGCTGAGATGCCAGGCTGACGACTCCCTGGAGCGCTTCTTTGACTCT	905						
DB	541	GGGTGGCCCTATGCTGAGATGGCCAG-----GCTTTGTGGTGGCTTTC	566						
QY	906	CTGGTAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTCGAGCTTTGTGGTGGCTTTC	965						
DB	567	-----GCTTTGTGGTGGCTTTC	585						
QY	966	CCCTCAACAGCTGAAGTGTGGCTCTGTGGAGGAGCATGATCATTTGGAGGTATC	1025						
DB	586	CCCTCAACAGCTGAAGTGTGGCTCTGTGGAGGAGCATGATCATTTGGAGGTATC	645						
QY	1026	GACCACTCGTGTACAGGCGAGTCTGTGATACACCCATCCGGGGGAGTGGTATTAT	1085						
DB	646	GACCACTCGTGTACAGGCGAGTCTGTGATACACCCATCCGGGGGAGTGGTATTAT	705						
QY	1086	GAGGTGATCATTTGGGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	1145						
DB	706	GAGGTGATCATTTGGGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	765						
QY	1146	TACAACCTATGACAGAGCATTTGGACAGTGGCACCACCACTCGTTTGGCCCAAGAAA	1205						
DB	766	TACAACCTATGACAGAGCATTTGGACAGTGGCACCACCACTCGTTTGGCCCAAGAAA	825						
QY	1206	GTGTTTGAAGCTGCGTCAAAATCCATCAAGGCGAGCTCCCTCCACGGAGAAGTTCCCTGAT	1265						
DB	826	GTGTTTGAAGCTGCGTCAAAATCCATCAAGGCGAGCTCCCTCCACGGAGAAGTTCCCTGAT	885						
QY	1266	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAGGAGGACCACTTGGAAACATT	1325						

DB	886	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGACCACTTGGAAACATT	945						
QY	1326	TTCCAGTCATCTCACTTACCTAATGGGTGAGGTACCAACCAAGTCTTCCGGATCACC	1385						
DB	946	TTCCAGTCATCTCACTTACCTAATGGGTGAGGTACCAACCAAGTCTTCCGGATCACC	1005						
QY	1386	ATCCTTCCGCGAGCAATACCTCGCGGCGAGTGGGAAGTGTGCCACGTCCTCAAGACACAT	1445						
DB	1006	ATCCTTCCGCGAGCAATACCTCGCGGCGAGTGGGAAGTGTGCCACGTCCTCAAGACACAT	1065						
QY	1446	TACAAGTTTGGCATCTCAGATCATCCACGGGCACTGTATATGGAGCTGTATCATATGAG	1505						
DB	1066	TACAAGTTTGGCATCTCAGATCATCCACGGGCACTGTATATGGAGCTGTATCATATGAG	1125						
QY	1506	GGCTTCTACGTTTGTCTTGTATCGGGCCGGAAGCAATTTGGCTTGTGTCAGCGCTTGC	1565						
DB	1126	GGCTTCTACGTTTGTCTTGTATCGGGCCGGAAGCAATTTGGCTTGTGTCAGCGCTTGC	1185						
QY	1566	CATGTGACGATGAGTTTCAAGGACGCGGCGGCTGGAAGGCGCTTTTGTACCTTGGACATG	1625						
DB	1186	CATGTGACGATGAGTTTCAAGGACGCGGCGGCTGGAAGGCGCTTTTGTACCTTGGACATG	1245						
QY	1626	GAGACTGTGCTTACAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT	1685						
DB	1246	GAGACTGTGCTTACAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT	1305						
QY	1686	GTCAATGCTGCCATCTGCCCTCTTCATGCTGCCACTCTGCCCTCATGCTGTGTCAGTGG	1745						
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DB	1726	TTGTCCACCACTTCCCTTTAAATTTCTCAACCCCAAGATTTCTCTTTTCTTTCAGAA	1785						
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QY	2226	AGACCAAGCTTGTTCCTTCTGCTGGCCAAAGTCACTAGGAGAGGATGCACAGTTTGTCT	2285						
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RESULT 13
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; Sequence 5, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-743-5

Query Match 80.1%; Score 1881; DB 10; Length 1977;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1966; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

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RESULT 15

US-09-794-925-5
; Sequence 5, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-925-5

Query Match 80.1%; Score 1881; DB 10; Length 1977;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1966; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

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Job time : 125 secs

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2003, 14:26:30 ; Search time 2167.5 Seconds

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Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1649	70.2	3859	AK014464	AK014464 Mus muscu
2	990	42.2	1114	AF150387	AF150387 AF150387
3	954.2	40.6	2503	AK014390	AK014390 Mus muscu
4	819.6	34.9	913	BQ949536	BQ949536 AGENCOURT
5	740.6	31.5	1059	BI084083	BI084083 602869445
6	728	31.0	747	BQ018588	BQ018588 UI-H-DHL

C	7	723.8	30.8	865	13	BI084878	BI084878 602869445
C	8	713.8	30.4	761	13	BM016288	BM016288 603642760
C	9	688.6	29.3	700	9	AL570757	AL570757 AL570757
C	10	688.6	29.3	904	10	BE378929	BE378929 601237528
C	11	681.4	29.0	718	12	BF057767	BF057767 7K53ell.x
C	12	664.4	28.3	945	14	BQ669630	BQ669630 AGENCOURT
C	13	657.8	28.0	684	12	BF338951	BF338951 602036021
C	14	647.4	27.6	730	13	BM048418	BM048418 603625683
C	15	634.2	27.0	840	12	BE885725	BE885725 601508937
C	16	631.4	26.9	789	12	BF204338	BF204338 601866411
C	17	624	26.6	635	10	BE296749	BE296749 601175134
C	18	598.6	25.5	684	10	AV725513	AV725513 AV725513
C	19	595	25.3	623	13	BI828125	BI828125 603075385
C	20	594.8	25.3	862	13	BI157614	BI157614 602922587
C	21	579	24.7	720	12	BG288435	BG288435 602383404
C	22	574.2	24.5	649	12	BE837592	BE837592 RC2-EN009
C	23	563.8	24.0	644	12	BE783981	BE783981 601472451
C	24	556.4	23.7	939	12	BF203806	BF203806 601868788
C	25	533	22.7	836	9	AL544727	AL544727 AL544727
C	26	524	22.3	525	9	AI005033	AI005033 ou91b12.x
C	27	514.4	21.9	541	10	AW770546	AW770546 hl86c06.x
C	28	511.4	21.8	513	14	BQ637035	BQ637035 hs04g12.y
C	29	508	21.6	864	12	BE872035	BE872035 601448124
C	30	476.2	20.3	605	12	BE793449	BE793449 601588510
C	31	475.2	20.2	514	12	BF439471	BF439471 nab65a03.
C	32	472	20.1	487	13	BM313609	BM313609 ig72h03.y
C	33	464	19.8	464	9	AA701598	AA701598 zi34h07.s
C	34	464	19.8	464	9	AI127789	AI127789 qc32c02.x
C	35	453.2	19.3	458	9	AL700814	AL700814 DKFZp686H
C	36	451.2	19.2	542	10	AV667139	AV667139 AV667139
C	37	447.4	19.1	537	13	BG927600	BG927600 HNC43-1-E
C	38	445	19.0	461	9	AL700831	AL700831 DKFZp686I
C	39	445	19.0	493	12	BF443234	BF443234 260654 MA
C	40	444	18.9	444	9	AI095556	AI095556 qb19f04.x
C	41	443	18.9	443	9	AI127822	AI127822 qc36f02.x
C	42	426.4	18.2	428	9	AI094243	AI094243 qa43c11.s
C	43	425.6	18.1	1092	13	BM454007	BM454007 AGENCOURT
C	44	424.2	18.1	573	12	BE799078	BE799078 601588381
C	45	423.6	18.0	447	10	AW015855	AW015855 UI-H-BIO-

ALIGNMENTS

RESULT 1	AK014464	3859 bp	mRNA	linear	HTC 19-JAN-2002
LOCUS	AK014464	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:4122401C04;beta-site APP cleaving enzyme, full insert sequence.			
DEFINITION	AK014464	AK014464.1 GI:12852334			
ACCESSION	AK014464	HTC; CAP trapper.			
VERSION	AK014464	Mus musculus (strain:C57BL/6J) 16 days embryo head cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1				
TITLE	Carninci, P. and Hayashizaki, Y.				
JOURNAL	High-efficiency full-length cDNA cloning				
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	99279253				
REFERENCE	2				
AUTHORS	10349636				
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)				
PUBMED	20499374				
PUBMED	11042159				


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DB 723 CTTTGCAGTGGGGCTGCCCCCAGCCCTTCCCTGCAATCGCTACTACAGAGGAGCTGTC 782
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DB 903 CAACATTGCTGCCATCACTGAATCAGACAAAGTTCTTTCATCAATGTTTCCAACTGGGAGG 962
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QY 1739 TCAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1798
DB 1863 TCAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1922
QY 1799 CTTGCTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1858
DB 1923 CTTGCTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1982
QY 1859 TGGTTTCACTTTTGGTGCACA--AGTAGGAGACAGATGGGACCTGTGGCCAGAGACACCTCA 1916
DB 1983 TGGTTTCACTTTTGGTGCACA--AGTAGGAGACAGATGGGACCTGTGGCCAGAGACACCTCA 2042
QY 1917 GGACCTTCCCAACCCCAACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1976
DB 2043 GGACCTTCCCAACCCCAACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2101
QY 1977 GGGTTCCAGGAGCTGTACCTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2036
DB 2102 GGGTTCCAGGAGCTGTACCTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2161
QY 2037 GGGAACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2096
DB 2162 AGGAATATCTTTAGACACACCAACTTGAAGT-TGGAAATTTTCTGCTGCTGCTGCTGCTGCT 2220
QY 2097 CTTGAACCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2156
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QY 2157 GTTTCAGAGTACTGGCATCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2216
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DB 2337 GCAGAGAAGAGACCAAGCTTTGTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2393
QY 2277 TTTGCTATTTGCTTTTAGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2336
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DB 2453 GCCTCTTGA 2461

RESULT 2
AF150387
LOCUS
DEFINITION
AF150387 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone
CBMAPH03, mRNA sequence.
ACCESSION
AF150387
VERSION
AF150387.1 GI:5133823
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1114)
AUTHORS
Ye,M., Zhang,Q.H., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L.,
Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z.
TITLE
Human mRNA from cd34+ stem cells
JOURNAL
Unpublished (1999)
```

COMMENT

Contact: Ye M
Shanghai Institute of Hematology
Shanghai Second Medical University, Rui-Jin Hospital
197 Rui-Jin Road II, Shanghai, 200025, P. R. China
Email: zchen@stn.sh.cn

FEATURES
source

Location/Qualifiers
1. l114
/organism="Homo sapiens"
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/tissue_type="umbilical cord blood"
/cell_type="cd34+ stem cell"
/note="cloned by differential display method after
chemical induction of terminal differentiation of cell
line"

BASE COUNT 275 a 300 c 286 g 253 t
ORIGIN

Query Match

Best Local Similarity 97.3%; Pred. No. 4.8e-232;
Matches 1092; Conservative 0; Mismatches 20; Indels 10; Gaps 8;

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DB 1 GGAGGTATCGACCACTCGCTGTACACAGCAGCTCTCTGGTATACACCATCCGGCGGGAG 60

QY 1077 TGGTATTATGAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGAC 1136
DB 61 TGGTATTATGAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGAC 120

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QY 1437 GACGACTGTTTACAAAGTTTGGCATCTCACAGTATCCACGGGCACTGTTATGGAGCTGTT 1496
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QY 1497 ATCATGGAGGCTTCTA - CGTTGCTTTGATCGGGCCCAAAACGAATTCGCTTTGCTGT 1555
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QY 1855 TCCGTGGTTCACCTTTGGTTCACAAAGTAGGACACAGATGCGACCTGTGGCCAGACACCT 1914
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DB 894 CAGGACCTCTCCACCCACCAATGCCTCTGCCTTCGCTGAGAGAGAAAGGCTGGCAAG 953
QY 1975 GTGGGTTCCAGGGAGCTGTACCTGTAGGAAACACAAAGAGAGAAAGACGACCTGTGCTG 2034
DB 954 GTGGGTTCCAGGGAGCTG - ACCTGTAGGAAACACAAAGAGAGAGAAAGACGACCTGTGCTG 1012
QY 2035 GCGGAATACCTTTGGTTCACCTCAATTTAAGTCGGGAAATTCCTGCTGCTTTGAAACTTCA 2094
DB 1013 GCGGAATACCTTTGGTTCACCTCAATTTAAGTCGGGAAATTCCTGCTGCTTTGAAACTTCA 1072
QY 2095 GCCTGAAACCTTTGTCCACCATTCCTTTAAATTCCTCAACCC 2136
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RESULT 3
AK014390
LOCUS
DEFINITION
Mus musculus adult male brain cDNA, RIKEN full-length enriched
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insert sequence.
ACCESSION
AK014390.1 GI:12852207
VERSION
H7C; CAP trapper.
KEYWORDS
Mus musculus (strain:C57BL/6J) adult male brain cDNA to mRNA,
clone_11b:RIKEN full-length enriched mouse cDNA library
SOURCE
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
ORGANISM
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999);
99279253
10349636
PUBMED
REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
PUBMED
REFERENCE
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
PUBMED
REFERENCE
4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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FEATURES		Location/Qualifiers	
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		/note="Organ: lung; Vector: pORF7; Site: 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
BASE COUNT		207 a	259 c 232 g 206 t
ORIGIN		Query Match 34.9%; Score 819.6; DB 14; Length 913; Best Local Similarity 96.8%; Pred. No. 3e-190; Matches 864; Conservative 0; Mismatches 26; Indels 3; Gaps 3;	
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 The following repetitive elements were found in this cDNA
 sequence: 1-22, >AT-rich#Low_complexity
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..747

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5823683"
 /clone_lib="NCI CGAP DHL"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
 modified polylinker; Site_1: Ecor I; Site_2: Not I;
 NCI CGAP DHL is a normalized cDNA library containing the
 following tissue(s): VS-8 Cell line from Metastatic
 Chondrosarcoma in Lung. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an Ecor I adaptor, digested
 with Not I, and cloned directionally into p773-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is AGATCATTCG.

TAG_LIB=UI-H-DH1

TAG_TISSUE=Lung

TAG_SEQ=AGATCATTCG

BASE COUNT 176 a 178 c 192 g 200 t 1 others

ORIGIN

Query Match 31.0%; Score 728; DB 14; Length 747;

Best Local Similarity 99.9%; Pred. No. 8.8e-168;

Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1620 GACATGGAAGACTGTGGCTACAACTCCAGACAGATGAGTCAACCCCTCATGACCATA 1679

Db 747 GACATGGAAGACTGTGGCTACAACTCCAGACAGATGAGTCAACCCCTCATGACCATA 688

Qy 1680 GCCTATGTCATGCTGCCATCTGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGT 1739

Db 687 GCNTATGTCATGCTGCCATCTGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGT 628

Qy 1740 CAGTGGCGTCCCTCGCTCGCCAGCAGCATGATGATCTTGTCTGATGACATCTCC 1799

Db 627 CAGTGGCGTCCCTCGCTCGCCAGCAGCATGATGATCTTGTCTGATGACATCTCC 568

Qy 1800 CTGCTGAAGTAGAGGCCCATGGGACAGATAGAGATTCCTCCCTGGACACACCTCCGT 1859

Db 567 CTGCTGAAGTAGAGGCCCATGGGACAGATAGAGATTCCTCCCTGGACACACCTCCGT 508

Qy 1860 GCTTCACTTTGGTTCACAAGTAGGAGACACATGGCACCCTGTGGCCAGACACCTCAGGA 1919

Db 507 GGTTCACCTTTGGTTCACAAGTAGGAGACACATGGCACCCTGTGGCCAGACACCTCAGGA 448

Qy 1920 CCCTCCACCCACCAATTCCTCGCTTCATGGAGAGGAAAGGCTGGCAAGGTGGG 1979

Db 447 CCCTCCACCCACCAATTCCTCGCTTCATGGAGAGGAAAGGCTGGCAAGGTGGG 388

Qy 1980 TTCCAGGGACTGTACCTGTAGGAACAGAAAGAGAAAGCACTCTGCTGGCGGG 2039

Db 387 TTCCAGGGACTGTACCTGTAGGAACAGAAAGAGAAAGCACTCTGCTGGCGGG 328

Qy 2040 ATACTCTTGGTCACTCAATTTAAGTCGGGAATTCGTGCTTGAACCTTCAGCCCT 2099

Db 327 AATACTCTTGGTCACTCAATTTAAGTCGGGAATTCGTGCTTGAACCTTCAGCCCT 268

Qy 2100 GAACCTTTGTCCACCATTCTTTAAATTTCTCCAACCAAGATATCTCTTTCTTACTT 2159
 Db 267 GAACCTTTGTCCACCATTCTTTAAATTTCTCCAACCAAGATATCTCTTTCTTACTT 208
 Qy 2160 TCAGAACTACTGGCATCACACGACGAGTTACCTTGGGGTGTGTCCTGTGGTACCTGGCA 2219
 Db 207 TCAGAACTACTGGCATCACACGACGAGTTACCTTGGGGTGTGTCCTGTGGTACCTGGCA 148
 Qy 2220 GAGAAGAGACCAAGCTTTGTTTCCCTGCTGGCCAAAGTCTAGTAGGAGGATGCACAGTTT 2279
 Db 147 GAGAAGAGACCAAGCTTTGTTTCCCTGCTGGCCAAAGTCTAGTAGGAGGATGCACAGTTT 88
 Qy 2280 GCTATTGCTTTAGACACAGGACTGTATAAACAAGCCCTAAACATTTGGTGCACCAAGATGCC 2339
 Db 87 GCTATTGCTTTAGACACAGGACTGTATAAACAAGCCCTAAACATTTGGTGCACCAAGATGCC 28
 Qy 2340 TCTTGAATT 2348
 Db 27 TCTTGAATT 19

RESULT 7

BI084878/c

LOCUS

DEFINITION 602869445T1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5013994 3',
 mRNA sequence.

ACCESSION BI084878

VERSION BI084878.1 GI:14503208

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-f@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONETECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCMI820 row: j column: 11

High quality sequence start: 18

High quality sequence stop: 821.

Location/Qualifiers

1..865

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5013994"

/clone_lib="NIH_MGC_102"

/tissue_type="epidermoid carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;

Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGACGAG(G). Library constructed

by Ling Hong in the laboratory of Gerald M. Rubin

(University of California, Berkeley) using ZAP-cDNA

synthesis kit (Stratagene) and Superscript II RT (Life

Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 207 a 224 c 228 g 205 t

ORIGIN

Query Match 30.88;

Best Local Similarity 95.3%;

Matches 810; Conservative 0; Mismatches 33; Indels 7; Gaps 6;

Score 723.8; DB 13; Length 865;

Pred. No. 9.7e-167;

QY	1413	GTGAAGATGTGCCACGTCCCAAGACGACTGTTACAAGTTTCCCATCTCACAGTCATCC	1472
Db	865	GTGAAGATGTGCCACGTCCCAAGACGACTGTTAC-AGTTGCCATCTCACAGTCATCC	807
QY	1473	ACGGGCACTGTTATGGAG-CTGTTATCATCGAGGCTTCTACGTGCTTTTTCATCGGGC	1531
Db	806	ACGGCAACTGTTATGGAGGCTTTCATCGAGGCTTCTACGTGCTTTTTCATCGGGC	747
QY	1532	CCGAAAACGAATTTGGCTTCTGCTCAGCGCTTGCCA-TGTGCACGATGACTTCAGGACGG	1590
Db	746	CCGAAAACGAATTTGGCTTCTGCTCAGCGCTTGCCATTGTGCACGATGACTTCAGGACGG	687
QY	1591	CAGCGTGGAGGCCCTTTTGTCCACCTTGACATGGAAGACTGTGGC--TACAACATTC	1648
Db	686	CAGCGTGGAGGCCCTTTTGTCCACCTTGACATGGAAGACTGTGGCATTACANACATTC	627
QY	1649	ACAGACAGATGAGTCAACCTCATGACCATAGCTATGTGATGCTGCCATCTGCCCCCT	1708
Db	626	ACAGACAGATGAGTCAACCTCATGACCATAGCTATGTGATGCTGCCATCTGCCCCCT	567
QY	1709	CTTCATGCTGCCACTCTGCCCTCATGTGTGTCAGTGGCGTGCCTCGCTGCCTGGGCCA	1768
Db	566	CTTCATGCTGCCACTCTGCCCTCATGTGTGTCAGTGGCGTGCCTCGCTGCCTGGGCCA	507
QY	1769	GCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTAGAGGCCCCATGGGCAGA	1828
Db	506	GCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTAGAGGCCCCATGGGCAGA	447
QY	1829	AGATAGAGATTCCTCCCTGGACCACTCCGTTGCTACTTTGCTCACAAGTAGGACAC	1888
Db	446	AGATAGAGATTCCTCCCTGGACCACTCCGTTGCTACTTTGCTCACAAGTAGGACAC	388
QY	1889	AGATGGCACCTGTGGCAGAGCACCTCAGGACCTCCGCCACCCACCAATGCTCTGCCCT	1948
Db	387	AGATGGCACCTGTGGCAGAGCACCTCAGGACCTCCGCCACCCACCAATGCTCTGCCCT	328
QY	1949	TGATGGAGAGGAAAAGGCTGGCAAGTGGTTCAGGAGTCTTACCTGTAGGAAACAGA	2008
Db	327	TGATGGAGAGGAAAAGGCTGGCAAGTGGTTCAGGAGTCTTACCTGTAGGAAACAGA	268
QY	2009	AAGAGAAGAAAGAACGACTCTGCTGGCGGAATACTCTTGGTCACTCAATTTAAGTC	2068
Db	267	AAGAGAAGAAAGAACGACTCTGCTGGCGGAATACTCTTGGTCACTCAATTTAAGTC	208
QY	2069	GGGAAATTCGCTGCTTGAACCTTCAGCCCTGAACCTTGTCCACCAATTCCTTTAAATTC	2128
Db	207	GGGAAATTCGCTGCTTGAACCTTCAGCCCTGAACCTTGTCCACCAATTCCTTTAAATTC	148
QY	2129	TCAACCCCAAGATATCTTCTTTTCTTAGTTTCAGAACTACTGGCATCAACGAGGTTA	2188
Db	147	TCAACCCCAAGATATCTTCTTTTCTTAGTTTCAGAACTACTGGCATCAACGAGGTTA	88
QY	2189	CTTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2248
Db	87	CTTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	29
QY	2249	GCCAAAGTCA 2258	
Db	28	GCCAAAGTCA 19	
RESULT	8		
LOCUS	BM016288		
DEFINITION	603642760F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5418687 5',	761 bp	mRNA linear EST 30-OCT-2001
ACCESSION	BM016288		mRNA sequence.
VERSION	BM016288.1		GI:16530642
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		

REFERENCE	1 (bases 1 to 761)	
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12068 row: h column: 16 High quality sequence stop: 728.	
FEATURES	Location/Qualifiers	
source	1..761	
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	/clone="IMAGE:5418687"	
	/clone_lib="NIH_MGC_87"	
	/tissue_type="mammary adenocarcinoma, cell line"	
	/lab_host="DH10B (phage-resistant)"	
	/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."	
BASE COUNT	170 a 221 c 197 g 171 t	2 others
ORIGIN		
	Query Match 30.4%; Score 713.8; DB 13; Length 761;	
	Best Local Similarity 99.3%; Pred. No. 2.7e-164;	
	Matches 726; Conservative 0; Mismatches 4; Indels 1; Gaps 1;	
QY	1221	GTCAATCCATCAAGGAGGCTCTCTCCACGGAGAAGTTCCCTGTATGTTCTTGCTAGGA 1280
Db	1	GTCAATCCATCAAGGAGGCTCTCTCCACGGAGAAGTTCCCTGTATGTTCTTGCTAGGA 60
QY	1281	GAGCAGCTGTGTCTGGCAAGCAGGACCCCTTTGGAAACATTTCCCAAGTCATCTCA 1340
Db	61	GAGCAGCTGTGTCTGGCAAGCAGGACCCCTTTGGAAACATTTCCCAAGTCATCTCA 120
QY	1341	CTCTACCTAATGGTGTAGTTTACCAACAGTCTCTCCGCATCACCCTCTTCCGACGAA 1400
Db	121	CTCTACCTAATGGTGTAGTTTACCAACAGTCTCTCTCCGCATCACCCTCTTCCGACGAA 180
QY	1401	TACCTGGGCGCAGTGGAAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATC 1460
Db	181	TACCTGGGCGCAGTGGAAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATC 240
QY	1461	TCACAGTCATCCACGGGCACCTGTTATGGAGCTGTTATCATGGAGGCTTCTACGTTGTC 1520
Db	241	TCACAGTCATCCACGGGCACCTGTTATGGAGCTGTTATCATGGAGGCTTCTACGTTGTC 300
QY	1521	TTTGATCGGGCCCCGAAAACGAATTTGGCTTTGCTGTACAGCGCTTGCCATGTGCACGATGAG 1580
Db	301	TTTGATCGGGCCCCGAAAACGAANTGGCTTTGCTGTACAGCGCTTGCCATGTGCACGATGAG 360
QY	1581	TTCAGGACGCGGTGGAAAGGCCCTTTTGTACCTTTGGACATGGAAGACTGTGGGTAC 1640
Db	361	TTCAGGACGCGGTGGAAAGGCCCTTTTGTACCTTTGGACATGGAAGACTGTGGGTAC 420
QY	1641	AACATTCACAGACAGATGAGTCAACCTCATGACCATAGCTATGTCATGGCTGCCATC 1700
Db	421	AACATTCACAGACAGATGAGTCAACCTCATGACCATAGCTATGTCATGGCTGCCATC 480
QY	1701	TGGCCCTCTTCATGCTGCCACTCTGCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGC 1760
Db	481	TGGCCCTCTTCATGCTGCCACTCTGCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGC 540
QY	1761	CTGCGCCACGACGATGATGACTTTGCTGTGATGACATCTCCCTGCTGAAAGTAGAGGCCCA 1820

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Db 541 CTCGCCAGCAGCATGATGACATTGCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCA 600
QY 1821 TGGCAGAGATAGAGATTCCCTGGACCACACCTCGTGGTTTCACATTGCTCAAGTA 1880
Db 601 TGGCAGAGATAGAGATTCCCTGGACCACACCTCGTGGTTTCACATTGCTCAAGTA 660
QY 1881 GGAGACACAGATGGCAGCCTGTGGCCAGAGACACCTCAGGACCCTCCGCCACCCACCAATGTC 1940
Db 661 GGAGACACAGATGGCAGCCTGTGGCCAGAGACACCTCAGGACCCTCCGCCA-CCACAAATGTC 719
QY 1941 CTCGCTGCTTGA 1951
Db 720 CTCGCTGCTTGA 730

RESULT 9
AL570757/c
LOCUS AL570757 LTI_NFL006_PL2 700 bp mRNA linear EST 16-FEB-2001
DEFINITION prime, mRNA sequence.
ACCESSION AL570757
VERSION AL570757.1 GI:12927378
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J. and Pollayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 700
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODI022YE22"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 169 a 173 c 191 g 161 t 6 others
ORIGIN

Query Watch 29.3%; Score 688.6; DB 9; Length 700;
Best Local Similarity 99.3%; Pred. No. 4e-158;
Matches 688; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1555 TCAGCGCTTGCATGTGCACCATGATGATTCAGGACGCGCGGTGGAAGGCCCTTTTGTCA 1614
Db 693 TCAGCGCTTGCATGTGCACCATGATGATTCAGGACGCGCGGTGGAAGGCCCTTTTGTCA 634
QY 1615 CTTTGGACATGGAAGACTGTGGCTACAACTTCCACAGACAGATGAGTCAACCCCTCATGA 1674
Db 633 CTTTGYACATGGAAGACTGTGGCTACAACTTCCACAGACAGATGAGTCAACCCCTCATGA 574
QY 1675 CCATAGCCTATGTGATGGCTGCCATCTTGGCCCTCTTTCATGTGCGCACTCTGCCCTCATGG 1734
Db 573 CCATAGCCTATGTGATGGCTGCCATCTTGGCCCTCTTTCATGTGCGCACTCTGCCCTCATGG 514
QY 1735 TGTGTAGTGCCTGCTCCCTGCTCCGTCGCGCAGCAGCATGATGACTTTCCTGATGACA 1794

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Db 513 TGTGTCACTGGCGCTGCCCTCCGCTGCTGCGCCACAGCATGATGACTTGTGCTGATGACA 454
QY 1795 TCTCCCTCTGAAGTCAAGTGAGAGGCCCATGGCAGAGATAGAGATTCCCTTGACACACACC 1854
Db 453 TCTCCCTCTGAAGTCAAGTGAGAGGCCCATGGCAGAGATAGAGATTCCCTTGACACACACC 394
QY 1855 TCCGTGGTTTCACTTTGGTCAACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGACACCT 1914
Db 393 TCCGTGGTTTCACTTTGGTCAACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGACACCT 334
QY 1915 CAGGACCTCCGCCACCCACCAATGCTCTGCTTGTAGGAGAGAGAAAGCTGGCAAG 1974
Db 333 CAGGACCTCCGCCACCCACCAATGCTCTGCTTGTAGGAGAGAGAAAGCTGGCAAG 274
QY 1975 GTGGGTTCCAGGAGCTGTACCTGTAGGAAACAGAAAGAGAAAGAGCACTCTGCTG 2034
Db 273 GTGGGTTCCAGGAGCTGTACCTGTAGGAAACAGAAAGAGAGAAAGAGCACTCTGCTG 214
QY 2035 GCGGGAATACCTTGTGCTACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTCAAACTTCA 2094
Db 213 GCGGGAATACCTTGTGCTACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTCAAACTTCA 154
QY 2095 GCCCTGAACCTTTGTGCCACCATTCCTTTAAATTTCTTCAACCCAAAGATATCTCTTTTCT 2154
Db 153 GCCCTGAACCTTTGTGCCACCATTCCTTTAAATTTCTTCAACCCAAAGATATCTCTTTTCT 94
QY 2155 TAGTTTTCAGAGTACTTGGCATCACACGAGTACCTTGGCGTGTGCTGCTGCTGCTGCTGCTGCT 2214
Db 93 TAGTTTTCAGAGTACTTGGCATCACACGAGTACCTTGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCT 34
QY 2215 TGGCAGAGAAGAGACCAAGCTTTGTTTCCCTGCT 2247
Db 33 TGGCAGAGAAGAGACCAAGCTTTGTTTCCCTGCT 1

RESULT 10
BE378929
LOCUS BE378929
DEFINITION 601237528F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609631 5',
mRNA sequence.
ACCESSION BE378929
VERSION BE378929.1 GI:9324294
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM264 row: g column: 08
High quality sequence stop: 735.
Location/Qualifiers
1. 904
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3609631"
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/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="pHL0B (phage-resistant)"
/note="Organ: uterus; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'

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adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 191 a 240 c 256 g 217 t

Query Match 29.3%; Score 688.6; DB 10; Length 904;
Best Local Similarity 98.0%; Pred. No. 4.2e-158;
Matches 740; Conservative 0; Mismatches 9; Indels 6; Gaps 4;

QY 1054 GGTATACCCATCCGCGGGAGTGTATATAGGTG-ATCAATGTGGGGTGGAGATC 1112
Db 1 GGTATACCCATCCGCGGGAGTGTATATAGGTGTCATTCGCGGGTGGAGATC 60
QY 1113 AATGGACAGATCTGAATGGAGTCAAGGAGTCAACTATCACAAGACATTTGGAC 1172
Db 61 AATGGACAGATCTGAATGGAGTCAAGGAGTCAACTATCACAAGACATTTGGAC 120
QY 1173 AGTGGCACCACCAACCTTCGTTTGGCCCAAGAAAGTGTGGAAGCTGCAGTCAATCCATC 1232
Db 121 AGTGGCACCACCAACCTTCGTTTGGCCCAAGAAAGTGTGGAAGCTGCAGTCAATCCATC 180
QY 1233 AA-GGCAGGCTCTCCACGGAGAAGTTCCCTGATGTTTCTGGCTAGGAGAGCAGCTGGT 1291
Db 181 AAGGCGAGGCTCTCCACGGAGAAGTTCCCTGATGTTTCTGGCTAGGAGAGCAGCTGGT 240
QY 1292 GTGCTGGCAGCAGGACCAACCCCTTGGACATTTTCCAGTCTATCTCACTTACCTAAT 1351
Db 241 GTGCTGGCAGCAGGACCAACCCCTTGGACATTTTCCAGTCTATCTCACTTACCTAAT 300
QY 1352 GGTGAGGTTTACCAACGAGTCCCTCCGATCACCATCTTCCGACGAATACCTGGGGC 1411
Db 301 GGTGAGGTTTACCAACGAGTCCCTCCGATCACCATCTTCCGATCACCATCTGGGGC 360
QY 1412 AGTGAAGATGTGGCCACGTCCTCAAGACGACTGTTACAAGTTTGGCATCTCAAGTCAATC 1471
Db 361 AGTGAAGATGTGGCCACGTCCTCAAGACGACTGTTACAAGTTTGGCATCTCAAGTCAATC 420
QY 1472 CACGGGCACGTGTTATGGGAGCTGTTATCATGGAGGCTTCTACGTTGCTCTTTCATCGGGC 1531
Db 421 CACGGGCACGTGTTATGGGAGCTGTTATCATGGAGGCTTCTACGTTGCTCTTTCATCGGGC 480
QY 1532 CCGAAAACGAATTTGGCTTTCGCTGTCAGCGCTTGCCATGTGCAGATGAGTTCAGGACGGC 1591
Db 481 CCGAAAACGAATTTGGCTTTCGCTGTCAGCGCTTGCCATGTGCAGATGAGTTCAGGACGGC 540
QY 1592 AGCGGTGGAAGGCCCTTTTGTACCTTTGGACATGGAAGAGTGTGGCTTACAACTTCCACA 1651
Db 541 AGCGGTGGAAGGCCCTTTTGTACCTTTGGACATGGAAGAGTGTGGCTTACAACTTCCACA 600
QY 1652 GACAGATGAGTCAACCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTT 1711
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Db 661 CATGCTG-CACTCTGCTCATGTGTGTGTCAGTGGCGTG---CTCCGTGCTGCGCCAGCA 716
QY 1772 GCATGATGACTTTGGTGATGACATCTCCCTGCTGA 1806
Db 717 GCATGATGACTTTGGTGATGACATCTCCCTGCTGA 751

RESULT 11
BF057767/c 718 bp mRNA linear EST 16-OCT-2000
LOCUS 7k53ell.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3479156 3'
DEFINITION similar to TR:Q9ULS1 Q9ULS1 KIAA1149 PROTEIN ;, mRNA sequence.
ACCESSION BF057767
VERSION BF057767.1 GI:10811663
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 718)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 465.

FEATURES
Source
1..718
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/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clones IDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 174 a 177 c 190 g 176 t
ORIGIN
Query Match 29.0%; Score: 681.4; DB 12; Length 718;
Best Local Similarity 99.3%; Pred. No. 2.4e-156;
Matches 715; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

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Db 718 GTCACTTGGACATGGAGACTGTGGCTAC-ACATTCACAGACAGATGAGTCAA-CCTC 661
QY 1671 ATGACATAGCCTATGTCAATGGCTGCTGCGCCCTCTTCATGCTGCCACTCTGCCTC 1730
Db 660 ATGACATAGCCTATGTCAATGGCTGCTGCGCCCTCTTCATGCTGCCACTCTGCCTC 601
QY 1731 ATGCTGTGTCAGTGGCGCTGCTCCGCTGCTGCGCCAGCAGCATGATGACTTTGCTGAT 1790
Db 600 ATGCTGTGTCAGTGGCGCTGCTCCGCTGCTGCGCCAGCAGCATGATGACTTTGCTGAT 541
QY 1791 GACATCTCCCTGCTGAAGTGAAGGAGGCGCCATGGCACAAGATAGAGATTCCTCCCTGGACCA 1850
Db 540 GACATCTCCCTGCTGAAGTGAAGGAGGCGCCATGGCACAAGATAGAGATTCCTCCCTGGACCA 481
QY 1851 CACCTCGTGGTTCACCTTTGGTCAACAGTAGGAGACACAGATGGCAGCTGTGGCAGAGC 1910
Db 480 CACCTCGTGGTTCACCTTTGGTCAACAGTAGGAGACACAGATGGCAGCTGTGGCAGAGC 421
QY 1911 ACCTCAGGACCCCTCCACCCCAAAATGCCTCTGCCTTGTATGAGAAGGAAAAGGCTGG 1970
Db 420 ACCTCAGGACCCCTCCACCCCAAAATGCCTCTGCCTTGTATGAGAAGGAAAAGGCTGG 361
QY 1971 CAAGGTGGGTTCAGGAGACTGTACCTGTAGGAACACAGAAAGAGAAAGAACCACTCT 2030
Db 360 CAAGGTGGGTTCAGGAGACTGTACCTGTAGGAACACAGAAAGAGAAAGAACCACTCT 301

QY 2031 GCTGGCGGAATACCTCTTGGTCACCTCAAAATTTAAGTCGGAAATCTGCTGCTTGAAC 2090
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Db 300 GCTGGCGGAATACCTCTTGGTCACCTCAAAATTTAAGTCGGAAATCTGCTGCTTGAAC 241
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QY 2091 TTCAGCCCTGAACCTTTTCTCCACCATTCCTTTAAATTTCTCAACCCAAAGATATCTTCT 2149
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QY 2150 TTTCTTAGTTTTCAGAGTACTGGCATCACACGAGGTTTACCTTGGCGGTGTCTCCCTGTGG 2209
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Db 180 TTTCTTAGTTTTCAGAGTACTGGCATCACACGAGGTTTACCTTGGCGGTGTCTCCCTGTGG 121
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QY 2210 TACCTGCGCAGAGAGACCAAGCTTGTTCCTCTGCTGCCAAAGTCAGTAGGAGAGGA 2269
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Db 120 TACCTGCGCAGAGAGACCAAGCTTGTTCCTCTGCTGCCAAAGTCAGTAGGAGAGGA 61
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5', mRNA sequence.
ACCESSION BO669630
VERSION BO669630.1 GI:21780464
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 945)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
JOURNAL Email: cgapbs-r@mail.nih.gov
COMMENT Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM2459 row: 0 column: 22
High quality sequence stop: 506.
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/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 253 a 231 c 245 g 214 t 2 others
ORIGIN
Query Match 28.3%; Score 664.4; DB 14; Length 945;
Best Local Similarity 99.4%; Pred. No. 3.7e-152;
Matches 676; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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QY 1850 ACACCTCCGTGGTTCACCTTTGGTTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAG 1909
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Db 181 ACACCTCCGTGGTTCACCTTTGGTTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAG 240
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QY 1910 CACCTCAGAGCCCTCCCCACCCACCAATTCCTTGCCTTTCATGGAGAGGAAAAGGCTG 1969
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Db 241 CACCTCAGAGCCCTCCCCACCCACCAATTCCTTGCCTTTCATGGAGAGGAAAAGGCTG 300
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QY 1970 GCAAGTGGGTTTCCAGGGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGACACATC 2029
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Db 301 GCAAGTGGGTTTCCAGGGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGACACATC 360
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Db 361 TGCTGGCGGGAATACCTCTTGGTTCACCTCAAAATTTAAGTCGGAAATCTGCTGCTTGAAC 420
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Db 421 CTTCAGCCCTGAACCTTTCTGCACACATTCCTTTAAATTTCTCCAAACCCAAAGATATCTTCT 480
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QY 2150 TTTCTTAGTTTTCAGAGTACTGGCATCACACGAGGTTTACCTTGGCGGTGTGCTCCCTGTGG 2209
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Db 481 TTTCTTAGTTTTCAGAGTACTGGCATCACACGAGGTTTACCTTGGCGGTGTGCTCCCTGTGG 540
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QY 2210 TACCTT-GGCAGAGAGACCAAGCTTTTTCCTGCTGCCAAAGTCAGTAGGAGAGG 2268
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Db 541 TACCTTGGCGAGAGAGACCAAGCTTTTTCCTGCTGCCANAGTCAGTAGGAGAGG 600
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QY 2269 ATGCACAGTTTGTCTATTTGCTTTAGAGACAGGAGCTGTATAAACAAGCCTTAACATTTGGT 2328
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Db 601 ATGCACAGTTTGTCTATTTGCTTTANAGACAGGAGCTGTATAAACAAGCCTTAACATTTGGT 660
QY 2329 CAAAGATTGCTCTTTGAATTT 2348
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Db 661 CAAAGATTGCTCTTTGAATTT 680
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RESULT 13
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LOCUS
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5', mRNA sequence.
ACCESSION BF338951
VERSION BF338951.1 GI:11285371
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 684)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
JOURNAL Email: cgapbs-r@mail.nih.gov
COMMENT Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM9501 row: 1 column: 05

High quality sequence stop: 652.

FEATURES

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/organism="Homo sapiens"
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/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="organ: brain; Vector: PCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 161 a 189 c 172 g 162 t
ORIGIN

Query Match 28.0%; Score 657.8; DB 12; Length 684;
Best Local Similarity 99.4%; Pred. No. 1.5e-150;
Matches 681; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 1534 GAAAGCAATTGGCTTGTGTCAGCGCTTGCATGTGCACGATGAGTTTCAGGACGGCAG 1593
DB 1 GAAAGCAATTGGCTTGTGTCAGCGCTTGCATGTGCACGATGAGTTTCAGGACGGCAG 60
QY 1594 CGGTGGAAGCGCCCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACTTCCACAGA 1653
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QY 1654 CAGATGAGTCAACCTTCATGACATAGCCCTATGTATGCTGCGCATCTGCGCCCTTTTCA 1713
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QY 1894 GCACCTGTGGCCAGACGACCTCAGGACCTCCGCCACCCACCAATCCCTCTGCTTTGATG 1953
DB 361 GCACCTGTGGCCAGACGACCTCAGGACCTCCGCCACCCACCAATCCCTCTGCTTTGATG 420
QY 1954 GAGAAGAAAGGCTGGCAAGGTGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGA 2013
DB 421 GAGAAGAAAGGCTGGCAAGGTGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGA 479
QY 2014 GAAGAAGAAGCACCTGCTGGGGGAATACCTTGGTCAACCTCAATTTAAGTCGGGA 2073
DB 480 GAAGAAGAAGCACCTGCTGGGGGAATACCTTGGTCAACCTCAATTTAAGTCGGGA 539
QY 2074 ATTCTGCTGCTTGAACACTTTCAGCCCTTGAACCTTGTGTCACCATTCCTTTAAATTCACCA 2133
DB 540 ATTCTGCTGCTTGAACACTTTCAGCCCTTGAACCTTGTGTCACCATTCCTTTAAATTCACCA 599
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QY 2193 GCGGTGTCCCTGTGGTACCCCTGG 2217
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RESULT 14

BM048418 730 bp mRNA linear EST 07-NOV-2001
LOCUS 603625683F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5452052 5',
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

mRNA sequence.

BM048418
BM048418.1 GI:16777685
EST
human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/

1 (bases 1 to 730)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue procurement: DCTD/Dnp

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1943 row: f column: 21

High quality sequence stop: 696.

Location/Qualifiers

1. 730

/organism="Homo sapiens"

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/clone="IMAGE:5452052"

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/tissue_type="carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: prostate; Vector: pOTB7; Site.1: XhoI;

Site.2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."

BASE COUNT 163 a 210 c 206 g 151 t

ORIGIN

Query Match 27.6%; Score 647.4; DB 13; Length 730;
Best Local Similarity 97.0%; Pred. No. 5.2e-148;
Matches 713; Conservative 0; Mismatches 16; Indels 6; Gaps 5;

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QY 599 CTTTGAGTGGGTGCTGCCCGCCCGCCCGCTTCCCTGCTGCTTACCAGAGGAGCTGTC 658

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QY 659 CAGCACATACCGGGAGCTCCGGAAGGTGTGTATGTGCCCTACACCCAGGGCAGGTGGA 718

DB 121 CAGCACATACCGGGA-CTCCGGAAGGTGTGTATGTGCCCTACACCCA-GGCAAGTGGGA 178

QY 719 AGGGGAGCTGGGACCGACCTGTGTAAGCATCCCGCCCGCCCGCTTCCCTGCTGCTGTC 778

DB 179 AGGGGAGCTGGGACCGACCTGTGTAAGCATCCCGCCCGCTTCCCTGCTGCTGTC 237

QY 779 CAACATTGCTGCCATCCTGAGATTGCCAGGCTTCCATCAACGGCTCCCACTGGGAAGG 838

DB 238 CAACATTGCTGCCATCCTGAGATTGCCAGGCTTCCATCAACGGCTCCCACTGGGAAGG 297

QY 839 CATCTCTGGGCTGGCCTATGCTGAGATTGCCAGGCTTCCAGCTTCCCTGAGGCTTTCTT 898

DB 298 CATCTCTGGGCTGGCCTATGCTGAGATTGCCAGGCTTCCAGCTTCCCTGAGGCTTTCTT 357

QY 899 TGACTCTCTGGTAAAGCAGACCCACGCTTCCCAACCTCTTCTCCCTGAGCTTTGTGTGTC 958

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RESULT 15
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ACCESSION BE885725
VERSION BE885725.1 GI:10339345
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9725 row: j column: 09
High quality sequence stop: 628.
FEATURES
Location/Qualifiers
BASE COUNT 167 a 216 c 248 g 209 t
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/db_xref="taxon:9606"
/clone="IMAGE:3910376"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
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Best Local Similarity 94.4%; Pred. NO. 9.3e-145;
Matches 690; Conservative 0; Mismatches 38; Indels 3; Gaps 3;
QY 944 GCAGCTTGTGGTCTGGCTTCCCTCAACAGTCTGAAGTCTGCTGCTGCGGAGG 1003
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Search completed: March 2, 2003, 05:48:13
Job time: 2198.5 secs

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5	1881	80.1	1977	4	US-09-548-372D-5	Sequence 5, Appli
6	1835.4	78.2	2370	4	US-09-548-367D-5	Sequence 5, Appli
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12	1355.8	57.7	1380	4	US-09-548-372D-31	Sequence 31, Appl
13	1298	55.3	1506	4	US-09-548-367D-31	Sequence 31, Appl
14	1293.8	55.1	1341	4	US-09-713-158-1	Sequence 1, Appli
15	1293.8	55.1	1341	4	US-09-548-372D-21	Sequence 21, Appl
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25	1180	50.3	1278	4	US-09-548-372D-27	Sequence 27, Appl
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27	397.4	16.9	1804	4	US-09-280-116-30	Sequence 30, Appl
28	397.4	16.9	1804	4	US-09-548-372D-1	Sequence 1, Appli

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Db 301 GTGGTGTGCCCCCACCACCCCTTCTCGATCGCTACTACAGAGGACGCTGCCAGCACA 360
Qy 666 TACCGGGACCTCCGGGAAGGCTGTATGTATGTCCTTACACCCAGGCAAGTGGGAAGGGGAG 725
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Db 1081 ATCTCTCCGACCAATACCTCGGCCAGTGGAGATGGGCCAGCTCCCAAGACCACTGT 1140
Qy 1446 TACAAGTTTGGCATCTCAGATCATCCACGGGCACTCTTATGGGAGCTGTATCATGGAG 1505
Db 1141 TACAAGTTTGGCATCTCAGATCATCCACGGGCACTGTATGGAGCTGTATCATGGAG 1200
Qy 1506 GGCTTCTACGTTGTCTTTGATCGGGCCGCAAGAAAGAAATTTGCTGTACGCGCTTCC 1565
Db 1201 GGCTTCTACGTTGTCTTTGATCGGGCCGCAAGAAAGAAATTTGCTGTACGCGCTTCC 1260
Qy 1566 CATGTGCAGGATGAGTTGAGGAGCGGAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1625
Db 1261 CATGTGCAGGATGAGTTGAGGAGCGGAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320
Qy 1626 GAAGACTGTGGCTACAACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT 1685
Db 1321 GAAGACTGTGGCTACAACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT 1380

Qy 1686 GTCATGGCTGCCCATTCGGCCCTCTTCATGCTGGCACCTCTGCCTCATGCTGTGTCACTGG 1745
Db 1381 GTCATGGCTGCCCATTCGGCCCTCTTCATGCTGGCACCTCTGCCTCATGCTGTGTCACTGG 1440
Qy 1746 CGCTGGCTCCGCTGGCTGGCCAGCAGCATGATGACTTTTGTGTGATGACATCTCCCTCTG 1805
Db 1441 CGCTGGCTCCGCTGGCTGGCCAGCAGCATGATGACTTTTGTGTGATGACATCTCCCTCTG 1500
Qy 1806 AAGTGAAGGAGGCCATGGGCAGAGATAGAGATTCCCTGGACACACCTCCGTGGTTC 1865
Db 1501 AAGTGAAGGAGGCCATGGGCAGAGATAGAGATTCCCTGGACACACCTCCGTGGTTC 1560
Qy 1866 CTTTGGTCAACAGTAGGAGACACAGATGGCACCTGTGGCCAGAGACCTTCAGGACCTCC 1925
Db 1561 CTTTGGTCAACAGTAGGAGACACAGATGGCACCTGTGGCCAGAGACCTTCAGGACCTCC 1620
Qy 1926 CCACCCACCAATGGCTCTGCTTGTATGGAGAAGAAAGGCTGGCAAGGTGGGTTCAG 1985
Db 1621 CCACCCACCAATGGCTCTGCTTGTATGGAGAAGAAAGGCTGGCAAGGTGGGTTCAG 1680
Qy 1986 GGAAGTGTACCTGTAGGAAACAGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGT 2045
Db 1681 GGAAGTGTACCTGTAGGAAACAGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGT 1740
Qy 2046 CTTGCTCACCTCAAAATTTAAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 2105
Db 1741 CTTGCTCACCTCAAAATTTAAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 1800
Qy 2106 TTGTCACCACTTCCTTTAAATTTCTCAACCCAAAGTATTTCTTTCTTTAGTTTCAGAA 2165
Db 1801 TTGTCACCACTTCCTTTAAATTTCTCAACCCAAAGTATTTCTTTCTTTAGTTTCAGAA 1860
Qy 2166 GTACTGGCATCACACGAGGTACCTTTGGCGTGTCTCCCTGTGGTACCCTGGCAGAGAG 2225
Db 1861 GTACTGGCATCACACGAGGTACCTTTGGCGTGTCTCCCTGTGGTACCCTGGCAGAGAG 1920
Qy 2226 AGACCAAGCTTTGCTTCCCTGCTGGCCAAAGTCAGTAGGAGAGATGCACAGTTTGTCTATT 2285
Db 1921 AGACCAAGCTTTGCTTCCCTGCTGGCCAAAGTCAGTAGGAGAGATGCACAGTTTGTCTATT 1980
Qy 2286 TGCTTTAGAGACAGGAGCTGTATAAACAAGCCTAACATTTGGTGAAGATTTGCCTCTGA 2345
Db 1981 TGCTTTAGAGACAGGAGCTGTATAAACAAGCCTAACATTTGGTGAAGATTTGCCTCTGA 2040
Qy 2346 ATT 2348
Db 2041 ATT 2043

RESULT 2

US-09-548-367D-3
: Sequence 3, Application US/09548367D
: Patent No. 6440698
: GENERAL INFORMATION:
: APPLICANT: GURNEY ET AL.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: 29915/6280H
: CURRENT APPLICATION NUMBER: US/09/548.367D
: CURRENT FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 3
: LENGTH: 2070
: TYPE: DNA

; ORGANISM: Homo sapiens
US-09-548-367D-3

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Query Match      86.9%; Score 2041.4; DB 4; Length 2070;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 2042; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy	306	ATGGCCCAAGCCCTGCCCTTGGCTCTCTCTGTGGATGGCGCGGGAGTGCCTGCCCTGCCAC	365
Db	1	ATGGCCCAAGCCCTGCCCTTGGCTCTCTGTGGATGGCGCGGGAGTGCCTGCCCTGCCAC	60
Qy	366	GGCACACAGCAGGCATCCGGCTGCCCTTGCCGACAGCGCCTGGGGGGGCCCCCTCGGGG	425
Db	61	GGCACACAGCAGGCATCCGGCTGCCCTTGCCGACAGCGCCTGGGGGGGCCCCCTCGGGG	120
Qy	426	CTCGGGTGCCTGGGAGACCACGAAGAAGCCCGAGGAGCCCGCGGAGGGCAGCTTT	485
Db	121	CTCGGGTGCCTGGGAGACCACGAAGAAGCCCGAGGAGCCCGCGGAGGGCAGCTTT	180
Qy	486	GTGGAGATGTTGACAACTTGAGGGCAAGTCGGGGCAGGCTACTACGTGGAGATGACC	545
Db	181	GTGGAGATGTTGACAACTTGAGGGCAAGTCGGGGCAGGCTACTACGTGGAGATGACC	240
Qy	546	GTGGGAGCCCCCGCAGACGCTCAACATCTCTGTGGATACAGGCAGCAGTAACCTTGCA	605
Db	241	GTGGGAGCCCCCGCAGACGCTCAACATCTCTGTGGATACAGGCAGCAGTAACCTTGCA	300
Qy	606	GTGGGTGTCCTCCCCACACCCCTTCTGTCATCCGTACTACAGAGGCAGCTCTCCAGACA	665
Db	301	GTGGGTGTCCTCCCCACACCCCTTCTGTCATCCGTACTACAGAGGCAGCTCTCCAGACA	360
Qy	666	TACCGGACCTCCGGAAAGGTTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	725
Db	361	TACCGGACCTCCGGAAAGGTTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	726	CTGGGCACCGACTGTTAAGCATGCCCATGCCCCCAACGTCATCTGCGTGCACAATTT	785
Db	421	CTGGGCACCGACTGTTAAGCATGCCCATGCCCCCAACGTCATCTGCGTGCACAATTT	480
Qy	786	GCTGCCATCACTCAATCAGACAAAGTTCTTATCAACGGCTCCAACTGGGAAGGCATCTG	845
Db	481	GCTGCCATCACTCAATCAGACAAAGTTCTTATCAACGGCTCCAACTGGGAAGGCATCTG	540
Qy	846	GGGCTGGCCCTATGCTGAGATTGCCAGGCGTCAGCACTCCCTGGAGCCCTTCTTTGACTCT	905
Db	541	GGGCTGGCCCTATGCTGAGATTGCCAGGCGTCAGCACTCCCTGGAGCCCTTCTTTGACTCT	600
Qy	906	CTGTTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGGCTTC	965
Db	601	CTGTTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGGCTTC	660
Qy	966	CCCTCAACCACTGAAGTGTGGGCTCTGTCGAGGGAGCATGATCATTTGGAGGTATC	1025
Db	661	CCCTCAACCACTGAAGTGTGGGCTCTGTCGAGGGAGCATGATCATTTGGAGGTATC	720
Qy	1026	GACCACTCGTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	1085
Db	721	GACCACTCGTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	1086	GAGTGTATCATTTGCGGGTGGAGATCAATGACACAGGATCTGAAATGGACTGCAAGGAG	1145
Db	781	GAGTGTATCATTTGCGGGTGGAGATCAATGACACAGGATCTGAAATGGACTGCAAGGAG	840
Qy	1146	TACAACATGACAAGAGCATTTGGGACATGGGACACCAACACTTCTGTTTGGCCCAAGAA	1205
Db	841	TACAACATGACAAGAGCATTTGGGACATGGGACACCAACACTTCTGTTTGGCCCAAGAA	900
Qy	1206	GTGTTTCAAGCTCAGTCAAACTCATCAAGGCAGGCTCTCCACGAGGAAGTTCCTGTAT	1265
Db	901	GTGTTTCAAGCTCAGTCAAACTCATCAAGGCAGGCTCTCCACGAGGAAGTTCCTGTAT	960
Qy	1266	GGTTTCTTGCTAGGAGAGCAGCTTGTTGCTGGCAAGCAGGCACCAACCCCTTGGAACAT	1325

Db	961	GGTTTCTGGCTAGGAGCAGCTGGTGTGCTGGCAAGCAGGCACCCCTTTGGAACTT	1021
Qy	1326	TTCCGAGTCATCTCACTTACCTAATGGGTGAGGTTTACCAACCACTCCTTCGCATCACC	1385
Db	1021	TTCCAGTCATCTCACTTACCTAATGGGTGAGGTTTACCAACCACTCCTTCGCATCACC	1080
Qy	1386	ATCCTTCCGAGCAATACCTGGGGCCAGTGGGAAGATGTGGCCACGTGCCAAGACGACTGT	1445
Db	1081	ATCCTTCCGAGCAATACCTGGGGCCAGTGGGAAGATGTGGCCACGTGCCAAGACGACTGT	1140
Qy	1446	TACAAGTTTCCCATCTCACAGTCATCCACGGGCACCTGTTATGGGAGCTGTTATCATCGAG	1505
Db	1141	TACAAGTTTCCCATCTCACAGTCATCCACGGGCACCTGTTATGGGAGCTGTTATCATCGAG	1200
Qy	1506	GGCTTCTACCTTGTCTTTGATGGGGCCGAAACGAATTTGGCTTTGTCTCAGCGCTTGC	1565
Db	1201	GGCTTCTACCTTGTCTTTGATGGGGCCGAAACGAATTTGGCTTTGTCTCAGCGCTTGC	1260
Qy	1566	CATGTGCACGATGAGTTTCAGGAGCGCGGTGGGAAGGCCCTTTTGTCCACTTGGACATG	1625
Db	1261	CATGTGCACGATGAGTTTCAGGAGCGCGGTGGGAAGGCCCTTTTGTCCACTTGGACATG	1320
Qy	1626	GAAGACTTGTGGCTTACAACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	1685
Db	1321	GAAGACTTGTGGCTTACAACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	1380
Qy	1686	GTCATGGCTGCCATCTGCGGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1745
Db	1381	GTCATGGCTGCCATCTGCGGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1440
Qy	1746	CGCTGCCCTCCGCTGCCCTGGCCAGCAGCATGATGACTTTGTGTGATGACATCTCCCTGCTG	1805
Db	1441	CGCTGCCCTCCGCTGCCCTGGCCAGCAGCATGATGACTTTGTGTGATGACATCTCCCTGCTG	1500
Qy	1806	AAGTAGGAGGCCCATTTGGGCAGAGATACAGATTTCCCTTGGACACACACCTCCGTGGTTCA	1865
Db	1501	AAGTAGGAGGCCCATTTGGGCAGAGATACAGATTTCCCTTGGACACACACCTCCGTGGTTCA	1560
Qy	1866	CTTTGGTTCACAACTAGGAGACACAGATGCACCTGTGGCCAGAGCACCTTCAGGACCCCTCC	1925
Db	1561	CTTTGGTTCACAACTAGGAGACACAGATGCACCTGTGGCCAGAGCACCTTCAGGACCCCTCC	1620
Qy	1926	CCACCCACCAATGCCCTCTGCCCTTGATGGAGAAGAAAGCGTGGCAAGTGGGTTCAG	1985
Db	1621	CCACCCACCAATGCCCTCTGCCCTTGATGGAGAAGAAAGCGTGGCAAGTGGGTTCAG	1680
Qy	1986	GGACTGTACCTGTAGGAAACAGAAAGACAGAAAGACACTCTGCTGGCGGGAATACT	2045
Db	1681	GGACTGTACCTGTAGGAAACAGAAAGACAGAAAGACACTCTGCTGGCGGGAATACT	1740
Qy	2046	CTTGCTCACCTCAAAATTAAGTCGGGAAATCTGCTGCTTGAACCTTCAGCCCTGAACT	2105
Db	1741	CTTGCTCACCTCAAAATTAAGTCGGGAAATCTGCTGCTTGAACCTTCAGCCCTGAACT	1800
Qy	2106	TTGTCCACCATTCCTTTAAATTTCTCCAAACCCCAAAGTATTCTTTCTTTAGTTTCAGAA	2165
Db	1801	TTGTCCACCATTCCTTTAAATTTCTCCAAACCCCAAAGTATTCTTTCTTTAGTTTCAGAA	1860
Qy	2166	GTACTGGCATCACACGAGGTTTACCTTGGCGTGTGTCCCTGTGGTGTACCTTGGCAGAGAG	2225
Db	1861	GTACTGGCATCACACGAGGTTTACCTTGGCGTGTGTCCCTGTGGTGTACCTTGGCAGAGAG	1920
Qy	2226	AGACCAAGCTTGTTCCTCTCGCCCAAAAGTCAGTAGGAGAGATGCACAGTTTGTCTATT	2285
Db	1921	AGACCAAGCTTGTTCCTCTCGCCCAAAAGTCAGTAGGAGAGATGCACAGTTTGTCTATT	1980
Qy	2286	TGCTTTTAGACACAGGACTGTATAAACAAAGCCCTAACATTTGGTGCAAGATTCGCTCTTGA	2345
Db	1981	TGCTTTTAGACACAGGACTGTATAAACAAAGCCCTAACATTTGGTGCAAGATTCGCTCTTGA	2040
Qy	2346	ATT 2348	
Db	2041	ATT 2043	

RESULT 3

US-09-009-191-1

; Sequence 1, Application US/09009191

; Patent No. 6319689

; GENERAL INFORMATION:

; APPLICANT: POWELL, DAVID

; APPLICANT: CHAPMAN, CONRAD

; APPLICANT: MURPHY, KAY

; APPLICANT: SMITH, TRUDI

; TITLE OF INVENTION: ASP2

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,191

; FILING DATE: 20-JAN-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: UK 9701684.4

; FILING DATE: 28-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F.

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70368

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2541 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-009-191-1

Query Match 86.2%; Score 2024; DB 4; Length 2541;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2038; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY	306	ATGGCCCAAGCCCTGCCCTGGCTCTGCTGTGATGGGGGGGAGTGTCTGCTGCCAC	365
DB	1	ATGGCCCAAGCCCTGCCCTGGCTCTGCTGTGATGGGGGGGAGTGTCTGCTGCCAC	60
QY	366	GGCACCAGCAGCGATCGGCTGCCCTGCCAGCGCGCTGGGGGGGCGCCCTGGGG	425
DB	61	GGCACCAGCAGCGATCGGCTGCCCTGCCAGCGCGCTGGGGGGGCGCCCTGGGG	120
QY	426	CTGGGGCTGCCCGGAGACCCGACGAAGACCGCCGAGGAGCGCGCGGGGCGGCA	485
DB	121	CTGGGGCTGCCCGGAGACCCGACGAAGACCGCCGAGGAGCGCGCGGGGCGGCA	180
QY	486	GTGAGATGTGGGACAACTGAGGGCAAGTCTGGGGGAGGCTACTAGTGGAGATGAC	545
DB	181	GTGAGATGTGGGACAACTGAGGGCAAGTCTGGGGGAGGCTACTAGTGGAGATGAC	240
QY	546	GTGGGACGCCCCCGCAGACGCTCAACATCTGTGTGATACAGGACGAGTAACCTT	605
DB	241	GTGGGACGCCCCCGCAGACGCTCAACATCTGTGTGATACAGGACGAGTAACCTT	300

QY	606	GTGGTGCTGCTGCCCGCCACCCCTTCTGCTGCTACTACAGAGCAGCTGTCCAGACA	665
DB	301	GTGGTGCTGCTGCCCGCCACCCCTTCTGCTGCTACTACAGAGCAGCTGTCCAGACA	360
QY	666	TACCGGGACCTCCGGAAAGGTGTATGTGCCCTTACACCCAGGGAAGTGGAAAGGGAG	725
DB	361	TACCGGGACCTCCGGAAAGGTGTATGTAGAGCCCTACACCCAGGGAAGTGGAAAGGGAG	420
QY	726	CTGGGACCGGACCTGCTAAGCATCCCCATGGCCCCCAACGTCACCTGTGGTGGCCACAT	785
DB	421	CTGGGACCGGACCTGCTAAGCATCCCCATGGCCCCCAACGTCACCTGTGGTGGCCACAT	480
QY	786	GCTGCCATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCTG	845
DB	481	GCTGCCATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCTG	540
QY	846	GGCTGGGCTATGCTGAGATTGCCAGGCTTGACGACTCCCTGGAGCCCTTCTTTGACTCT	905
DB	541	GGCTGGGCTATGCTGAGATTGCCAGGCTTGACGACTCCCTGGAGCCCTTCTTTGACTCT	600
QY	906	CTGTTAAAGCAGACCCACCTTCCCAACCTCTTCTCCCTGCGAGCTTTGTGGTCTGGCTTC	965
DB	601	CTGTTAAAGCAGACCCACCTTCCCAACCTCTTCTCCCTGCGAGCTTTGTGGTCTGGCTTC	660
QY	966	CCCTCAACACCTCTGAAGTGTGGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC	1025
DB	661	CCCTCAACACCTCTGAAGTGTGGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC	720
QY	1026	GACCACTCGCTACACAGGACGTCTCTGTTATACCCATCCCGGGGAGTGGTATAT	1085
DB	721	GACCACTCGCTACACAGGACGTCTCTGTTATACCCATCCCGGGGAGTGGTATAT	780
QY	1086	GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGACATGCAAGGAG	1145
DB	781	GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGACATGCAAGGAG	840
QY	1146	TACAACTATGACAAGAGCATTTGTGACAGTGGCAGCACCAACCTTCCTTTGCCCAAGAA	1205
DB	841	TACAACTATGACAAGAGCATTTGTGACAGTGGCAGCACCAACCTTCCTTTGCCCAAGAA	900
QY	1206	GTGTTTGAAGCTGCAGTCAATCCATCAAGCAGCCCTCTCCACGGGAGTTCCTTGAT	1265
DB	901	GTGTTTGAAGCTGCAGTCAATCCATCAAGCAGCCCTCTCCACGGGAGTTCCTTGAT	960
QY	1266	GGTTTCTGGCTAGGAGCAGCTGCTGTGCTGGAAGCAGCAGCACCCCTTTGGAACT	1325
DB	961	GGTTTCTGGCTAGGAGCAGCTGCTGTGCTGGAAGCAGCAGCACCCCTTTGGAACT	1020
QY	1326	TTCCAGTCACTCACTCTACCTTAATGGGTGAGGTACCAACAGTCTCTCCGCACTACC	1385
DB	1021	TTCCAGTCACTCACTCTACCTTAATGGGTGAGGTACCAACAGTCTCTCCGCACTACC	1080
QY	1386	ATCTTCCGACAGCAATACCTGCGGCGAGTGAAGATGTGGGCCAGCTCCCAAGCAGCTGT	1445
DB	1081	ATCTTCCGACAGCAATACCTGCGGCGAGTGAAGATGTGGGCCAGCTCCCAAGCAGCTGT	1140
QY	1446	TACAAGTTTGCCATCTCAGTCACTCACCGGCACTGTTATGGAGCTGTTATCATCGAG	1505
DB	1141	TACAAGTTTGCCATCTCAGTCACTCACCGGCACTGTTATGGAGCTGTTATCATCGAG	1200
QY	1506	GGCTTCTACGTTCTCTTTGATCGGGCCGAAAGCAATTTGGCTTTGCTCAGCGCTTCG	1565
DB	1201	GGCTTCTACGTTCTCTTTGATCGGGCCGAAAGCAATTTGGCTTTGCTCAGCGCTTCG	1260
QY	1566	CATGTGACGAGTGTGATTCAGGACGCGAGCGTGAAGGCCCTTTTGTCACTTGGACATG	1625
DB	1261	CATGTGACGAGTGTGATTCAGGACGCGAGCGTGAAGGCCCTTTTGTCACTTGGACATG	1320
QY	1626	GAAGACTGTGGCTACAACTTTCCACAGACAGATCAGTCAACCTCATCACCATAGCTAT	1685
DB	1321	GAAGACTGTGGCTACAACTTTCCACAGACAGATCAGTCAACCTCATCACCATAGCTAT	1380
QY	1686	GTCAATGGCTGCCATCTGCGCCCTCTTTCATGCTGCCACTCTGCCCTCATGGTGTCACTGG	1745

QY 1326 TTCCAGTCACTCTACTCTACCTAATGGTGAGGTTTACCAACCAAGTCTCTCCCGCATCACC 1385
Db 946 TTCCAGTCACTCTACTCTACCTAATGGTGAGGTTTACCAACCAAGTCTCTCCCGCATCACC 1005
QY 1386 ATCCTTCGGCAGCAATACCTCGCGGCAGTGGAGATGTGGCCAGGTCCCAAGAGACTGT 1445
Db 1006 ATCTTCGGCAGCAATACCTCGCGGCAGTGGAGATGTGGCCAGGTCCCAAGAGACTGT 1065
QY 1446 TACAAGTTTGGCATCTCACAGTCATCCACGGGCAGTGTATGGAGCTGTATCATCATGGAG 1505
Db 1066 TACAAGTTTGGCATCTCACAGTCATCCACGGGCAGTGTATGGAGCTGTATCATCATGGAG 1125
QY 1506 GGCTTCTACGTTGTCTTTGATGGGCCCGGAAACAAATGGCTTTGTGTGTCAGGCTTGC 1565
Db 1126 GGCTTCTACGTTGTCTTTGATGGGCCCGGAAACAAATGGCTTTGTGTGTCAGGCTTGC 1185
QY 1566 CATGTGCACGATGAGTTTCAGGACGCGAGCGGTGGAGGCCCTTTTGTACCTTGGACATG 1625
Db 1186 CATGTGCACGATGAGTTTCAGGACGCGAGCGGTGGAGGCCCTTTTGTACCTTGGACATG 1245
QY 1626 GAAGACTGTGGCTTACAACATTCACAGACAGATGAGTCAACCTTCATGACCATAGCCCTAT 1685
Db 1246 GAAGACTGTGGCTTACAACATTCACAGACAGATGAGTCAACCTTCATGACCATAGCCCTAT 1305
QY 1686 GTCATGGCTGCCATCTGCGCCCTCTTCATGTGCCACTCTGCCACTCTGCCCTCATGTTGTGTCAGTGG 1745
Db 1306 GTCATGGCTGCCATCTGCGCCCTCTTCATGTGCCACTCTGCCACTCTGCCCTCATGTTGTGTCAGTGG 1365
QY 1746 CGCTGCCCTCCGCTCGCTCGCCAGCAGCATGATGACTTGTCTGATGACATCTCCCTGCTG 1805
Db 1366 CGCTGCCCTCCGCTCGCTCGCCAGCAGCATGATGACTTGTCTGATGACATCTCCCTGCTG 1425
QY 1806 AAGTGGAGAGGCCATGGGCAAGATAGAGATTCCTCCCTGGACACACCTCCGTTGTCTCA 1865
Db 1426 AAGTGGAGAGGCCATGGGCAAGATAGAGATTCCTCCCTGGACACACCTCCGTTGTCTCA 1485
QY 1866 CTTTGGTCAAGTAGGAGACACAGATGGCAGCTGTGGCCAGAGACCTCAGGACCCCTCC 1925
Db 1486 CTTTGGTCAAGTAGGAGACACAGATGGCAGCTGTGGCCAGAGACCTCAGGACCCCTCC 1545
QY 1926 CCACCCACCAATGCTCTGCTTGTGAGAGAGGAAAGGCTGGCAAGTGGGTTCAG 1985
Db 1546 CCACCCACCAATGCTCTGCTTGTGAGAGAGGAAAGGCTGGCAAGTGGGTTCAG 1605
QY 1986 GGAAGTACCTGTAGGAAACAGAAAGAGAAAGAAAGCACTGTGCTGGCGGAATACT 2045
Db 1606 GGAAGTACCTGTAGGAAACAGAAAGAGAAAGAAAGCACTGTGCTGGCGGAATACT 1665
QY 2046 CTTGGTCAACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 2105
Db 1666 CTTGGTCAACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 1725
QY 2106 TTGTCCACCATTCCTTTAAATTTCTCAACCCCAAGATTTCTCTTTTCTTAGTTTCAGAA 2165
Db 1726 TTGTCCACCATTCCTTTAAATTTCTCAACCCCAAGATTTCTCTTTTCTTAGTTTCAGAA 1785
QY 2166 GTACTGGCATCACAGCAGGTTACCTTTGGCGTGTGCTCCCTGTGGTACCCCTGGCAGAGAG 2225
Db 1786 GTACTGGCATCACAGCAGGTTACCTTTGGCGTGTGCTCCCTGTGGTACCCCTGGCAGAGAG 1845
QY 2226 AGACCAAGCTTTTCCCTGCTGGCCAAAGTCAAGTAGGAGAGATGACAGTTTGTCTATT 2285
Db 1846 AGACCAAGCTTTTCCCTGCTGGCCAAAGTCAAGTAGGAGAGATGACAGTTTGTCTATT 1905
QY 2286 TGCTTTAGAGACAGGAGCTGTATAAACAAGCCCTAATTTGGTGCAGAGATTGGCTCTTTGA 2345
Db 1906 TGCTTTAGAGACAGGAGCTGTATAAACAAGCCCTAATTTGGTGCAGAGATTGGCTCTTTGA 1965
QY 2346 A 2346
Db 1966 A 1966

RESULT 5
US-09-548-367D-5
; Sequence 5, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: "THEROF"
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-367D-5

Query Match 80.1%; Score 1881; DB 4; Length 1977;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1966; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

QY 306 ATGCCCCAAGCCCTCCCTGGCTCTCTGCTGTGGATGGCGCGGAGTGTCTGCTGCCAC 365
Db 1 ATGCCCCAAGCCCTCCCTGGCTCTCTGCTGTGGATGGCGCGGAGTGTCTGCTGCCAC 60
QY 366 GGCACCCAGCAGCGGATCGGGCTGCCCTCTGCGCAGCGGCTGGGGGGGCCCCCTGGGG 425
Db 61 GGCACCCAGCAGCGGATCGGGCTGCCCTCTGCGCAGCGGCTGGGGGGGCCCCCTGGGG 120
QY 426 CTGCGGCTGCCCGGAGACCGAGCCGAGAGCCGAGAGCCGCGGAGGCGGAGGCGAGCTTT 485
Db 121 CTGCGGCTGCCCGGAGACCGAGCCGAGAGCCGAGAGCCGCGGAGGCGGAGGCGAGCTTT 180
QY 486 GTGAGATGTTGGACAACCTGAGGGGCAAGTTCGGGCGAGGCTTACTAGTGGAGATGACC 545
Db 181 GTGAGATGTTGGACAACCTGAGGGGCAAGTTCGGGCGAGGCTTACTAGTGGAGATGACC 240
QY 546 GTGGGCGACCCCGCGCAGACGCTCAACATCTCTGGTGGATACAGGACGAGTAACCTTGA 605
Db 241 GTGGGCGACCCCGCGCAGACGCTCAACATCTCTGGTGGATACAGGACGAGTAACCTTGA 300
QY 606 GTGGGCTGTCGCCCGCCACCCCTTCTGCTGCTGCTTACTACAGAGGCGAGCTGTCCAGCACA 665
Db 301 GTGGGCTGTCGCCCGCCACCCCTTCTGCTGCTGCTTACTACAGAGGCGAGCTGTCCAGCACA 360
QY 666 TACCGGACCTCCCGAAGGTTGTATGTGCCCTACACCCAGGCGCAAGTGGGAAGGGAG 725
Db 361 TACCGGACCTCCCGAAGGTTGTATGTGCCCTACACCCAGGCGCAAGTGGGAAGGGAG 420
QY 726 CTGGGCGACCGAGCTGGTAAAGCATCCCGCATGGCCCCCAACGCTACTGTGCGTGCACCATTT 785
Db 421 CTGGGCGACCGAGCTGGTAAAGCATCCCGCATGGCCCCCAACGCTACTGTGCGTGCACCATTT 480
QY 786 GCTGCCATCACTGAATCAGACAAGTTCTTCTCATCAACCGGCTCCAACTGGGAAGGCACTCCTG 845
Db 481 GCTGCCATCACTGAATCAGACAAGTTCTTCTCATCAACCGGCTCCAACTGGGAAGGCACTCCTG 540
QY 846 GGGCTGGCCTATGCTGAGATTCGCCAGCTGTACGACTTCCCTGGAGCCCTTTCTTTTGAATCT 905
Db 541 GGGCTGGCCTATGCTGAGATTCGCCAG- - - - - 566
QY 906 CTGTAAGACAGACCCACGTTTCCCAACCTTCTTCCCTGCGAGCTTTGTGGTGGCTGGCTTC 965

Db 567 -----||||| 585
QY 966 CCCTCAACAGTCTGAAGTCTGGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC 1025
Db 586 CCCTCAACAGTCTGAAGTCTGGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC 645
QY 1026 GACCACTCGCTGACACAGCAGTCTCTGGTATACACCCATCCGCGGGAGTGGTATTAT 1085
Db 646 GACCACTCGCTGACACAGCAGTCTCTGGTATACACCCATCCGCGGGAGTGGTATTAT 705
QY 1086 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGATCTGAAAATGGAGTGAAGGAG 1145
Db 706 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGATCTGAAAATGGAGTGAAGGAG 765
QY 1146 TACAACATATGACAAAGACATTTGGAGCAGTGGCACACCAACCTTCCTTTGCCCAAGAAA 1205
Db 766 TACAACATATGACAAAGACATTTGGAGCAGTGGCACACCAACCTTCCTTTGCCCAAGAAA 825
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QY 1566 CATGTGCACGATGAGTTTCAGGACGGCAGCGTGGAGGCGCTTTGTACCTTGGACATG 1625
Db 1186 CATGTGCACGATGAGTTTCAGGACGGCAGCGTGGAGGCGCTTTGTACCTTGGACATG 1245
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Db 1306 GTCATGGCTGCCATCTCGGCCCTCTTCATGCTGCACTCTGCCCTCATGGTGTGTCAGTGG 1365
QY 1746 CGCTGCCCTCGCTCGCTCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTCGTG 1805
Db 1366 CGCTGCCCTCGCTCGCTCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTCGTG 1425
QY 1806 AAGTGAGAGGCCCATGGGAGAGATAGAGATTTCCCTTGGACACACACCTCCCGTGGTTCA 1865
Db 1426 AAGTGAGAGGCCCATGGGAGAGATAGAGATTTCCCTTGGACACACACCTCCCGTGGTTCA 1485
QY 1866 CTTTGGTTCACAAGTGAAGACACAGATGGCACCTGTGGCCAGCAGCCTCAGAGACCTCC 1925
Db 1486 CTTTGGTTCACAAGTGAAGACACAGATGGCACCTGTGGCCAGCAGCCTCAGAGACCTCC 1545
QY 1926 CCACCCACCAATGCCTCTGCTTTGATGGAGAGAAAGGCTGGCAAGTGGGTTCCAG 1985
Db 1546 CCACCCACCAATGCCTCTGCTTTGATGGAGAGAAAGGCTGGCAAGTGGGTTCCAG 1605
QY 1986 GGACTGTACCTGTAGGAACAGAAAGAGAGAAAGCACTCTGCTGGCGGGAATACT 2045
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Db 1606 GGACTGTACCTGTAGGAACAGAAAGAGAAAGCACTCTGCTGGCGGAATACT 1665
QY 2046 CTTGGTCACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 2105
Db 1666 CTTGGTCACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 1725
QY 2106 TTGTCCACCATTCTCTTAAATTTCCAAACCCAAAGTATTCCTCTTTCTTTAGTTTCAGAA 2165
Db 1726 TTGTCCACCATTCTCTTAAATTTCCAAACCCAAAGTATTCCTCTTTCTTTAGTTTCAGAA 1785
QY 2166 GTACTGTCATCACAGCAGGTTACCTTTGGCGTGTGTCCTGTGTCACCTGGCAGAGAG 2225
Db 1786 GTACTGTCATCACAGCAGGTTACCTTTGGCGTGTGTCCTGTGTCACCTGGCAGAGAG 1845
QY 2226 AGACCAAGCTTGTTCCTCTGCTGCCAAAGTCAGTAGGAGGATGCACAGTTCCTATT 2285
Db 1846 AGACCAAGCTTGTTCCTCTGCTGCCAAAGTCAGTAGGAGGATGCACAGTTCCTATT 1905
QY 2286 TGCTTTAGACAGAGGGACTGTATAAACAAGCCTTAACATTTGGTGCAAGATTTGCCTCTTGA 2345
Db 1906 TGCTTTAGACAGAGGGACTGTATAAACAAGCCTTAACATTTGGTGCAAGATTTGCCTCTTGA 1965
QY 2346 A 2346
Db 1966 A 1966
RESULT 6
US-09-009-191-3
; Sequence 3, Application US/09009191
; Patent No. 6319689
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID
; APPLICANT: CHAPMAN, CONRAD
; APPLICANT: MURPHY, KAY
; APPLICANT: SMITH, TRUDI
; TITLE OF INVENTION: ASP2
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,191
; FILING DATE: 20-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9701684.4
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2370 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-009-191-3

Query Match 78.2%; Score 1835.4; DB 4; Length 2370;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1856; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY	477	GGCAGCTTTGTGGAGATGTTGACAACTGAGGGGCAAGTCGGGGCAGGGCTACTACGTG	536
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QY	537	GAGATGACCGTGGGAGCCCCCGCAGACGCTCAACATCTCTGGTGGATACAGGCAGCAGT	596
Db	61	GAGATGACCGTGGGAGCCCCCGCAGACGCTCAACATCTCTGGTGGATACAGGCAGCAGT	120
QY	597	AACCTTTGAGTGGGTGCTGCCGCCACCCCTTCTGCTGCTACTACAGAGGCGAGGTG	656
Db	121	AACCTTTGAGTGGGTGCTGCCGCCACCCCTTCTGCTGCTACTACAGAGGCGAGGTG	180
QY	657	TCCAGCAGATACCGGAGCTCCGGAAGGTGTGTATGTGCTTACACCCAGGCGCAAGTGG	716
Db	181	TCCAGCAGATACCGGAGCTCCGGAAGGTGTGTATGTGCTTACACCCAGGCGCAAGTGG	240
QY	717	GAAGGGAGCTGGGACGACCTGTAAGCATCCCCCATGCCCAAGCTCAGCTGTGCTG	776
Db	241	GAAGGGAGCTGGGACGACCTGTAAGCATCCCCCATGCCCAAGCTCAGCTGTGCTG	300
QY	777	GCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCAACAGGCTCCAACTGGAA	836
Db	301	GCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCAACAGGCTCCAACTGGAA	360
QY	837	GGCATCTGGGGCTGGCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCTTTC	896
Db	361	GGCATCTGGGGCTGGCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCTTTC	420
QY	897	TTTGACTCTCTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGACGCTTTGTGT	956
Db	421	TTTGACTCTCTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGACGCTTTGTGT	480
QY	957	GCTGGCTTCCCGCTCAACAGCTCTGAAGTCTGGGCTCTCTCGGAGGAGCATGATCAT	1016
Db	481	GCTGGCTTCCCGCTCAACAGCTCTGAAGTCTGGGCTCTCTCGGAGGAGCATGATCAT	540
QY	1017	GGAGTATCGACCACTGCTGTACACAGGAGCTCTCTGGTATACACCCATCCGGCGGAG	1076
Db	541	GGAGTATCGACCACTGCTGTACACAGGAGCTCTCTGGTATACACCCATCCGGCGGAG	600
QY	1077	TGGTATTATGAGGTGATCATTTGCGGGTGGAGATCAATGACAGGATCTGAAATGGAC	1136
Db	601	TGGTATTATGAGGTGATCATTTGCGGGTGGAGATCAATGACAGGATCTGAAATGGAC	560
QY	1137	TGCAAGGAGTACAATATGACAAGAGCATTTGGACAGTGGCACCCACCACTTCGTTTG	1196
Db	661	TGCAAGGAGTACAATATGACAAGAGCATTTGGACAGTGGCACCCACCACTTCGTTTG	720
QY	1197	CCCAAGAAGTGTGAGCTGAGTCAATCCATCAAGGAGCTCTCCACGAGAGAG	1256
Db	721	CCCAAGAAGTGTGAGCTGAGTCAATCCATCAAGGAGCTCTCCACGAGAGAG	780
QY	1257	TTCCCTGATGTTCTGCTGAGAGAGCAGCTGTGTGCTGGCAAGCAGGACCAACCCCT	1316
Db	781	TTCCCTGATGTTCTGCTGAGAGAGCAGCTGTGTGCTGGCAAGCAGGACCAACCCCT	840
QY	1317	TGGAACATTTTCCAGTCACTCTACCTAATGGGTGAGGTTACCAACAGTCCCTTC	1376
Db	841	TGGAACATTTTCCAGTCACTCTACCTAATGGGTGAGGTTACCAACAGTCCCTTC	900
QY	1377	GGCATCACCATCTTCCGAGCAATACCTGGCGCCAGTGGAGATGGGCCAGTCCCAA	1436
Db	901	GGCATCACCATCTTCCGAGCAATACCTGGCGCCAGTGGAGATGGGCCAGTCCCAA	960
QY	1437	GACGACTGTTTACAGTTTCCCATCTCACAGTCAATCCAGGCGACTGTTATGGAGCTGT	1496
Db	961	GACGACTGTTTACAGTTTCCCATCTCACAGTCAATCCAGGCGACTGTTATGGAGCTGT	1020

QY	1497	ATCATGGAGGGCTTCTACGTTGTCTTTGATGCGGGCCGAAACGAATTTGGCTTTGCTGTC	1556
Db	1021	ATCATGGAGGGCTTCTACGTTGTCTTTGATGCGGGCCGAAACGAATTTGGCTTTGCTGTC	1080
QY	1557	AGCGCTTGCCATGTGACAGATGAGTTTCAGGACGCGAGCGGTGGAAGGCCCTTTTGTAC	1616
Db	1081	AGCGCTTGCCATGTGACAGATGAGTTTCAGGACGCGAGCGGTGGAAGGCCCTTTTGTAC	1140
QY	1617	TTGGACATGGAAGACTGTGGCTCAACATTCACAGACAGATGACTCAACCCCTCATCAC	1676
Db	1141	TTGGACATGGAAGACTGTGGCTCAACATTCACAGACAGATGACTCAACCCCTCATCAC	1200
QY	1677	ATAGCTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1736
Db	1201	ATAGCTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1260
QY	1737	TGTCAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1796
Db	1261	TGTCAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1320
QY	1797	TCCCTGCTGAAGTGAAGGAGGCCCATGGCAGAGATAGAGATTTCCCTT-GGACCAACCT	1855
Db	1321	TCCCTGCTGAAGTGAAGGAGGCCCATGGCAGAGATAGAGATTTCCCTTGGGACCAACCT	1380
QY	1856	CCGTGGTTTCACTTTGGTCAACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGACCTC	1915
Db	1381	CCGTGGTTTCACTTTGGTCAACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGACCTC	1440
QY	1916	AGGACCTTCCCAACCCACCAATGGCTTCTGCTTGTGAGAGAGAAAGGCTGGCAAG	1975
Db	1441	AGGACCTTCCCAACCCACCAATGGCTTCTGCTTGTGAGAGAGAAAGGCTGGCAAG	1500
QY	1976	TGGGTTTCAGAGGACTGTACCTGTAGGAAACAGAAAGAGAAAGAGAGAGAGAGAGAG	2035
Db	1501	TGGGTTTCAGAGGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGAGAGAGAGAGAG	1360
QY	2036	CGGGAATACTCTTTGGTCACTCAAAATTAAGTCGGGAAATTTCTGCTGTTGAAACTTCAG	2095
Db	1561	CGGGAATACTCTTTGGTCACTCAAAATTAAGTCGGGAAATTTCTGCTGTTGAAACTTCAG	1620
QY	2096	CCCTCAACCTTTGTCACCAATTCCTTTAAATTTCCCAACCCAAAGATTTCTTCTTTCTTT	2155
Db	1621	CCCTCAACCTTTGTCACCAATTCCTTTAAATTTCCCAACCCAAAGATTTCTTCTTTCTTT	1680
QY	2156	AGTTTTCAGAAGTACTGGCATCACACGAGGTTTACCTTTGGCGTGTCTCCCTGTGGTACCCCT	2215
Db	1681	AGTTTTCAGAAGTACTGGCATCACACGAGGTTTACCTTTGGCGTGTCTCCCTGTGGTACCCG	1740
QY	2216	GGCAG	2275
Db	1741	GGCAG	1800
QY	2276	GTTTCTATTTCTGCTTTAGAGACAGGAGGACTGTATTAACAGGCTTACATTGGTGCAGAG	2335
Db	1801	GTTTCTATTTCTGCTTTAGAGACAGGAGGACTGTATTAACAGGCTTACATTGGTGCAGAG	1860
QY	2336	TGCCTCTTGAATTT 2348	
Db	1861	TGCCTCTTGAATTT 1873	

RESULT 7
US-09-548-372D-7
; Sequence 7, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548, 372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493

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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-548-372D-7

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	Query Match	46.0%;	Score 1550;	DB 4;	Length 2043;
	Best Local Similarity	87.9%;	Pred. No. 0;		
	Matches 1794;	Conservative	0;	Mismatches 235;	Indels 13; Gaps
Qy	306	ATGGCCCAAGCCCTGCCCCTGCTCTGCTGTGGATGGCGCGGGAGTGCTGCTGCTGCCAC	365		
Db	1	ATGGCCCAAGCGCTGCACTGGCTCTGCTATATGGGTGGGCTCGGAATGCTGCTGCTGCCAG	60		
Qy	366	GGCACACGACACGGCATCCGGCTGCGCCCTGCGCAGCGCCTGGGGGGGGCCCCCTGGGG	425		
Db	61	GAACCCATCTCGGCATCCGGCTGCCCTTCGACGGCCTTGGCAGGCCACCCCTGGGC	120		
Qy	426	CTGGCGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGGAGCGCTTT	485		
Db	121	CTGAGGCTGCCCGGGAGACTGACGAGAAATCGGAGGAATCGGCGGAGGCGAGCTTT	180		
Qy	486	GTGAGATGTTGACAACTGAGGGCAAGTCGGGGCAGGCTACTACTGGAGATGACC	545		
Db	181	GTGAGATGTTGGAACAACCTGAGGGAAGTCCGGCCAGGGCTACTATGTGGAGATGACC	240		
Qy	546	GTGGGACGCCCGCCGACAGCCTCAACATCTGTGTGATACAGGCAGCAGTAACCTTTCGA	605		
Db	241	GTAGGACGCCCGCCACAGACGCTCAACATCTGTGTGGACACGGCAGTAGTAACCTTTCGA	300		
Qy	606	GTGGGTGCTGCCCGCCACCCTTCTGCATCGCTACTACAGAGGACGCTGTCCAGACACA	665		
Db	301	GTGGGGCTGCCCGACACACCTTCTGCATCGCTACTACAGAGGACGCTGTCCAGCACA	360		
Qy	666	TACGGGACCTCCGGAGGGTGTATGTGCCCTACACCGAGGCAAGTGGGAGGGGAG	725		
Db	361	TATCGAGACCTCCGAAGGGTGTATGTGCCCTACACCGAGGCAAGTGGGAGGGGGA	420		
Qy	726	CTGGGACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACGTGCGTGCCCAACAT	785		
Db	421	CTGGGACCGACCTGGTGAGCATCCCTCATGGCCCCAACGTCACGTGCGTGCCCAACAT	480		
Qy	786	GCTGCCATCACTGAATCAGACAAGTTCTTCATACGCGCTCCAACCTGGGAGGCAATCTG	845		
Db	481	GCTGCCATCACTGAATCGGACAAGTTCTTCATATGTTCCAACTGGGAGGGCAATCTA	540		
Qy	846	GGGTGGCCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCCCTTCTTTGACTCT	905		
Db	541	GGGTGGCCTATGCTGAGATTGCCAGGCTGACGACTCTTTGGAGCCCTTCTTTGACTCC	600		
Qy	906	CTGTAAAGCAGACCCACGTTCCCAACCTCTTCCTCCCTGCAGCTTTGTGCTGGCTTC	965		
Db	601	CTGTGAAGCAGACCCACATTTCCCAACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTC	660		
Qy	966	CCCTCAACCACTGTGAAGTCTGGCTCTTCCAGGAGGACATGATCATTTGGAGGTATC	1025		
Db	661	CCCTCAACCACTGTGAAGTCTGGCTCTTCCAGGAGGACATGATCATTTGGTGGTATC	720		
Qy	1026	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGAGTGGTATTAT	1085		
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGAGTGGTATTAT	780		
Qy	1086	GAGGTGATCATTTGTCCGGGTGGAGATCAATGGACAGGATCTTGAAATGGACTGCAAGGAG	1145		

Db	781	GAAGTGATCAATTGTACGCTGTGGAAATCAATAGTGTCAAGATCGATTCGAAGGAG	840
Qy	1146	TACAACATATGACAAGAGCATTTGTGGACAGTGGCACACCAACATCTTGTTCGCCAAGAAA	1205
Db	841	TACAACATACGACAAGAGCATTTGTGGACAGTGGGACACCAACATCTCGCTTGCCTTGC	900
Qy	1206	GTGTTTGAAGCTGAGTCAATTCATCAAGGAGGCTCTCTCCACGGAGAAGTTTCCTGTGA	1265
Db	901	GTAATTGAAGCTCGCTCAAGTCCATCAAGGAGGCTCTCTCGACGAGAAAGTTCCCGGAT	960
Qy	1266	GGTTTCTCGCTAGGAGAGAGCTGTGTGCTGGCAAGGAGGACACCAACCCCTTGGACATT	1325
Db	961	GGCTTTTGGCTAGGGAGAGCTGTGTGCTGGCAAGGAGGACACCAACCCCTTGGACATT	1020
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Db	1021	TTCCAGCTCATTTCACTTTACCTCATGTGGTGTGAAGTCAACCAATCACTCTCTCCGATCAC	1080
Qy	1386	ATCCTTCCGAGCAATACCTTGGGGCAGTGTGAAGATGTGGCACGTGCCAAGAGACTGT	1445
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Qy	1446	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTATGGGAGCTGTATCATGGAG	1505
Db	1141	TACAAGTTTGGCTGTCTCACAGTCATCCACGGGCACTGTATGGGAGCCGTCTCATGGAA	1200
Qy	1506	GGCTTCTACCTGTCTTTGATCGGGCCGAAAGCAATTTGGCTTTCGTCTCAGCGCTTGC	1565
Db	1201	GGTTTCTATGTCTGTTCGATCGAGCCCGAAAGCAATTTGGCTTTCGTCTCAGCGCTTGC	1260
Qy	1566	CATGTGCAGATGAGTTCAGGACGGGCGGTGGAAAGCCCTTTTGTCAACCTTGGACATG	1625
Db	1261	CATGTGCAGATGAGTTCAGGACGGGCGGAGTGGAAAGTTCCTTTTGTACGGACATG	1320
Qy	1626	GAAGACTGTGGCTACACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	1685
Db	1321	GAAGACTGTGGCTACACATTTCCACAGACAGATGAGTCAACCACTTATGACCATAGCCTAT	1380
Qy	1686	GTCATGGCTGCCATCTGGCGCCCTCTTCATGTCTGCCACTCTGCCTCATGTGTGTCACTGG	1745
Db	1381	GTCAATGGCGGCATCTGGCGCCCTCTTCATGTCTGGCCACTCTGCCTCATGTATGTCACTGG	1440
Qy	1746	CGCTGCTCTCGCTTGGCCAGCAGCATGATGATCTTGTGTGATGACATCTCCCTGCTGT	1805
Db	1441	CGCTGCTCTCGCTTGGCCAGCAGCATGATGATGATCTTGTGTGATGACATCTCCCTGCTGT	1500
Qy	1806	AAGTGAGAGGCCCATGGCAGAAAGATAGAGATTCCTCTGGACCACTCCCTCGTGGTTCA	1865
Db	1501	AAGTAAAGAGGCTCGTGGGCAGATGATGAGAGCGCCCTTGGACCACTCTGGTGTGTTC	1560
Qy	1866	CTTTTGTGTACA--AGTAGGAGACAGATGGCACTGTGGCCAGAGCACTCAGGACCTT	1923
Db	1561	CTTTTGTGTACATGATGGAGCTATCGATGTGTACCTTGTGGCCAGAGCACTCAGGACCT	1620
Qy	1924	CCCCACCCCAATGCTCTGCTTGTATGGAGAAGAAAGGCTGGCAAGTGGGTTTCC	1983
Db	1621	CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGCAAGCTGGSATTAC	1679
Qy	1984	AGGAGCTGTACCTGTAGGAACAAGAAAGAGAAAGAGCACTCTCTGTGGCGGAATA	2043
Db	1680	AGGGCTTGCACCTGTAGGACAGAGAGAGGGAAGGAGCGCTTCTGTGGCAGGAATA	1739
Qy	2044	CTCTTGTGTACCTCAAAATTTAAGTCGGGAAATTCGTCTGCTTGAACCTTCAGCCCTGAAC	2103
Db	1740	TCCTTAGGCACCAAACTTGAAT-TGGAAATTTTCTCTGCTTGAAGCTTCAGCCCTGACC	1798
Qy	2104	CTTTGTGCCAATTCCTTTAAATTCCTCAACCCCAAGTATCTCTCTTTTCTTGTAGTTTCAG	2163
Db	1799	CTCTGCCAGCA-TCTTTTAGAGTCTCCAACCTAAGATATCTTTATGTC--CTTCCAG	1854
Qy	2164	AAGTACTGGCATCACAGCAGTTACCTTTGGCGTGTGTCCCTGTGTACCTCTGGCAGAGA	2233
Db	1955	AAGTACTGGCGCTATACCTCAAGGCTACC-CGGCATGTGTCCCTGTGGTACCTCTGGCAGAGA	1913

Db 1501 AAGTAAGGAGGCTCGTGGGAGAGATGATGGAGACGCCCTGGACACATCTGGGTGGTTC 1560
Qy 1866 CTTTGGTGCACA--AGTAGGAGACACAGATGGCACCCTGTGGCCAGAGCACCTCAGGACCCT 1923
Db 1561 CTTTGGTGCATAGTGGAGCTATGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT 1620
Qy 1924 CCCACCCACCAATAGCTCTGCTTGTGAGAGAAAGGCTGGCAAGTGGGTTC 1983
Db 1621 CACCAACTGCCAATGCTTCTGGGTGACAGA-ACAGAGAAATCAGCAAGCTGATTAC 1679
Qy 1984 AGGACTGTACCTGTAGGAACAGAAAGAGAGAAAGACACTGTGCTGGGGGGAATA 2043
Db 1680 AGGCTTGCACCTGTAGGACACAGGAGGAGGAAGGAGCGCTTCTGGTGGCAGGAATA 1739
Qy 2044 CTCTGTGTCACCTCAAAATTTAAGTCGGGAAATCTGCTGTGAAACTTTCAGCCCTGAAC 2103
Db 1740 TCCTTAGGCAACCAAACTTGAGT-TGGAATTTTGTGCTTGAAGCTTCAGCCCTGACC 1798
Qy 2104 CTTTGTCCAGCATTCCTTTAAATTTCCAAACCAAGATTTCTTTTCTTAGTTTCAG 2163
Db 1799 CTCTGCCACGCA-TCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTC---CTTCCAG 1854
Qy 2164 AAGTACTGGCATCAGCAGGAGTTACCTTGGCGTGTGTCCCTGTGTGTTACCTTGGCAGAGA 2223
Db 1855 AAGTACTGGCGTCTACTCAGGCTACC-CGGCATGTCTCCCTGTGTGTACCTTGGCAGAGA 1913
Qy 2224 AGAGCAAAAGCTGCTTTCCTCTGTGGCCAAAGTCAGTAGGAGAGATGTCACAGTTTCCCTA 2283
Db 1914 AAGGCCAAATC-TCATTTCCCTGTGGCCAAAGTCAGCAGAGAAGGTG--AAGTTTCCCA 1970
Qy 2284 TTTGCTTTAGAGACAGGAGCTGTATAAACAAAGCCTAACATTTGGTGCAAGATTCGCTCTT 2343
Db 1971 GTTGTCTTAGTAGGAGCTGCAGACTCAAGCT-ACACTGCTACAAAGACTGCGTCTT 2029
Qy 2344 GA 2345
Db 2030 GA 2031

RESULT 9

US-09-548-372D-29
; Sequence 29, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548, 372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-29

Query Match 57.7%; Score 1355.8; DB 4: Length 1362;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1357; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 306 ATGCCCAAGCCCTGCCTGCTGCTGTGGATGGCGGGGAGTGTGCTGCCAC 365
|||||

Db 1 ATGCCCAAGCCCTGCCTGGCTCTCTGCTGTGATGGCGGGAGTGTCTGCCTGCCAC 60
Qy 366 GGCACCCAGACGCGCATCCGGCTCGCCCTGGCAGCGCCCTGGGGGGCGCCCTGGG 425
Db 61 GGCACCCAGACGCGCATCCGGCTCGCCCTGGCAGCGCCCTGGGGGGCGCCCTGGG 120
Qy 426 CTGGGCTGCCCCGGGAGACCGAGAGAGCCGAGGAGCCCGGCGGAGGCGGAGGCTTT 485
Db 121 CTGGGCTGCCCCGGGAGACCGAGAGAGCCGAGGAGCCCGGCGGAGGCGGAGCTTT 180
Qy 486 GTGAGATGTGGACAACCTGTAGGGGCAAGTGGGGGAGGCTTACTAGTGGAGATGACC 545
Db 181 GTGAGATGTGGACAACCTGTAGGGGCAAGTGGGGGAGGCTTACTAGTGGAGATGACC 240
Qy 546 GTGGGAGCCCCCGCAGACGCTCAACATCTCTGTGTGATACAGCAGCAGTAACCTTGC 605
Db 241 GTGGGAGCCCCCGCAGACGCTCAACATCTCTGTGTGATACAGCAGCAGTAACCTTGC 300
Qy 606 GTGGGCTGCTGCCCCCGCAGACGCTTCTCTGATGCTTACTACCAGAGGCGAGCTTCCAGCACA 665
Db 301 GTGGGCTGCTGCCCCCGCAGACGCTTCTCTGATGCTTACTACCAGAGGCGAGCTTCCAGCACA 360
Qy 666 TACCGGACCTCCGGAAGGCTGTATGTGCCCTTACACCCAGGCAAGTGGGAAGGGAG 725
Db 361 TACCGGACCTCCGGAAGGCTGTATGTGCCCTTACACCCAGGCAAGTGGGAAGGGAG 420
Qy 726 CTGGGACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACCTGCTGCCCAACATT 785
Db 421 CTGGGACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACCTGCTGCCCAACATT 480
Qy 786 GCTGCCATCACTGAATCAGACAAGTTCTTCAACAGGCTCCAACCTGGGAAGGCGATCCTG 845
Db 481 GCTGCCATCACTGAATCAGACAAGTTCTTCAACAGGCTCCAACCTGGGAAGGCGATCCTG 540
Qy 846 GGGCTGCCCTATGCTGAGATTTGCCAGGCTGACGACTCCCTTGGAGCCTTTCTTTGACTCT 905
Db 541 GGGCTGCCCTATGCTGAGATTTGCCAGGCTGACGACTCCCTTGGAGCCTTTCTTTGACTCT 600
Qy 906 CTGGTAAAGCAGACCCACGTTTCCCAACCTCTTCTCCCTGCGAGCTTTGTGGTGGCTTC 965
Db 601 CTGGTAAAGCAGACCCACGTTTCCCAACCTCTTCTCCCTGCGAGCTTTGTGGAGTATC 660
Qy 966 CCCCTCAACAGCTCTGAAGTCTGGCCTCTGTGGAGGAGGAGCATGATCATTTGGAGTATC 1025
Db 661 CCCCTCAACAGCTCTGAAGTCTGGCCTCTGTGGAGGAGGAGCATGATCATTTGGAGTATC 720
Qy 1026 GACCACTGCTGTACACAGGAGCTCTCTGATATACACCCATCCCGGGGAGTGGTATTAT 1085
Db 721 GACCACTGCTGTACACAGGAGCTCTCTGATATACACCCATCCCGGGGAGTGGTATTAT 780
Qy 1086 GAGTGTATCATTTGGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 1145
Db 781 GAGTGTATCATTTGGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 840
Qy 1146 TACAATCATGACAAGAGCATTTGTGGACATGGGACACCAACCTTCTGTTCCCAAGAAA 1205
Db 841 TACAATCATGACAAGAGCATTTGTGGACATGGGACACCAACCTTCTGTTCCCAAGAAA 900
Qy 1206 GTGTTTCAAGCTGACGTCATAATCCATCAAGGACGCTCTCCAGGAGAAAGTTCCTGTAT 1265
Db 901 GTGTTTCAAGCTGACGTCATAATCCATCAAGGACGCTCTCCAGGAGAAAGTTCCTGTAT 960
Qy 1266 GGTTCCTGGCTAGGAGAGCAGCTGCTGTGCTGGCAAGCAGCAGCACCCTTGGAAACATT 1325
Db 961 GGTTCCTGGCTAGGAGAGCAGCTGCTGTGCTGGCAAGCAGCAGCACCCTTGGAAACATT 1020
Qy 1326 TTCCAGTCTATCTCAGCTTACCTAATGGTGAGGTTTACCACCAAGCTCCTTCCCGATCACC 1385
Db 1021 TTCCAGTCTATCTCAGCTTACCTAATGGTGAGGTTTACCACCAAGCTCCTTCCCGATCACC 1080
Qy 1386 ATCCTTCCGAGCAATACCTGCGGCCAGTGGAAAGATGTGGCCACGTTGCCCAAGAGACTGT 1445
Db 1081 ATCCTTCCGAGCAATACCTGCGGCCAGTGGAAAGATGTGGCCACGTTGCCCAAGAGACTGT 1140

QY	306	ATGGCCCAAGCCCTGCGCTTCTCTGTGTGGATGGCGCGGGAGTCTGCCTGCCAC	365
Db	1	ATGCCCAAGCCCTGCGCTTCTGTGTGGATGGCGCGGGAGTCTGCCTGCCAC	60
		ATGCCCAAGCCCTGCGCTTCTGTGTGGATGGCGCGGGAGTCTGCCTGCCAC	60
QY	366	GGCACCACGACGGCATCCGGCTGCCCTGCGCACGCGCCTGGGGGGGCCCCCTCGGG	425
Db	61	GGCACCACGACGGCATCCGGCTGCCCTGCGCACGCGCCTGGGGGGGCCCCCTCGGG	120
		GGCACCACGACGGCATCCGGCTGCCCTGCGCACGCGCCTGGGGGGGCCCCCTCGGG	120
QY	426	CTGCGGCTCCCCGGGAGACCGACAAGAGCCCGAGGAGCCCGCGGAGGGGACGCTTT	485
Db	121	CTGCGGCTCCCCGGGAGACCGACAAGAGCCCGAGGAGCCCGCGGAGGGGACGCTTT	180
		CTGCGGCTCCCCGGGAGACCGACAAGAGCCCGAGGAGCCCGCGGAGGGGACGCTTT	180
QY	486	GTGGAGATGGTGGACAAACCTGAGGGGCAAGTCGGGGCAGGCGTACTAGTGGAGATGACC	545
Db	181	GTGGAGATGGTGGACAAACCTGAGGGGCAAGTCGGGGCAGGCGTACTAGTGGAGATGACC	240
		GTGGAGATGGTGGACAAACCTGAGGGGCAAGTCGGGGCAGGCGTACTAGTGGAGATGACC	240
QY	546	GTGGGACGCCCCCGGACAGCGCTCAACATCTCTGGTGGATCAGGACGACGTAACCTTGCA	605
Db	241	GTGGGACGCCCCCGGACAGCGCTCAACATCTCTGGTGGATCAGGACGACGTAACCTTGCA	300
		GTGGGACGCCCCCGGACAGCGCTCAACATCTCTGGTGGATCAGGACGACGTAACCTTGCA	300
QY	606	GTGGTGTCTGCCCGCCACCCCTTCTGTGCATCGCTACTACCAGAGCGAGCTGTCCAGCAC	665
Db	301	GTGGTGTCTGCCCGCCACCCCTTCTGTGCATCGCTACTACCAGAGCGAGCTGTCCAGCAC	360
		GTGGTGTCTGCCCGCCACCCCTTCTGTGCATCGCTACTACCAGAGCGAGCTGTCCAGCAC	360
QY	666	TACCGGGACCTCGGGAAGGGTGTGTATGTGCCCTACACCCAGGCGAAGTGGGAAGGGGAG	725
Db	361	TACCGGGACCTCGGGAAGGGTGTGTATGTGCCCTACACCCAGGCGAAGTGGGAAGGGGAG	420
		TACCGGGACCTCGGGAAGGGTGTGTATGTGCCCTACACCCAGGCGAAGTGGGAAGGGGAG	420
QY	726	CTGGGACACGACCTGTGTAAAGCATCCCCATGCCGCCAACGTCAGCTGCGTGCACCAAT	785
Db	421	CTGGGACACGACCTGTGTAAAGCATCCCCATGCCGCCAACGTCAGCTGCGTGCACCAAT	480
		CTGGGACACGACCTGTGTAAAGCATCCCCATGCCGCCAACGTCAGCTGCGTGCACCAAT	480
QY	786	GCTGCCATCACTGAATCAGACAAGTCTTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	845
Db	481	GCTGCCATCACTGAATCAGACAAGTCTTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
		GCTGCCATCACTGAATCAGACAAGTCTTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
QY	846	GGGCTGGCCTATGCTCAGATTGCCAGGGCTGAGAGCTCCCTGGAGCCCTTCTTTGACTCT	905
Db	541	GGGCTGGCCTATGCTCAGATTGCCAGGGCTGAGAGCTCCCTGGAGCCCTTCTTTGACTCT	600
		GGGCTGGCCTATGCTCAGATTGCCAGGGCTGAGAGCTCCCTGGAGCCCTTCTTTGACTCT	600
QY	906	CTGGTAAAGCAGACCCACGCTTCCCAACCTCTTCTCCCTGACGCTTTGTGGTGGCTTC	965
Db	601	CTGGTAAAGCAGACCCACGCTTCCCAACCTCTTCTCCCTGACGCTTTGTGGTGGCTTC	660
		CTGGTAAAGCAGACCCACGCTTCCCAACCTCTTCTCCCTGACGCTTTGTGGTGGCTTC	660
QY	966	CCCTCAACCAAGTCTGAAGTGTGGCCTCTGTGCGAGGGAGCATGATCATTTGGAGGTATC	1025

Query Match 57.7%; Score 1355.8; DB 4; Length 1380;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1357; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 306 ATGGCCCAAGCCCTGCGCTCTGCTGTGGATGGCGCGGAGTGTGCTGCCAC 365
Db 1 ATGGCCCAAGCCCTGCGCTCTGCTGTGGATGGCGCGGAGTGTGCTGCCAC 60

QY 366 GGCACCCAGCAGCCGCTGCGCTGCGCAGCGGCTGGGGCGGCCCTGGGG 425
Db 61 GGCACCCAGCAGCCGCTGCGCTGCGCAGCGGCTGGGGCGGCCCTGGGG 120

QY 426 CTGCGGCTGCGCCCGGAGACCGAGAGAGCCGAGGAGCCGCGGAGGCGAGCTTT 485
Db 121 CTGCGGCTGCGCCCGGAGACCGAGAGAGCCGAGGAGCCGCGGAGGCGAGCTTT 180

QY 486 GTGGAGATGTGGACACCTGAGGGCAAGTCGGGCGAGGCTACTACGTGGAGATGACC 545
Db 181 GTGGAGATGTGGACACCTGAGGGCAAGTCGGGCGAGGCTACTACGTGGAGATGACC 240

QY 546 GTGGGACGCCCGCGCAGACGCTCAACATCTGTTGGATACAGGACGAGTAACTTTGCA 605
Db 241 GTGGGACGCCCGCGCAGACGCTCAACATCTGTTGGATACAGGACGAGTAACTTTGCA 300

QY 606 GTGGGTGCTGCGCCCGCAGCCCTTCTGCTGCTACTACAGAGGCGAGCTGTCCAGCACA 665
Db 301 GTGGGTGCTGCGCCCGCAGCCCTTCTGCTGCTACTACAGAGGCGAGCTGTCCAGCACA 360

QY 666 TACCGGACCTCCGGAGGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGAGGGAG 725
Db 361 TACCGGACCTCCGGAGGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGAGGGAG 420

QY 726 CTGGGACCCAGCTGTGAAGTATCCCATGCGCCCAAGCTGCTGCTGCTGCTGCTGCT 785
Db 421 CTGGGACCCAGCTGTGAAGTATCCCATGCGCCCAAGCTGCTGCTGCTGCTGCTGCT 480

QY 786 GCTGCCATCACTGAATCAGACAACTTCTTCAATCAACGGCTTCAACCTGGGAAGCATCTCG 845
Db 481 GCTGCCATCACTGAATCAGACAACTTCTTCAATCAACGGCTTCAACCTGGGAAGCATCTCG 540

QY 846 GGCTGCGCTATGCTGAGATGCGCAGGCTGACGACTCCCTGGAGCTTTCTTTGACTCT 905
Db 541 GGCTGCGCTATGCTGAGATGCGCAGGCTGACGACTCCCTGGAGCTTTCTTTGACTCT 600

QY 906 CTGGTAAAGCAGACCCAGCTTCCCAACCTTCTTCCCTGCGAGCTTTGTGTGCTGCTGCT 965
Db 601 CTGGTAAAGCAGACCCAGCTTCCCAACCTTCTTCCCTGCGAGCTTTGTGTGCTGCTGCT 660

QY 966 CCGCTCAACGAGCTGAAGTCTGCGCTCTGTCGGAGGAGCATGATCATTTGGAGGTATC 1025
Db 661 CCGCTCAACGAGCTGAAGTCTGCGCTCTGTCGGAGGAGCATGATCATTTGGAGGTATC 720

QY 1026 GACCACTGCTGTACAGGAGTCTCTGGTATACACCCATCGCGCGGAGTGGTATTAT 1085
Db 721 GACCACTGCTGTACAGGAGTCTCTGGTATACACCCATCGCGCGGAGTGGTATTAT 780

QY 1086 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 1145
Db 781 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 840

QY 1146 TACAATATGACAAGAGATTTGGACAGTGGCACACCACTTCTGTTTGGCCCAAGAAA 1205
Db 841 TACAATATGACAAGAGATTTGGACAGTGGCACACCACTTCTGTTTGGCCCAAGAAA 900

QY 1206 GTCTTTGAAGCTGAGTCAATCAATCAAGGAGCTTCTCCACGAGAGTTCCTCTGAT 1265
Db 901 GTCTTTGAAGCTGAGTCAATCAATCAAGGAGCTTCTCCACGAGAGTTCCTCTGAT 960

QY 1266 GGTCTTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGACCACTTGGAAACATT 1325
Db 961 GGTCTTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGACCACTTGGAAACATT 1020

QY 1326 TTCCCAAGTATCTACATCTACCTAATGGTGAGGTTACCAACAGTCTCTTCCGATCACC 1385
Db 1021 TTCCCAAGTATCTACATCTACCTAATGGTGAGGTTACCAACAGTCTCTTCCGATCACC 1080

QY 1386 ATCTCTTCCGAGCAATACCTGCGGCAAGTGAAGATGTGGCCACAGTCTCCCAAGAGTGT 1445
Db 1081 ATCTCTTCCGAGCAATACCTGCGGCAAGTGAAGATGTGGCCACAGTCTCCCAAGAGTGT 1140

QY 1446 TACAAGTTTCCCATCTCACAGTATCCACGGGCACTGTTATGGAGCTGTATTATCATGAG 1505
Db 1141 TACAAGTTTCCCATCTCACAGTATCCACGGGCACTGTTATGGAGCTGTATTATCATGAG 1200

QY 1506 GCGTTCTACGTTGCTTTTGTATCGGCGCCGAAACAAATTTGGCTGTGTCAGCGCTTGC 1565
Db 1201 GCGTTCTACGTTGCTTTTGTATCGGCGCCGAAACAAATTTGGCTGTGTCAGCGCTTGC 1260

QY 1566 CATGTGCAGATGAGTTTCAGGACGCGCGGTGGAGGCGCTTTTGTCTACCTTTGGACATG 1625
Db 1261 CATGTGCAGATGAGTTTCAGGACGCGCGGTGGAGGCGCTTTTGTCTACCTTTGGACATG 1320

QY 1626 GAAGACTGTGCTTACAACTTCCACAGACAGATGAGTCA 1664
Db 1321 GAAGACTGTGCTTACAACTTCCACAGACAGATGAGTCA 1359

RESULT 13
US-09-713-158-1
; Sequence 1, Application US/09713158
; Patent No. 6361975
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; APPLICANT: LI, XIAOTONG
; APPLICANT: POWELL, DAVID J.
; APPLICANT: CHRISTIE, GARY
; TITLE OF INVENTION: MOUSE ASPARTIC SECRETASE-2 (MASP-2)
; FILE REFERENCE: GP-70660
; CURRENT APPLICATION NUMBER: US/09/713.158
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 60/165,800
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: MUS MUSCULUS
US-09-713-158-1

Query Match 55.3%; Score 1298; DB 4; Length 1506;
Best Local Similarity 91.4%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 306 ATGGCCCAAGCCCTGCGCTCTGCTGTGGATGGCGCGGAGTGTGCTGCCAC 365
Db 1 ATGGCCCAAGCCCTGCGCTCTGCTGTGGATGGCGCGGAGTGTGCTGCCAC 60

QY 366 GGCACCCAGCAGCCGCTGCGCTGCGCAGCGGCTGGGGCGGCCCTGGGG 425
Db 61 GGCACCCAGCAGCCGCTGCGCTGCGCAGCGGCTGGGGCGGCCCTGGGG 120

QY 426 CTGCGGCTGCGCCCGGAGACCGAGAGCCCGAGGAGCCCGCGGAGGCGAGCTTT 485
Db 121 CTGCGGCTGCGCCCGGAGACCGAGAGATCGGAGGAGCTTGGCCGAGGAGCTTT 180

QY 486 GTGGAGATGTGGACAACTGAGGGCAAGTGGGGGAGGCTACTACGTGGAGATGACC 545
Db 181 GTGGAGATGTGGACAACTGAGGGCAAGTGGGGGAGGCTACTACGTGGAGATGACC 240

QY 546 GTGGGAGCCCGCGCAGACGCTCAACATCTGTTGGATACAGGACGAGTAACTTTGCA 605
Db 241 GTGGGAGCCCGCGCAGACGCTCAACATCTGTTGGATACAGGACGAGTAACTTTGCA 300

QY 606 GTGGGTGCTGCGCCCGCAGCCCTTCTGCTGCTACTACAGAGGCGAGCTGTCCAGCACA 665

Db 301 GTGGGGCTGCCACACACCCCTTTCCTGCTGCTACTACACAGGCGAGCTGTCCAGCACA 360
Qy TACCGGAGCTCCGGAGGGTGTATGTGCTTACACCCAGGCAAGTGGGAAGGGAG 725
Db 361 TATCGAGACCTCCGAAGGGTGTATGTGCTTACACCCAGGCAAGTGGGAAGGGAA 420
Qy 726 CTGGGACCGACCTGGTGAAGCATCCGCCATGCGCCCAACGCTCACTGTGCGTGCACATTT 785
Db 421 CTGGGACCGACCTGGTGAAGCATCCCTCATGCGCCCAACGCTCACTGTGCGTGCACATTT 480
Qy 786 GTGGCCATCACTGAATCAGACAAGTTCTTCATCAAGGGCTCCAACTGGGAAGGATCCTG 845
Db 481 GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAACTGGGAGGCACTCCTA 540
Qy 846 GGCTGGCTATGCTGAGATTGCGAGGCTTGAGGACTCCCTGGAGCTTCTTTTGACTCT 905
Db 541 GGCTGGCTATGCTGAGATTGCGAGGCTTGAGGACTTCTTTGAGGCTTCTTTGACTCC 600
Qy 906 CTGGTAAAGCAGACCCACAGCTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGGCTTC 965
Db 601 CTGGTAAAGCAGACCCACAGCTTCCCAACATCTTTCCCTGCAGCTGTGGCGCTGGCTTC 660
Qy 966 CCCCTCAACAGTCTGAAGTGTGGGCTCTGTGCGAGGGAGCATGATCATTTGGAGGTATC 1025
Db 661 CCCCTCAACAGACCCGAGGCACTGGGCTCGGTGGAGGGAGCATGATCATTTGGTGGTATC 720
Qy 1026 GACCACTCGCTTACACAGCAGTCTGCTGATACACCCATCGCGGGGAGTGGTATTAT 1085
Db 721 GACCACTCGCTTACACAGGCACTCTGCTGATACACCCATCGCGGGGAGTGGTATTAT 780
Qy 1086 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGATCTGAAATGGACTGCAAGGAG 1145
Db 781 GAAGTATCATTTGCTGCTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG 840
Qy 1146 TACAACATGACAAAGAGCATTTGGAGAGTGGACAGTGGCACCAACCACTTCGTTTGGCCAAAGAA 1205
Db 841 TACAACATGACAAAGAGCATTTGGAGAGTGGACAGTGGGACCAACCACTTCGTTTGGCCAAAGAA 900
Qy 1206 GTCTTTGAAGCTGAGTCAATCCATCAAGGAGCTTCCCTCCAGGAGAGTTCCTTGAT 1265
Db 901 GTATTTGAAGCTGCCGTCAAGTCCATCAAGGAGCTTCCCTCCAGGAGAGTTCCTCGGAT 960
Qy 1266 GTTTTCTGGCTAGGAGAGCAGTGGTGTGCTGGCAAGCAGCACCCCTTGGAACTT 1325
Db 961 GGCTTTGGCTAGGAGAGCAGTGGTGTGCTGGCAAGCAGCACCCCTTGGAACTT 1020
Qy 1326 TTCCCACTCATCTCACTTCACTTAATGGGTGAGGTTTACCAACCACTTCCTTCCGCATCAC 1385
Db 1021 TTCCCACTCATCTCACTTCACTTAATGGGTGAGGTTTACCAACCACTTCCTTCCGCATCAC 1080
Qy 1386 ATCTTTCCGAGCAATACCTGCGGCCAGTGGAAAGATGTGGCCACGTCCTCCAGAGCACTGT 1445
Db 1081 ATCTTTCCCTCAGCAATACCTTACGCGGGTGGAGAGCTGGCCACGTCCTCCAGAGCACTGT 1140
Qy 1446 TACAAGTTTCCCATCTCACAGTCATCACAGGCACTGTTATGGAGCTGTTATCATGGAG 1505
Db 1141 TACAAGTTTCCCTGTCTCACAGTCATCACAGGCACTGTTATGGAGCCGTCATCATGGAA 1200
Qy 1506 GGCTTTCTACGTTGTCTTTGATCGGGCCGAAACGAATTTGGCTTGTGTGTCAGGCGTTGC 1565
Db 1201 GGTTTCTATGCTGCTTTCGATCGAGCCCGAAAGCGAATTTGGCTTGTGTGTCAGGCGTTGC 1260
Qy 1566 CATGTGCACCATGATTCAGAGCGGAGCGGTGGAGGCTTGTGTCACCTTTGGACATG 1625
Db 1261 CATGTGCACCATGATTCAGAGCGGCGGAGTGGAGGCTTGTGTCACCTTTGGACATG 1320
Qy 1626 GAAGACTGTGGCTTACAACATTTCCACAGACAGATGAGTCAACCTTCATGACCATAGCCAT 1685
Db 1321 GAAGACTGTGGCTTACAACATTTCCACAGACAGATGAGTCAACATTTATGACCATAGCCAT 1380
Qy 1686 GTCATGGCTGCCATCTGCGCCCTTTCATGCTGCCACTCTGCCCTCATGTTGTGTCAGTGG 1745

Db 1381 GTCATGGCGCCATCTGGCCCTTTCATGTTGCCACTCTGCCTCATGTTGTCAGTGG 1440
Qy 1746 CGCTGCTCGCTGCTGCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1805
Db 1441 CGCTGCTCGCTGCTGCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
Qy 1806 AAGTGA 1811
Db 1501 AAGTGA 1506
RESULT 14
US-09-548-372D-21
; Sequence 21, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-21
Query Match 55.1%; Score 1293.8; DB 4; Length 1341;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 368 CACCCAGCAGCGATCCGGCTGCCCCCTGCGCAGCGGCTGGGGGCGCCCTTGGGGCT 427
Db 42 CACCCAGCAGCGATCCGGCTGCCCCCTGCGCAGCGGCTGGGGGCGCCCTTGGGGCT 101
Qy 428 GCGGCTCCCCGGGAGACCGAGAGAGCCGCGAGAGCCGCGCGGAGGCGAGCTTTGT 487
Db 102 GCGGCTCCCCGGGAGACCGAGAGAGCCGCGAGAGCCGCGCGGAGGCGAGCTTTGT 161
Qy 488 GGAGATGCTGGACAACCTGAGGGCAAGTGGGGCAGGCTACTACCTGGAGATGACCGT 547
Db 162 GGAGATGCTGGACAACCTGAGGGCAAGTGGGGCAGGCTACTACCTGGAGATGACCGT 221
Qy 548 GGCAGAGCCCCCGCAGACGCTCAACATCTCGTGGATACAGGACGAGTAACTTTGCAGT 607
Db 222 GGCAGAGCCCCCGCAGACGCTCAACATCTCGTGGATACAGGACGAGTAACTTTGCAGT 281
Qy 608 GGTGCTGCCCCCGCAGACCCCTTCCCTGATCGTACTACAGAGGAGCTGTCCACACATA 667
Db 282 GGTGCTGCCCCCGCAGACCCCTTCCCTGATCGTACTACAGAGGAGCTGTCCACACATA 341
Qy 668 CCGGAGCTCCGGAAGGCTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAGCT 727
Db 342 CCGGAGCTCCGGAAGGCTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAGCT 401
Qy 728 GGCACCGACCTGTTAAGCATGCCCATGCCCAAGCTCACTGCTGGTGGCAACATTTGC 787
Db 402 GGCACCGACCTGTTAAGCATGCCCATGCCCAAGCTCACTGCTGGTGGCAACATTTGC 461
Qy 788 TGCATCACTGAATCAGACAAGTTCTTCATCAACGGTTCACAGGATCCCACTGGGAAGGCATCTCGGG 847
Db 462 TGCATCACTGAATCAGACAAGTTCTTCATCAACGGTTCACAGGATCCCACTGGGAAGGCATCTCGGG 521

QY	848	GCTGGCCTATGCTGAGATTGCCAGGCCTCACGACTCCCTTGGACCCTTTCTTTGACTCTCT	907
DB	522	GCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTTGGAGCCTTTCTTTGACTCTCT	581
QY	908	GGTAAAGCAGACCCACGTTCCCAACCTCTCTCCCTGACAGCTTTGTGGTGCTGGCTTCCC	967
DB	582	GGTAAAGCAGACCCACGTTCCCAACCTCTCTCCCTGACAGCTTTGTGGTGCTGGCTTCCC	641
QY	968	CCTCAACAGTCTGAAGTGCTGGCCTCTGCGAGGAGCATGATCATTTGGAGGATPCGA	1027
DB	642	CCTCAACAGTCTGAAGTGCTGGCCTCTGCGAGGAGCATGATCATTTGGAGGATPCGA	701
QY	1028	CCACTCGCTGTACACAGCAGTCTCTGGTATACACCATCCGGCGGAGTGGTATTATGA	1087
DB	702	CCACTCGCTGTACACAGCAGTCTCTGGTATACACCATCCGGCGGAGTGGTATTATGA	761
QY	1088	GGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTA	1147
DB	762	GGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTA	821
QY	1148	CAACTATCACAAAGACATTTGGCAGTGGCACCAACCTTCGTTGCCCAAGAAAGT	1207
DB	822	CAACTATCACAAAGACATTTGGCAGTGGCACCAACCTTCGTTGCCCAAGAAAGT	881
QY	1208	GTTTGAAGCTGCAGTCAATCATCAAGCAGCCTCTCCACGGAGAAAGTTCCTCATGG	1267
DB	882	GTTTGAAGCTGCAGTCAATCCATCAAGCAGCCTCTCCACGGAGAAAGTTCCTCATGG	941
QY	1268	TTTCTGGCTAGGAGAGCAGCTGGTGCTGGCAAGCAGCAGCACCCCTTGGAAACATTTT	1327
DB	942	TTTCTGGCTAGGAGAGCAGCTGGTGCTGGCAAGCAGCAGCACCCCTTGGAAACATTTT	1001
QY	1328	CCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAAGTCCTTCGCGATCACCAT	1387
DB	1002	CCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAAGTCCTTCGCGATCACCAT	1061
QY	1388	CCTTCCGAGCAATACCTTCGGGCCAGTGGAAAGATGGGCCAGTCCCAAGACAGCTGTTA	1447
DB	1062	CCTTCCGAGCAATACCTTCGGGCCAGTGGAAAGATGGGCCAGTCCCAAGACAGCTGTTA	1121
QY	1448	CAAGTTTGCCATCTCACAGTCATCACCGGCCACTGTTATTGGAGAGCTGTTATCATGAGGG	1507
DB	1122	CAAGTTTGCCATCTCACAGTCATCACCGGCCACTGTTATTGGAGAGCTGTTATCATGAGGG	1181
QY	1508	CTTCTACGTTGCTTTGATCGGGCCGGAAGCAATTTGGCTTTGCTGTACGCCCTTGCCCA	1567
DB	1182	CTTCTACGTTGCTTTGATCGGGCCGGAAGCAATTTGGCTTTGCTGTACGCCCTTGCCCA	1241
QY	1568	TGTCACCATGAGTTTCAGACGGCAGCGGTGGAAGGCCCTTTTGTCAACCTTGGACATGGA	1627
DB	1242	TGTCACCATGAGTTTCAGACGGCAGCGGTGGAAGGCCCTTTTGTCAACCTTGGACATGGA	1301
QY	1628	AGACTGTGGCTACAAATTTCCACAGACAGATGAGTCA	1664
DB	1302	AGACTGTGGCTACAAATTTCCACAGACAGATGAGTCA	1338

RESULT 15

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US-09-548-367D-21
; Sequence 21, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23

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Db 882 GTTTGAAGCTGCAGTCAAAATCCATCAAGGCAGCCTCTCCACGGAGAAGTTCCCTGATGG 941
QY 1268 TTTCTGGCTAGGAGAGCAGTGTGTGCTGGCAGCAGGACACCCCTTTGGAAACATTTT 1327
Db 942 TTTCTGGCTAGGAGAGCAGTGTGTGCTGGCAGCAGGACACCCCTTTGGAAACATTTT 1001
QY 1328 CCCAGTCATCTCACTCTACCTAATGGGTGAGGTTTACCAACAGTCCTTCCGCATCACCAT 1387
Db 1002 CCCAGTCATCTCACTCTACCTAATGGGTGAGGTTTACCAACAGTCCTTCCGCATCACCAT 1061
QY 1388 CCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCTCCCAAGACGACTGTTA 1447
Db 1062 CCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCTCCCAAGACGACTGTTA 1121
QY 1448 CAAGTTTGGCCATCTCACAGTCATCCACGGGCAGTGTATGGGAGCTGTTATCATGGAGGG 1507
Db 1122 CAAGTTTGGCCATCTCACAGTCATCCACGGGCAGTGTATGGGAGCTGTTATCATGGAGGG 1181
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Db 1242 TGTGCACGATGAGTTCAGGACGCGGTGGAAAGGCCCTTTTGTCACTTGGACATGGA 1301
QY 1628 AGACTGTGGCTACAAACATTCCACAGACAGATGAGTCA 1664
Db 1302 AGACTGTGGCTACAAACATTCCACAGACAGATGAGTCA 1338
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Search completed: March 2, 2003, 06:15:53
Job time : 79 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2003, 13:37:20 ; Search time 324.5 Seconds
(without alignments)
16294.891 Million cell updates/sec

Title: US-09-723-722A-42
Perfect score: 2348
Sequence: 1 ccatcgccgcccctcacagc.....caagattgctcttggaatt 2348

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :				N_Geneseq_101002:*			
Result No.	Score	Query Match	Length DB	ID	Description		
1	2347.6	100.0	2348	21	AAA59551	DNA encoding a hum	
2	2336.4	99.5	16080	21	AAA59553	DNA clone pCEK Cl.	
3	2181.2	92.9	5757	24	ABL39774	Human NS cDNA sequ	
4	2039.8	86.9	2070	21	AAAL5662	Human aspartyl pro	
5	2039.8	86.9	2070	22	AAD17865	Human aspartyl pro	
6	2039.8	86.9	2070	22	AAD13021	Human aspartyl pro	
7	2039.8	86.9	2070	22	AAAL1517	Human cDNA encodin	
8	2039.8	86.9	2070	22	AAAL1702	DNA encoding human	
9	2039.8	86.9	2070	22	AAD06739	Human aspartyl pro	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	2039.8	86.9	2070	24	ABL52457	Human Asp-2(a) nuc
11	2039.8	86.9	2070	24	ABL49914	Human aspartyl pro
12	2024	86.2	2541	19	AAV41696	Nucleotide sequenc
13	2004	85.3	3252	22	AAF31848	Human memapsin 2 c
14	2004	85.3	3252	22	AAF28101	CDNA encoding huma
15	2004	85.3	3252	24	ABK88641	CDNA encoding huma
16	1881	80.1	1977	21	AAAL5663	Human aspartyl pro
17	1881	80.1	1977	21	AAAL7866	Human aspartyl pro
18	1881	80.1	1977	22	AAD13022	Human aspartyl pro
19	1881	80.1	1977	22	AAAL1518	Human cDNA encodin
20	1881	80.1	1977	22	AAAL1703	DNA encoding human
21	1881	80.1	1977	22	AAD06740	Human aspartyl pro
22	1881	80.1	1977	24	ABL52458	Human Asp-2(b) nuc
23	1881	80.1	1977	24	ABL49915	Human aspartyl pro
24	1835.4	78.2	2370	19	AAV41697	Partial nucleotide
25	1792	76.3	1379	22	AAK94824	Human full-length
26	1648	70.2	1747	20	AAK97602	Extended human sec
27	1550	66.0	2043	21	AAAL5664	Murine aspartyl pr
28	1550	66.0	2043	22	AAD17867	Murine aspartyl pr
29	1550	66.0	2043	22	AAD13023	Murine aspartyl pr
30	1550	66.0	2043	22	AAAL1519	Mouse cDNA encodin
31	1550	66.0	2043	22	AAAL1704	DNA encoding mouse
32	1550	66.0	2043	22	AAD06741	Murine aspartyl pr
33	1550	66.0	2043	24	ABL52459	Mouse Asp-2(a) nuc
34	1511.2	64.4	2158	24	ABK63758	Rat sequence diffe
35	1504.4	64.1	2907	23	AAK82237	DNA encoding novel
36	1503	64.0	1503	21	AAK28278	Human cDNA encodin
37	1503	64.0	1503	21	AAK59550	DNA encoding a hum
38	1503	64.0	1527	24	ABA02406	FLAG-tagged human
39	1476.2	62.9	1911	22	AAK09485	Human aspartyl pro
40	1423	60.6	2914	23	AAK37398	DNA encoding novel
41	1355.8	57.7	1362	21	AAAL5668	Modified human asp
42	1355.8	57.7	1362	22	AAD17878	Human-Asp 2(a) pro
43	1355.8	57.7	1362	22	AAD13034	Human-Asp2(a) delt
44	1355.8	57.7	1362	22	AAAL1530	Human cDNA encodin
45	1355.8	57.7	1362	22	AAAL1715	DNA encoding human

ALIGNMENTS

RESULT 1	
AAA59551	
ID	AAA59551 standard; DNA; 2348 BP.
XX	
AC	AAA59551;
XX	
DT	14-NOV-2000 (first entry)
XX	
DE	DNA encoding a human beta-secretase enzyme.
XX	
KW	Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW	amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW	inhibitor; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	306..1811
FT	/*tag= a
FT	/product= "beta-secretase"
XX	
PN	WO200047618-A2.
XX	
PD	17-AUG-2000.
XX	
PF	10-FEB-2000; 2000WO-US03819.
XX	
PR	10-FEB-1999; 99US-0119571.
PR	15-JUN-1999; 99US-0139172.
XX	
PA	(ELAN-) ELAN PHARM INC.
XX	

PI Anderson JP, Basi G, Doane WT, Frigon N, John V, Power M;
PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;
DR WPI: 2000-533011/48.
DR P-PSDB: AAB07896.
XX
XX Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease -
XX
XX Disclosure; Fig 1B; 121pp; English.
XX
CC The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to
CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
CC disease-like pathology to test if they maintain or improve cognitive
CC ability or reduce the plaque burden. The compounds are used for the
CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
CC present sequence encodes a human beta-secretase enzyme.
XX
SQ Sequence 2348 BP: 489 A; 713 C; 661 G; 484 T; 1 other;

Query Match 100.0%; Score 2347.6; DB 21; Length 2348;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;
Matches 2348; Conservative 0; Indels 0;

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DB 1 CCATGCGGGCCCTCACAGCCCGCGGAGCCCGAGCCCGCTGCCAGGTGCGCGCG 60
QY 61 CSFTGCCGATGAGGGGCTCGGATGCCAGCTCTCCCTGCTCCCGTGTCTGCGGAT 120
DB 61 CSFTGCCGATGAGGGGCTCGGATGCCAGCTCTCCCTGCTCCCGTGTCTGCGGAT 120
QY 121 CTCCCTGACCGCTCTCACAGCCCGGACCCGGGGGTGCGCCAGGCGCTGACGGCCCT 180
DB 121 CTCCCTGACCGCTCTCACAGCCCGGACCCGGGGGTGCGCCAGGCGCTGACGGCCCT 180
QY 181 GCGTCTGTATGCCCCCAAGCTCCCTCTCTGAGAAGCCACAGCACCCAGACTTGG 240
DB 181 GCGTCTGTATGCCCCCAAGCTCCCTCTCTGAGAAGCCACAGCACCCAGACTTGG 240
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DB 241 GGCAGCGCCGAGGACGACGTGGCCAGTGGAGCCAGAGGCGCCGAGGCGCGGCG 300
QY 301 CCACCATGGCCCAAGCCCTGCCCTGGCTCTCTGATGGGCGGGAGTGTGCGCTG 360
DB 301 CCACCATGGCCCAAGCCCTGCCCTGGCTCTCTGATGGGCGGGAGTGTGCGCTG 360
QY 361 CCACAGCACCCAGCAGCGCATCCGCTGCCCTGGCAGCGCTGGGGCGCGCCCCC 420
DB 361 CCACAGCACCCAGCAGCGCATCCGCTGCCCTGGCAGCGCTGGGGCGCGCCCCC 420
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DB 421 TGGGGCTGCGGCTGCCCGGGAGACCGACAGAGCCCGAGGCGCCGCGGAGGGGCA 480
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DB 601 TTGCAGTGGGTGCTGCCCGCCACCCCTTCTGATCGCTACTACAGAGCAGCTGTCCA 660

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DB 661 GCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGSCAAGTGGGAAG 720
QY 721 GGGAGCTGGGACCGGACCTGGTAAGCATCCCCATGGCCCCCAACGCTCACTGCGTGGCA 780
DB 721 GGGAGCTGGGACCGGACCTGGTAAGCATCCCCATGGCCCCCAACGCTCACTGCGTGGCA 780
QY 781 ACATTGCTGCCATCACTGAATCAGACAAGTCTTTCATCAACGGCTCCCAACTGGGAAGCA 840
DB 781 ACATTGCTGCCATCACTGAATCAGACAAGTCTTTCATCAACGGCTCCCAACTGGGAAGCA 840
QY 841 TCCTGGGGTGGCCCTATGTGATGATGCCAGGCGCTGAGACTCTCCGAGCCCTTCTTTG 900
DB 841 TCCTGGGGTGGCCCTATGTGATGATGCCAGGCGCTGAGACTCTCCGAGCCCTTCTTTG 900
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DB 901 ACTCTCTGTTAAGCAGACCCAGCTTCCCAACCTTCTCTCCCTGACGCTTTGTGGTGGCTG 960
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DB 961 GCTTCCCTCTCAACCAAGTCTGAAGTGTGGCTCTGTGCGAGGAGCATGATCATTTGGAG 1020
QY 1021 GTATGACCACTCGGTGTACACAGGAGTCTCTGGTATACACCCATCCGCGGGAGTGGT 1080
DB 1021 GTATGACCACTCGGTGTACACAGGAGTCTCTGGTATACACCCATCCGCGGGAGTGGT 1080
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DB 1081 ATTATGAGGTGATCATTTGTCGGGTGGAGATCAATGACAGCATCTGAAAATGGACTGCA 1140
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DB 1141 AGGAGTACAACCTATGACAAGAGCATTTGGACAGCTGGCACCACCAACCTTCGTTGCCCA 1200
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DB 1321 ACATTTTCCAGTCACTCTACCTAATGGTGAGGTTTACCAACCAAGTCTTCCCGCA 1380
QY 1381 TCACCATCTTCCGAGCAATACCTGCGGCGAGTGGAGAGATGTGCGCCACGTCGCCAAGAG 1440
DB 1381 TCACCATCTTCCGAGCAATACCTGCGGCGAGTGGAGAGATGTGCGCCACGTCGCCAAGAG 1440
QY 1441 ACTGTTACAAGTTTGGCATCTCAGTCACTCCAGGCGCACTGTTATGGAGCTGTATCA 1500
DB 1441 ACTGTTACAAGTTTGGCATCTCAGTCACTCCAGGCGCACTGTTATGGAGCTGTATCA 1500
QY 1501 TGGAGGGCTTCTACGTTGTCTTTGATGCGGCCCGGAAAACAAATTTGGCTGTGTCAGGG 1560
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QY 1621 ACATGGAAGACTGTGGCTACACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAG 1680
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QY 1741 AGTGGCGCTGCTCCGCTGCCCGCAGCAGCATGATGACTTTGCTGATGACATCTCCC 1800

Db 1741 AGTGGCGCTGCTCCGCTGCTGGCAGCAGCATGATGATTTGCTGATGACATCTCCC 1800
Qy 1801 TGCTGAAGTGAAGGCGCCATGGCCAGCAAGATAGAGATTTCCCTGGACCACACTTCGGTG 1860
Db 1801 TGCTGAAGTGAAGGCGCCATGGCCAGCAAGATAGAGATTTCCCTGGACCACACTTCGGTG 1860
Qy 1861 GTTCACATTTGGTCACAAAGTAGGACACAGATGGCAGCTGTGGCCAGAGCACTTCAGGAC 1920
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Qy 1921 CTTCCCCACCCACCAATGCTCTGCTTGTGATGAGAGGAAAAGGCTGGCAAGGTGGGT 1980
Db 1921 CTTCCCCACCCACCAATGCTCTGCTTGTGATGAGAGGAAAAGGCTGGCAAGGTGGGT 1980
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Qy 2101 AACCTTTGTCACATTCCTTTAAATTTCTCAACCCAAAGATATTCCTTTCTTAGTTT 2160
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Qy 2161 CAGAAGTACTGGCATACAGCAGGTACTCTGGCGTGTGCTGCTGCTGCTGCTGCTGCTG 2220
Db 2161 CAGAAGTACTGGCATACAGCAGGTACTCTGGCGTGTGCTGCTGCTGCTGCTGCTGCTG 2220
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Qy 2341 CTTGAATT 2348
Db 2341 CTTGAATT 2348

RESULT 2
AAA59553
ID AAA59553 standard; DNA; 16080 BP.

AC AAA59553;

DT 14-NOV-2000 (first entry)

DE DNA clone pCEK C1.27 encoding a human beta-secretase enzyme.

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW Inhibitor; ss.
XX Homo sapiens.

OS Homo sapiens.

XX W0200047618-A2.

PN 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US03819.

XX 10-FEB-1999; 99US-0119571.

PR 15-JUN-1999; 99US-0139172.

XX (ELAN-) ELAN PHARM INC.

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

XX WPI; 2000-533011/48.
XX
DR Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease -
XX
PS Disclosure: Fig 13A-E; 121pp; English.
XX
CC The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to
CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
CC disease-like pathology to test if they maintain or improve cognitive
CC ability or reduce the plaque burden. The compounds are used for the
CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
CC present sequence encodes a human beta-secretase enzyme.
XX
SQ Sequence 16080 BP; 3627 A; 4556 C; 3962 G; 3913 T; 22 other;

Query Match 99.5%; Score 2336.4; DB 21; Length 16080;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2340; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CCATGCGCGCCCTCACAGCCCGCGGAGCCGCGCTGCCAGGCTGGCGCGG 60
Db 1370 CCATGCGCGCCCTCACAGCCCGCGGAGCCGCGCTGCCAGGCTGGCGCGG 1429
Qy 61 CSGTGCGGATGTAGCGGCTCCGGATCCAGCCTTCCCTTGCCTCCCTGCTCTGCGGAT 120
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Qy 241 GGCAGGCGCCAGGAGGAGCTGGGCGAGTSCGAGGCCAGAGGCCCGCGGCGG 300
Db 1610 GGCAGGCGCCAGGAGGAGCTGGGCGAGTSCGAGGCCAGAGGCCCGCGGCGG 1669
Qy 301 CCACATGGCCCAAGCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 1670 CCACATGGCCCAAGCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1729
Qy 361 CCCAGGCGCCAGGAGGAGCTGGGCGAGTSCGAGGCCAGAGGCCCGCGGCGG 420
Db 1730 CCCAGGCGCCAGGAGGAGCTGGGCGAGTSCGAGGCCAGAGGCCCGCGGCGG 1789
Qy 421 TGGGGCTGCGGCTGCCCGGAGACCGAGCAAGAGCCCGAGAGGCCCGCGGAGGGCA 480
Db 1790 TGGGGCTGCGGCTGCCCGGAGACCGAGCAAGAGCCCGAGAGGCCCGCGGAGGGCA 1849
Qy 481 GCTTTTGGAGATGGTGACAACTGAGGGGCAAGTGGGGCGGGCTACTACGTGGAGA 540
Db 1850 GCTTTTGGAGATGGTGACAACTGAGGGGCAAGTGGGGCGGGCTACTACGTGGAGA 1909
Qy 541 TGACCGTGGGCGAGCCCGCGCAGACGCTCAACATCTCTGGTGATACAGGAGCAGTAAC 600
Db 1910 TGACCGTGGGCGAGCCCGCGCAGACGCTCAACATCTCTGGTGATACAGGAGCAGTAAC 1969
Qy 601 TTGAGTGGGTGCTGCCCGCCACCCCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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Qy	841	TCCTGGGCTGGCCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGGCCCTTCCTTG	900
Db	2210	TCCTGGGCTGGCCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGGCCCTTCCTTG	2369
Qy	901	ACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTCTCCCTGCAAGCTTTGTGSGTGCCTG	960
Db	2270	ACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTCTCCCTGCAAGCTTTGTGSGTGCCTG	2329
Qy	961	GCTTCCCCCTCAACGAGTCTGAAGTCTGGCTCTGTGCGAGGGAGCATGATCATTTGGAG	1020
Db	2330	GCTTCCCCCTCAACGAGTCTGAAGTCTGGCTCTGTGCGAGGGAGCATGATCATTTGGAG	2389
Qy	1021	GTATCGACCACTCGCTGTATACAGACGAGTCTCTGGTATATACCCCATCCGGCGGAGTGGT	1080
Db	2390	GTATCGACCACTCGCTGTATACAGACGAGTCTCTGGTATATACCCCATCCGGCGGAGTGGT	2449
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Qy	1141	AGGAGTCAAACTATGACAAGACATTTGGAGAGTGGCACCACCAACCTTCGTTTGCCTCA	1200
Db	2510	AGGAGTCAAACTATGACAAGACATTTGGAGAGTGGCACCACCAACCTTCGTTTGCCTCA	2569
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Db	2570	AGAAAGTGTTTGAAGCTCGAGTCAAAATCCATCAAGCGACCTCTCCACGGAGAAATTCC	2629
Qy	1261	CTGATGGTTCCTGGCTAGGAGACGAGCTGGTGTCTGGCAAGCAGGCACACACCCCTTGA	1320
Db	2630	CTGATGGTTCCTGGCTAGGAGACGAGCTGGTGTCTGGCAAGCAGGCACACACCCCTTGA	2689
Qy	1321	ACATTTTCCAGTCATCTACCTCTACTTAATGGGTGAGGTTACCAACCAAGTCTCTCCGCA	1380
Db	2690	ACATTTTCCAGTCATCTACCTCTACTTAATGGGTGAGGTTACCAACCAAGTCTCTCCGCA	2749
Qy	1381	TCACCATCTTCCGAGCAATACCTTCGGCCAGTGGAAAGTGTGGCCACGTCCCACAGCG	1440
Db	2750	TCACCATCTTCCGAGCAATACCTTCGGCCAGTGGAAAGTGTGGCCACGTCCCACAGCG	2809
Qy	1441	ACTGTTACAAGTTTGCCATCTCACAGTCAATCCACGGGCACCTGTTATGGAGCTGTTATCA	1500
Db	2810	ACTGTTACAAGTTTGCCATCTCACAGTCAATCCACGGGCACCTGTTATGGAGCTGTTATCA	2869
Qy	1501	TGGAGGGCTTTCACGTTGTCTTTGATCGGGCCCGAAACGAATTGGCTTTGCTGTGTCAGCG	1560
Db	2870	TGGAGGGCTTTCACGTTGTCTTTGATCGGGCCCGAAACGAATTGGCTTTGCTGTGTCAGCG	2929
Qy	1561	CTTGCCATGTGCACATGAGTTTCAGGACGGCAGCGGTGGAAGCCCTTTTGTACCTTGG	1620
Db	2930	CTTGCCATGTGCACATGAGTTTCAGGACGGCAGCGGTGGAAGCCCTTTTGTACCTTGG	2989
Qy	1621	ACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAG	1680
Db	2990	ACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAG	3049
Qy	1681	CCTATGTCATGGCTGCCATCTCGGCCCTCTTTCATGCTGCCACTCTGCCTCATGGTGTGC	1740
Db	3050	CCTATGTCATGGCTGCCATCTCGGCCCTCTTTCATGCTGCCACTCTGCCTCATGGTGTGC	3109
Qy	1741	AGTGGCGCTCGCTCGCTGCGCCACGAGCATGATGACTTTTGTGTGATGACATCTCCC	1800
Db	3110	AGTGGCGCTCGCTCGCTGCGCCACGAGCATGATGACTTTTGTGTGATGACATCTCCC	3169

QY	1801	TGCTGAAGTCAGGAGGCCATGGGCAGAAATAGAGATTC	1866
Db	3170	TGCTGAAGTCAGGAGGCCATGGGCAGAAATAGAGATTC	3229
QY	1861	GTTCACCTTTGGTCTCAAGTAGGAGACACAGATGGC	1920
Db	3230	GTTCACCTTTGGTCTCAAGTAGGAGACACAGATGGC	3289
QY	1921	CCTCCCCACCCACCAATGCCCTCTGCCCTTGATGG	1980
Db	3290	CCTCCCCACCCACCAATGCCCTCTGCCCTTGATGG	3349
QY	1981	TCCAGGACTGTACCTGTAGAAACAGAAAGAGAAAG	2040
Db	3350	TCCAGGACTGTACCTGTAGAAACAGAAAGAGAAAG	3409
QY	2041	ATACTCTTGGTCACTCAAAATTAAGTCGGGAAATTC	2100
Db	3410	ATACTCTTGGTCACTCAAAATTAAGTCGGGAAATTC	3469
QY	2101	AACCTTTGTCCACCATTTCCCTTTAAATTCCTCAAC	2160
Db	3470	AACCTTTGTCCACCATTTCCCTTTAAATTCCTCAAC	3529
QY	2161	CAGAAGTACTGGCATCACACAGGTTACCTTTGGCGT	2220
Db	3530	CAGAAGTACTGGCATCACACAGGTTACCTTTGGCGT	3589
QY	2221	AGAAGAGACCAAGCTTGTTCCTTCCTGGCCAAAGTC	2280
Db	3590	AGAAGAGACCAAGCTTGTTCCTTCCTGGCCAAAGTC	3649
QY	2281	CTATTTTGTCTTAGAGACAGGACTGTATAACAAGCCT	2340
Db	3650	CTATTTTGTCTTAGAGACAGGACTGTATAACAAGCCT	3709
QY	2341	CTTGAATT	2348
Db	3710	CTTGAATT	3717

RESULT 3	
ABL39774	
ID	ABL39774 standard; cDNA; 5757 BP.
XX	
AC	ABL39774;
XX	
DT	10-MAY-2002 (first entry)
XX	
DE	Human NS cDNA sequence SEQ ID NO:84.
XX	
KW	Human; cytostatic; osteopathic; gyna-
KW	antirheumatic; antiarthritic; antipsy-
KW	vasotropic; antiarteriosclerotic; an-
KW	anorectic; muscular; antifertility; an-
KW	antifibrinolytic; hypotension; antia-
KW	nticonvulsant; antidiabetic; tranqui-
KW	gastrointestinal; virucide; antituce-
KW	contraceptive; vaccine; gene therapy
KW	endometriosis; degenerative disease;
KW	rheumatoid arthritis; cataract; resti-
KW	inflammation; skin disorder; obesity
KW	infertility; cardiovascular disease;
KW	ischemia; asthma; immune disease; e-
KW	diabetes; anxiety; depression; schiz-
KW	gastric ulcer; Alzheimer's disease;
XX	
OS	Homo sapiens.
XX	
PN	WO2000206315-A2.
XX	
PD	24-JAN-2002.
XX	

PF 17-JUL-2001; 2001WO-1L00653.
XX
PR 18-JUL-2000; 2000TL-0137345.
PR 15-DEC-2000; 2000TL-0140354.
XX
XX (COMP-) COMPUGEN LTD.
XX
PI Mintz L, Freilich S, Bernstein J;
XX
DR WPI: 2002-155037/20.
DR P-PSDB; ABB06120.
XX
XX One hundred and twenty eight novel nucleic acid sequences, useful for
PT treating and diagnosing e.g. cancer, asthma and Alzheimer's -
XX
XX Claim 1; Page 124-126; 290pp; English.
PS
XX ABL39691 to ABL39818 represent novel human nucleic acid sequences
CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
CC anorectic, muscular, anti-HIV, antifertility, cardiovascular,
CC anticoagulant, antifibrinolytic, hypotension, antidiabetic, cardiant,
CC immunomodulator, anticonvulsant, antidiabetic, tranquiliser, antiulcer,
CC antidepressant, gastrointestinal, neuroleptic, cerebroprotective,
CC nootropic and contraceptive activities. The NS can be used in vaccines,
CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
CC antibodies from the present invention can be used for treating and
CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC Alzheimer's disease and as a contraceptive.
XX
XX Sequence 5757 BP; 1485 A; 1490 C; 1392 G; 1388 T; 2 other;

Query Match 92.9%; Score 2181.2; DB 24; Length 5757;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 2268; Conservative 1; Mismatches 4; Indels 75; Gaps 1;

QY 1 CCATGCGGGCCCTCACAGCCCGCGGAGCCGCGAGCCGCTGCCAGGCTGGCCGCGG 60
DB 150 CCATGCGGGCCCTCCAGCCCGCGCGGAGCCGCGCGCTGCCAGGCTGGCCGCGG 209
QY 61 CSGTGCGCGATGTAGCGGGCTCCGGATCCCGAGCTCTCCCTGCTCCCGTCTCTGCGGAT 120
DB 210 CCGTGGCGATGTAGCGGGCTCCGGATCCCGAGCTCTCCCTGCTCCCGTCTCTGCGGAT 269
QY 121 CTCCTGACCGCTCTCCAGAGCCGAGCCCGGGGGTGGCCAGGCGCTGAGGCGCT 180
DB 270 CTCCTGACCGCTCTCCAGAGCCGAGCCCGGGGGTGGCCAGGCGCTGAGGCGCT 329
QY 181 GGGTCTCTGATGCCCAAGCTCCCTCTCTGAGAGCCAGCCAGCCAGACTTG 240
DB 330 GGGTCTCTGATGCCCAAGCTCCCTCTCTGAGAGCCAGCCAGACTTG 389
QY 241 GGGCAGCGCCAGGAGCGAGCTGGGCGAGTGGAGCCAGAGCGCCGAGCGCGGCG 300
DB 390 GGGCAGCGCCAGGAGCGAGTGGGCGAGTGGAGCCAGAGCGCCGAGCGCGGCG 449
QY 301 CCACCATGGGCCAAGCCCTGCCCTGGCTCTGCTGTGGATGGGCGCGGAGTGTGCTG 360
DB 450 CCACCATGGGCCAAGCCCTGCCCTGGCTCTGCTGTGGATGGGCGCGGAGTGTGCTG 509
QY 361 CCACGCGCCAGCAGCGGATCCGGCTGCCCTGCCAGCGGCGCTGGGCGGCGCCCC 420
DB 510 CCACGCGCCAGCAGCGGATCCGGCTGCCCTGCCAGCGGCGCTGGGCGGCGCCCC 569
QY 421 TGGGGCTGCGGCTGCCCGGGAGACCAGACGAGCCCGAGAGCCCGCGCGGAGGGCA 480

DB 570 TGGGGCTGCGGCTGCCCGGGAGACCAGGAAGAGCCCGAGGAGCCGCGCGGAGGGCA 629
QY 481 GCTTTTGGAGATGGTGGACAACTGAGGGGCAAGTGGGGCAGGGCTACTACGTGAGA 540
DB 630 GCTTTTGGAGATGGTGGACAACTGAGGGGCAAGTGGGGCAGGGCTACTACGTGAGA 689
QY 541 TGACCGTGGGCGAGCCCGCGCAGACGCTCAACATCCCTGGTGGATACAGGAGCAAGTAACT 600
DB 690 TGACCGTGGGCGAGCCCGCGCAGACGCTCAACATCCCTGGTGGATACAGGAGCAAGTAACT 749
QY 601 TTGACGTGGTGTGTCGCCCGCCCGCTTCCTGTGCATCGCTACTACAGGAGCGAGTGTCCA 660
DB 750 TTGACGTGGTGTGTCGCCCGCCCGCTTCCTGTGCATCGCTACTACAGGAGCGAGTGTCCA 809
QY 661 GCACATACCGGGAGCTCCGGAAGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAG 720
DB 810 GCACATACCGGGAGCTCCGGAAGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAG 869
QY 721 GGGAGCTGGGCGACCGACCTGTAAGCATCCCGCATGGCCCAAGCTCACTGTGCTGCCA 780
DB 870 GGGAGCTGGGCGACCGACCTGTAAGCATCCCGCATGGCCCAAGCTCACTGTGCTGCCA 929
QY 781 ACATGTGTCGCATCACTGAATTCAGACAAAGTTCTTCATCAACGGGTCCAACCTGGGAAGCA 840
DB 930 ACATGTGTCGCATCACTGAATTCAGACAAAGTTCTTCATCAACGGGTCCAACCTGGGAAGCA 989
QY 841 TCCTGGGGCTGGCTATGCTGAGATTGCCAGGCTGAGGACTCCCTGGAGGCTTTCTTTG 900
DB 990 TCCTGGGGCTGGCTATGCTGAGATTGCCAG----- 1020
QY 901 ACTCTCTGTTAAAGCAGACACCGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGTG 960
DB 1021 -----GCTTTGTGGTGTG 1034
QY 961 GCTTCCCGCTCAACAGTCTGAAAGTGTGGCTCTGTCGGAGGAGGATGATCATTTGGAG 1020
DB 1035 GCTTCCCGCTCAACAGTCTGAAAGTGTGGCTCTGTCGGAGGAGGATGATCATTTGGAG 1094
QY 1021 GTATCGACCACTCGCTGTACACAGGAGTCTCTGCTATACACCATCCGCGGGAGTGGT 1080
DB 1095 GTATCGACCACTCGCTGTACACAGGAGTCTCTGCTATACACCATCCGCGGGAGTGGT 1154
QY 1081 ATTATGAGGTGATCATTTGTGCGGTGGAGATCAATGGACAGGATCTGAAAATGGAGTCA 1140
DB 1155 ATTATGAGGTGATCATTTGTGCGGTGGAGATCAATGGACAGGATCTGAAAATGGAGTCA 1214
QY 1141 AGGAGTACAATATGACAAGAGCATTTGTGGACATGGCACACCAACCTTCGTTTGGCCA 1200
DB 1215 AGGAGTACAATATGACAAGAGCATTTGTGGACATGGCACACCAACCTTCGTTTGGCCA 1274
QY 1201 AGAAGTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCGCTCTCCACGGAGAGTTCC 1260
DB 1275 AGAAGTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCGCTCTCCACGGAGAGTTCC 1334
QY 1261 CTGATGCTTTCTGGCTAGGAGAGCAGCTGGTGTCTGGCAAGAGGACCAACCTTTGGA 1320
DB 1335 CTGATGCTTTCTGGCTAGGAGAGCAGCTGGTGTCTGGCAAGAGGACCAACCTTTGGA 1394
QY 1321 ACATTTTCCAGTCACTCTACCTTACCTAATGGGTGAGGTTTACCAACAGCTCTTCCGCA 1380
DB 1395 ACATTTTCCAGTCACTCTACCTTACCTAATGGGTGAGGTTTACCAACAGCTCTTCCGCA 1454
QY 1381 TCACCATCTTTCCGAGCAATACCTGGGCGCAGTGGAGATGTGGCCACGCTGCCAAGACG 1440
DB 1455 TCACCATCTTTCCGAGCAATACCTGGGCGCAGTGGAGATGTGGCCACGCTGCCAAGACG 1514
QY 1441 ACTGTTACAAGTTTGGCCATCTCAGATCATCCACGGGAGCTGTTATGGGAGCTGTATCA 1500
DB 1515 ACTGTTACAAGTTTGGCCATCTCAGATCATCCAGGCGACCTGTTATGGGAGCTGTATCA 1574
QY 1501 TGGAGGCTCTTACGTTGTCTTTGATCGGGCCGCAAAACGAATTTGGCTTCTGCTGACGCG 1560


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QY 726 CTGGGACCGACCTGTTAAGCATCCGCCATGCCCCCACTACTGTGGCTGCCAACATT 785
Db 421 CTGGGACCGACCTGTTAAGCATCCGCCATGCCCCCACTACTGTGGCTGCCAACATT 480
QY 786 GCTGGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAGGCATCCTG 845
Db 481 GCTGGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAGGCATCCTG 540
QY 846 GGCTGGCTATCTGCTGAGATTGGCAGGCTTGACGACTCCCTGGAGCCTTTCTTTGACTCT 905
Db 541 GGCTGGCTATCTGCTGAGATTGGCAGGCTTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
QY 906 CTGGTAAAGCAGACCCAGCTTCCCAACCTTTCTCCCTGACAGTTTGTGTGCTGGCTTC 965
Db 601 CTGGTAAAGCAGACCCAGCTTCCCAACCTTTCTCCCTGACAGTTTGTGTGCTGGCTTC 660
QY 966 CCCCTCAACGAGCTGAAGTGTGGCTCTGTGCGGAGGAGCATGATCATTTGAGGTATC 1025
Db 661 CCCCTCAACGAGCTGAAGTGTGGCTCTGTGCGGAGGAGCATGATCATTTGAGGTATC 720
QY 1026 GACCACTCGCTGTACACAGGCACTCTGTGTATACACCCATCCGGCGGAGTGGTATTAT 1085
Db 721 GACCACTCGCTGTACACAGGCACTCTGTGTATACACCCATCCGGCGGAGTGGTATTAT 780
QY 1086 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 1145
Db 781 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
QY 1146 TACAACATGACAAGAGCATTTGGACAGTGGACACCAACCTTCGTTTGGCCCAAGAAA 1205
Db 841 TACAACATGACAAGAGCATTTGGACAGTGGACACCAACCTTCGTTTGGCCCAAGAAA 900
QY 1206 GTGTTTGAAGCTGCAGTCAATCATCAAGGAGGCTTCCTCCAGGAGAGTTCCTCGTAT 1265
Db 901 GTGTTTGAAGCTGCAGTCAATCATCAAGGAGGCTTCCTCCAGGAGAGTTCCTCGTAT 960
QY 1266 GGTTCCTGGCTAGGAGAGCAGCTGTGTGTGCTGGCAGGAGCAGCACCCTTGGAAACATT 1325
Db 961 GGTTCCTGGCTAGGAGAGCAGCTGTGTGTGCTGGCAGGAGCAGCACCCTTGGAAACATT 1020
QY 1326 TTCCCACTCATCTCACTTACCTAATGGGTGAGGTACCAACCAAGTCTTCGGCATCACC 1385
Db 1021 TTCCCACTCATCTCACTTACCTAATGGGTGAGGTACCAACCAAGTCTTCGGCATCACC 1080
QY 1386 ATCTCTCCGAGCAATACCTCGCGCAGTGGAAAGATGTGGCCACGTCCTCCCAAGAGCAGCTGT 1445
Db 1081 ATCTCTCCGAGCAATACCTCGCGCAGTGGAAAGATGTGGCCACGTCCTCCCAAGAGCAGCTGT 1140
QY 1446 TACAAGTTTGGCCATCTCACAGTCACTCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1505
Db 1141 TACAAGTTTGGCCATCTCACAGTCACTCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
QY 1506 GGCTTCTACGTTCTTTGTATCGGGCCCGGAAACGAATTTGGCTTGTGTGTCAGGCTTGC 1565
Db 1201 GGCTTCTACGTTCTTTGTATCGGGCCCGGAAACGAATTTGGCTTGTGTGTCAGGCTTGC 1260
QY 1566 CATGTGCACCATGAGTTTCAGGAGCGGAGCGGTGGAAGCGCCCTTTTGTCACTTTGGACATG 1625
Db 1261 CATGTGCACCATGAGTTTCAGGAGCGGAGCGGTGGAAGCGCCCTTTTGTCACTTTGGACATG 1320
QY 1626 GAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1685
Db 1321 GAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1380
QY 1686 GTCATGGCTGCCATCTCGGCCCTTTCATGCTGCCACTCTGCCCTCATGGTGTGTCACTGG 1745
Db 1381 GTCATGGCTGCCATCTCGGCCCTTTCATGCTGCCACTCTGCCCTCATGGTGTGTCACTGG 1440
QY 1746 CGCTGCCCTCGCTGCTCGGCCAGCAGCATGATGACTTTTGTGTGATGACATCTCCCTGCTG 1805
Db 1441 CGCTGCCCTCGCTGCTCGGCCAGCAGCATGATGACTTTTGTGTGATGACATCTCCCTGCTG 1500
QY 1806 AAGTGAGGAGGCCCATGGGCGAGAAGATAGAGATTTCCCTGGACACACACCTCCGTGGTTCA 1865
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Db 1501 AAGTGGAGGCGCCCATGGGCGAGAAGATAGAGATTTCCCTGGACACACCTCCCGTGGTTCA 1560
QY 1866 CTTTGGTTCACAAGTAGGAGACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC 1925
Db 1561 CTTTGGTTCACAAGTAGGAGACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC 1620
QY 1926 CCACCCACCAAAATGCCCTCTGCCCTTGATGGAGAGAGAAAGCTGGCAAGGTGGGTTCAG 1985
Db 1621 CCACCCACCAAAATGCCCTCTGCCCTTGATGGAGAGAGAAAGCTGGCAAGGTGGGTTCAG 1680
QY 1986 GGAAGTGTACCTGTAGGAAACAGAAAGAGAGAAAGAGCACTCTGCTGGGCGGAATACT 2045
Db 1681 GGAAGTGTACCTGTAGGAAACAGAAAGAGAGAAAGAGCACTCTGCTGGGCGGAATACT 1740
QY 2046 CTTGGTCACCTCAAAATTTAAGTGGGGAATTTCTGCTCTTGAACCTTCAGCCCTGAACCT 2105
Db 1741 CTTGGTCACCTCAAAATTTAAGTGGGGAATTTCTGCTCTTGAACCTTCAGCCCTGAACCT 1800
QY 2106 TTGTCCACCAATTCCTTTAAATTTCTCCAAACCAAGATATTCTTTCTTTAGTTTCAGAA 2165
Db 1801 TTGTCCACCAATTCCTTTAAATTTCTCCAAACCAAGATATTCTTTCTTTAGTTTCAGAA 1860
QY 2166 GTACTGGCATCACACGAGGTTACCTTGGCGTGTGTGCTGTCACCTGGGAGAGAG 2225
Db 1861 GTACTGGCATCACACGAGGTTACCTTGGCGTGTGTGCTGTCACCTGGGAGAGAG 1920
QY 2226 AGACCAAGCTTGTTCCTCTGCTGGCCAAAGTCACTAGGAGAGGATGCACAGTTTGTATT 2285
Db 1921 AGACCAAGCTTGTTCCTCTGCTGGCCAAAGTCACTAGGAGAGGATGCACAGTTTGTATT 1980
QY 2286 TGCTTTAGACACAGGAGGACTGTATAAACAAGCCTAACATTTGGTGCAGAGATTGCCTCTTGA 2345
Db 1981 TGCTTTAGACACAGGAGGACTGTATAAACAAGCCTAACATTTGGTGCAGAGATTGCCTCTTGA 2040
QY 2346 ATT 2348
Db 2041 ATT 2043

RESULT 5.
AADI7865
ID AADI7865 standard; cDNA; 2070 BP.
XX
AC AADI7865;
XX
DT 10-DEC-2001 (first entry)
XX
Human aspartyl protease 2(a) [hu-Asp2(a)] cDNA.
Human; aspartyl protease 2(a); Asp2(a); amyloid precursor protein; App;
Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
amyloid plaque; neuronal loss; proteolytic; nontropic; neuroprotective;
chromosome 11q23.3-24.1; ss.
XX
Homo sapiens.
XX
Key Location/Qualifiers
CDS 1..1506
FT /*tag= a
FT /product= "Human aspartyl protease 2(a)"
FT sig_peptide 1..63
FT /*tag= b
FT mat_peptide 64..1503
FT /*tag= c
FT /product= "Mature human aspartyl protease 2(a)"
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XX GB2357767-A.
XX
XX 04-JUL-2001.
XX
XX 22-SEP-2000; 2000GB-0023315.
XX
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QY	1866	CTTTGGTCAAGTAGGAGACACAGATGGCACTGTGGCCAGAGCACCCTCAGGACCCCTCC	1925
Db	1561	CTTTGGTCAAGTAGGAGACACAGATGGCACTGTGGCCAGAGCACCCTCAGGACCCCTCC	1620
QY	1926	CCACCACCAAAATGCTCTGCCTTCATGAGAAAGCAAAAGGCTGCAAGGTGGGTTCAG	1985
Db	1621	CCACCACCAAAATGCTCTGCCTTCATGAGAAAGCAAAAGGCTGCAAGGTGGGTTCAG	1680
QY	1986	GGACTGTACCTGTAGGAAACAGAAAGAGAAAGAACGACACTCTGCTGGCGGGAATACT	2045
Db	1681	GGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGAGCAGCTCTGCTGGCGGGAATACT	1740
QY	2046	CTTGGTCACCTCAAAATTTAAGTCGGGAAATTCCTGCTTGAAACTTCAGGCCCTGAACCT	2105
Db	1741	CTTGGTCACCTCAAAATTTAAGTCGGGAAATTCCTGCTTGAAACTTCAGGCCCTGAACCT	1800
QY	2106	TTGTCACCAATTCCTTTAAATTTCTCAACCCCAAAAGTAATCTCTTTCTTAGTTTCAGAA	2165
Db	1801	TTGTCACCAATTCCTTTAAATTTCTCAACCCCAAAAGTAATCTCTTTCTTAGTTTCAGAA	1860
QY	2166	GTACTGGCATCACACGACAGTTTACCTTTGGCGTGTCTCCCTGTGTGATACCTTGGCAGAGAAG	2225
Db	1861	GTACTGGCATCACACGACAGTTTACCTTTGGCGTGTCTCCCTGTGTGATACCTTGGCAGAGAAG	1920
QY	2226	AGACCAAGCTTGTGTTCCCTTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	2285
Db	1921	AGACCAAGCTTGTGTTCCCTTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
QY	2286	TGCTTTAGAGACAGGAGCTGTATAACAAGCCTACACTTGGTGCAAGATTGCCTCTTTGA	2345
Db	1981	TGCTTTAGAGACAGGAGCTGTATAACAAGCCTTAACACTTGGTGCAAGATTGCCTCTTTGA	2040
QY	2346	ATT 2348	
Db	2041	ATT 2043	
RESULT 6			
AAD13021			
ID	AAD13021 standard; cDNA; 2070 BP.		
XX			
AC	AAD13021;		
XX			
DT	23-OCT-2001 (first entry)		
XX			
DE	Human aspartyl protease 2a (Hu-Asp2a) cDNA.		
XX			
KW	Human; aspartyl protease 2a; Asp 2a; beta-amyloid precursor protein; APP; beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;		
KW	neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;		
KW	neuroprotective; antisense therapy; gene therapy;		
KW	chromosome 11q23.2-24.1; ss.		
XX			
OS	Homo sapiens.		
XX			
PH	key	Location/Qualifiers	
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FT		/product= "Human aspartyl protease 2a (Hu-Asp2a)"	
FT	sig_peptide	1..63	
FT		/*tag= b	
FT	mat_peptide	64..1503	
FT		/*tag= c	
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XX			
XX	WO200150829-A2.		
PN			
XX			
PD	19-JUL-2001.		
XX			
XX	09-MAY-2001; 2001WO-IB00799.		
PF			
XX			
XX	09-MAY-2001; 2001WO-IB00799.		
PR			

(BIEN/) BIENKOWSKI M J.
 (GURN/) GURNEY M E.
 (HEIN/) HEINRIKSON R L.
 (PARO/) PARODI L A.
 (YANR/) YAN R.
 Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 WPI: 2001-483072/52.
 P-PSDB: AAE06859.
 Novel purified polypeptide comprising fragment of mammalian aspartyl
 protease 2, lacking Asp2 transmembrane domain and retaining beta
 secretase activity of Asp2 useful for identifying inhibitors of Asp2
 activity
 Claim 98; Fig 2: 185pp; English.
 The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
 precursor protein (APP) isoforms and their corresponding DNA molecules.
 Human aspartyl proteases can act as beta-secretase proteases useful for
 treating Alzheimer's disease. APP isoforms are useful for identifying
 modulators of amyloid-beta peptide production, for use in designing
 therapeutics for the treatment and prevention of Alzheimer's disease,
 dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
 and neuronal loss. APP isoforms are also used in methods for identifying
 inhibitors and modulators of human Asp2 activity. The invention relates
 to a method for identifying agents that modulate the activity of human
 aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
 as a means to screen in cellular assays for the inhibitors of beta- and
 gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
 polymerase chain reactions (PCR). The probes are useful for detecting
 Hu-Asp nucleic acids in *in vitro* assays and in Northern and Southern
 blots. The present cDNA sequence encodes human aspartyl protease 2
 (Hu-Asp2), a 'long' form designated as (Hu-Asp2a). Hu-Asp 2 gene is
 localised on chromosome 11q23.3-24.1.
 Sequence 2070 BP: 476 A: 583 C: 562 G: 449 T: 0 Other:
 Sequence 2070 BP: 476 A: 583 C: 562 G: 449 T: 0 Other:

Query Match	86.9%	Score 2039.8	DB 22	Length 2070
Best Local Similarity	99.9%	Pred. No. 0		
Matches 2041	Conservative 0	Mismatches 2	Indels 0	Gaps 0
Qy	306	ATGGCCCAAGCCCTCCCTCGCTCTGTGTGGATGGCGCGGAGTGTCTGCTGCCAC	365	
Db	1	ATGGCCCAAGCCCTGCCCCCTGCTCTGTGTGGATGGCGCGGAGTGTCTGCTGCCAC	60	
Qy	366	GGCACCCAGCACGGCATCCGGCTGCCCTGTGCAGCGGCTTGGGGGGCCCCCTTGGGG	425	
Db	61	GGCACCCAGCACGGCATCCGGCTGCCCTGTGCAGCGGCTTGGGGGGCCCCCTTGGGG	120	
Qy	426	CTGCGGCTGCCCGGAGACACGACCAAGACCCGAGGACCCGCGCGGAGGGGACGCTTT	485	
Db	121	CTGCGGCTGCCCGGAGACGACCAAGACCCGAGGACCCGCGCGGAGGGGACGCTTT	180	
Qy	486	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	545	
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240	
Qy	546	GTGGGACGCCCGCCGACAGCGTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTGCA	605	
Db	241	GTGGGACGCCCGCCGACAGCGTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTGCA	300	
Qy	606	GTGGGTGTGTGCCCGCCACCCCTTCCTGTGATCGCTACTACCAGAGGCAGCTGTCCAGCACA	665	
Db	301	GTGGGTGTGTGCCCGCCACCCCTTCCTGTGATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360	
Qy	666	TACCGGACCTCCGGAAGGTTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGAG	725	
Db	361	TACCGGACCTCCGGAAGGTTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGAG	420	
Qy	726	CTGGGACCGGACCTGGTAAGCATCCCCATGCCCCCAAGCTCACCTGCTGCGTGCCCACTTT	785	

Db 421 CTGGGACCGACCTGGTAAGCATCCCATGGCCCAAGCTCACTGTGCGTGCCAACATT 480
QY 786 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCCAACTGGGAAGGCATCCTG 845
Db 481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCCAACTGGGAAGGCATCCTG 540
QY 846 GGGTGGCCATATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 905
Db 541 GGGCTGGCCATATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
QY 906 CTGCTAAGCAGACCCAGCTTCCCAACCTCTTCTCCTCGCAGCTTTGTGTGCTGGCTTC 965
Db 601 CTGCTAAGCAGACCCAGCTTCCCAACCTCTTCTCCTCGCAGCTTTGTGTGCTGGCTTC 660
QY 966 CCCCTCAACCAAGTCTGAAGTGGCTGCTGCTCGGAGGAGCATGATCAATTTGAGGATTC 1025
Db 661 CCCCTCAACCAAGTCTGAAGTGGCTGCTGCTCGGAGGAGCATGATCAATTTGAGGATTC 720
QY 1026 GACCACTCGCTGTACACAGGAGTCTCTGTATATACACCCATCCGGGGAGTGGTATTAT 1085
Db 721 GACCACTCGCTGTACACAGGAGTCTCTGTATATACACCCATCCGGGGAGTGGTATTAT 780
QY 1086 GAGGTGATCTTTCGGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 1145
Db 781 GAGGTGATCTTTCGGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 840
QY 1146 TACAACATATGACAAGAGCATTTGTGACAGTGGCACCACCAACCTTCTGTTTGGCCCAAGAAA 1205
Db 841 TACAACATATGACAAGAGCATTTGTGACAGTGGCACCACCAACCTTCTGTTTGGCCCAAGAAA 900
QY 1206 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCCTCTCCACGGAGAAAGTTCCCTGAT 1265
Db 901 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCCTCTCCACGGAGAAAGTTCCCTGAT 960
QY 1266 GGTTCCTGGCTAGGAGACAGCTGTGTGCTGGCAAGCAGGACACCCCTTTGGAACATT 1325
Db 961 GGTTCCTGGCTAGGAGACAGCTGTGTGCTGGCAAGCAGGACACCCCTTTGGAACATT 1020
QY 1326 TTCCCACTGATCTCACTCTACTTAATGGGTGAGTTTACCAACCAAGTCTTCCCGCATCACC 1385
Db 1021 TTCCCACTGATCTCACTCTACTTAATGGGTGAGTTTACCAACCAAGTCTTCCCGCATCACC 1080
QY 1386 ATCCTTCGGCAGCAATACCTCGGGCCAGTGAAGATGTGGCCACGTGCCAAGACGACTGT 1445
Db 1081 ATCCTTCGGCAGCAATACCTCGGGCCAGTGAAGATGTGGCCACGTGCCAAGACGACTGT 1140
QY 1446 TACAAGTTGGCATCTCACAGTCAATCCAGGGCAGTGTATGGGAGCTGTATCATGAG 1505
Db 1141 TACAAGTTGGCATCTCACAGTCAATCCAGGGCAGTGTATGGGAGCTGTATCATGAG 1200
QY 1506 GGCTTCTACGTTGCTTTGATCGGGCCCGGAAACCAAGTGGCTTGTGTCAGGCGCTTC 1565
Db 1201 GGCTTCTACGTTGCTTTGATCGGGCCCGGAAACCAAGTGGCTTGTGTCAGGCGCTTC 1260
QY 1566 CATGTGCACGATAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1625
Db 1261 CATGTGCACGATAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320
QY 1626 GAAGACTGTGCTACAACTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT 1685
Db 1321 GAAGACTGTGCTACAACTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT 1380
QY 1686 GTCATGGCTGGCATCTGGCCCTCTTTCATGCTGCCACTCTGCTCATGTTGTGTCAGTGG 1745
Db 1381 GTCATGGCTGGCATCTGGCCCTCTTTCATGCTGCCACTCTGCTCATGTTGTGTCAGTGG 1440
QY 1746 CGTGTCCCTCGCTCGCTCGGCGAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1805
Db 1441 CGTGTCCCTCGCTCGCTCGGCGAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
QY 1806 AAGTGAAGAGGCCCATGGGACAGATAGAGATTCCCTGGACACACCTCCGCTGGTTCA 1865
|||||

Db 1501 AAGTGAAGAGGCCCATGGGACAGATAGAGATTCCCTGGACACACCTCCGCTGGTTCA 1560
QY 1866 CTTTGGTCAACAAGTAGGAGACACAGATGGCAGCTGTGGCCAGAGCAGCTCAGACCCCTCC 1925
Db 1561 CTTTGGTCAACAAGTAGGAGACACAGATGGCAGCTGTGGCCAGAGCAGCTCAGACCCCTCC 1620
QY 1926 CCACCCCAACAAATGCCCTTGGCTTGTATGGAGAAGGAAAAGGCTGGCAAGCTGGTTCAG 1985
Db 1621 CCACCCCAACAAATGCCCTTGGCTTGTATGGAGAAGGAAAAGGCTGGCAAGCTGGTTCAG 1680
QY 1986 GGAATGTACCTGTAGGAACACAGAAAGAGAAAGAAAGAAAGCTGCTGCGCGGAATACT 2045
Db 1681 GGAATGTACCTGTAGGAACACAGAAAGAGAAAGAAAGAAAGCTGCTGCGCGGAATACT 1740
QY 2046 CTTTGGTCAACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 2105
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QY 2106 TTGTCCCACTTCTTAAATTTCTCAACCCCAAGATTTCTTTCTTTAGTTTCAGAA 2165
Db 1801 TTGTCCCACTTCTTAAATTTCTCAACCCCAAGATTTCTTTCTTTAGTTTCAGAA 1860
QY 2166 GTACTGGCATCACAGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCCTGGCAGAGAAG 2225
Db 1861 GTACTGGCATCACAGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCCTGGCAGAGAAG 1920
QY 2226 AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGTCTATT 2285
Db 1921 AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGTCTATT 1980
QY 2286 TGCTTTAGAGACAGGAGCTGTATAAACAAGCCTTAACATTTGGTGCAAGATTGCTCTTTGA 2345
Db 1981 TGCTTTAGAGACAGGAGCTGTATAAACAAGCCTTAACATTTGGTGCAAGATTGCTCTTTGA 2040
QY 2346 ATT 2348
Db 2041 ATT 2043
|||||
RESULT 7
AAS11517
ID AAS11517 standard; cDNA: 2070 BP.
XX AAS11517;
XX AC
XX DT
XX DT
XX 24-OCT-2001 (first entry)
XX Human cDNA encoding Aspartyl protease 2(a), Asp2(a).
XX DE
XX Human: Aspartyl protease; Asp2(a); beta-secretase; neurotropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta; ss.
XX OS
XX Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 1..1506
FT FT /*tag= a
FT FT /product= "Asp2(a)"
FT FT sig_peptide 1..63
FT FT /*tag= b
FT FT sig_peptide 64..135
FT FT /*tag= c
FT FT sig_peptide 136..171
FT FT /label= Pre_pro_peptide
FT FT /*tag= d
FT FT /label= Pro_peptide
FT FT mat_peptide 172..1503
FT FT /*tag= e
FT FT /label= Mature_Asp2(a)
XX XX WO200149098-A2.
XX XX

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Db 1441 CGCTGCCCTCCGCTGCTGGCCAGCAGCATGATGACTTTGCTGTGATGACATCTCCCTGCTG 1500
QY 1806 AAGTGAGGAGGCCATGGGCAGAAGATAGAGATTCCCTGGACCACACCTCCGCTGGTTCA 1865
Db 1501 AAGTGAGGAGGCCATGGGCAGAAGATAGAGATTCCCTGGACCACACCTCCGCTGGTTCA 1560
QY 1866 CTTTGGTGCACAAATTAAGTAGGACACAGATGGCACTGTGGCCAGAGCACCTCAGGACCCCTCC 1925
Db 1561 CTTTGGTGCACAAATTAAGTAGGACACAGATGGCACTGTGGCCAGAGCACCTCAGGACCCCTCC 1620
QY 1926 CCACCCACCAATGCTCTGCTCTGTATGAGAGAGAAAGGCTGGCAAGCTGGGTTCCAG 1985
Db 1621 CCACCCACCAATGCTCTGCTCTGTATGAGAGAGAAAGGCTGGCAAGCTGGGTTCCAG 1680
QY 1986 GGACTGTACCTGTAGGAACAGAAAGAGAAAGAAAGCACTCTGCTGGCGGGAATACT 2045
Db 1681 GGACTGTACCTGTAGGAACAGAAAGAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740
QY 2046 CTTGGTCACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAAGCCCTGAACCT 2105
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QY 2106 TTGTCCACCATTCCTTTAAATTTCTCAACCCAAAGATTTCTTCTTTAGTTTCAGAA 2165
Db 1801 TTGTCCACCATTCCTTTAAATTTCTCAACCCAAAGATTTCTTCTTTAGTTTCAGAA 1860
QY 2166 GTACTGGCATCACAGCGAGTGTACCTTGGCGTGTGCTCCCTGTGTACCTGGCAGAGAG 2225
Db 1861 GTACTGGCATCACAGCGAGTGTACCTTGGCGTGTGCTCCCTGTGTACCTGGCAGAGAG 1920
QY 2226 AGACCAAGCTGTTTCCCTGCTGGCCAAAGTAGTAGGAGAGGATGCACAGTTTGCTATT 2285
Db 1921 AGACCAAGCTGTTTCCCTGCTGGCCAAAGTAGTAGGAGAGGATGCACAGTTTGCTATT 1980
QY 2286 TGCTTTAGAGACAGGAGCTGTATAACAAGCCTTAACATTGCTGCAAGATTGCCCTTTGA 2345
Db 1981 TGCTTTAGAGACAGGAGCTGTATAACAAGCCTTAACATTGCTGCAAGATTGCCCTTTGA 2040
QY 2346 ATT 2348
Db 2041 ATT 2043

RESULT 8

AAS11702
ID AAS11702 standard; DNA: 2070 BP.

XX AAS11702;
AC AAS11702;

XX 24-OCT-2001 (first entry)
DE DNA encoding human aspartyl protease 2a (Asp-2a).

XX Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; ds.
XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 1..1506
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FT /product= "Aspartyl protease-2a (Asp-2a)"
FT 1..63

FT sig_peptide /*tag= b
FT 64..135
FT misc_feature /*tag= c

FT misc_feature /note= "Pre-propeptide"
FT 136..171
FT /*tag= d
FT /note= "Propeptide"
FT 172..1503
FT /*tag= e
FT /note= "Mature Aspartyl protease-2a"

XX WO200149097-A2.

XX 12-JUL-2001.

XX 09-MAY-2001; 2001WO-IB00797.

XX 09-MAY-2001; 2001WO-IB00797.

XX (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX WPI; 2001-502548/55.
DR P-PSDB; AAU07102.

XX Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -

XX Claim 98: Fig 2; 185pp: English.

XX The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing
CC an APP cleavage site recognisable by a mammalian beta-secretase, and
CC further comprising two lysine residues at the carboxyl terminus of the
CC amino acid sequence of the mammalian APP or APP fragment. The
CC polypeptides are used for assaying for modulators of beta-secretase
CC activity; identifying agents that inhibit the APP processing activity
CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC modulate the activity of Asp2; and for reducing cellular production of
CC amyloid beta (Abeta) from APP. Agents identified by the above methods
CC are useful for treating Alzheimer's disease; and for identifying
CC modulators of amyloid-beta (Abeta) peptide production, for use in
CC designing therapeutics for the treatment or prevention of Alzheimer's
CC disease. Probes and primers derived from Asp nucleic acid sequences
CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence represents the
CC coding sequence of human Asp-2a used in the methods of the invention.

XX Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match 86.9%; Score 2039.8; DB 22; Length 2070;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 306 ATGGCCCAAGCCCTGCCCTGGCTCCTCTGTGGATGGCGCGGGAGTGTGCTGCCAC 365
Db 1 ATGGCCCAAGCCCTGCCCTGGCTCCTCTGTGGATGGCGCGGGAGTGTGCTGCCAC 60

QY 366 GGCACCCAGCAGGCATCCGGCTGCCCTGTGCGACGCGCCCTGGGGGGGCCCCCTCGGG 425
Db 61 GGCACCCAGCAGGCATCCGGCTGCCCTGTGCGACGCGCCCTGGGGGGGCCCCCTCGGG 120

QY 426 CTGGCGCTGCCCGGGGAGACCCGAGAGAGCCCGGAGGCGCGGAGGCGACGCTTT 485
Db 121 CTGGCGCTGCCCGGGGAGACCCGAGAGAGCCCGGAGGCGCGGAGGCGACGCTTT 180


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QY 506 GTGGTGTGTCGCCCCACCCCTTCTGCGATCGCTACACAGAGGCGAGCTGCCAGACA 665
DB 301 GTGGTGTGTCGCCCCACCCCTTCTGCGATCGCTACACAGAGGCGAGCTGCCAGACA 360
QY 666 TACCGGAGACCTCCGGAAGGCTGTATGTGCGCTACACCCAGGCAAGTGGGAAGGGAG 725
DB 361 TACCGGAGACCTCCGGAAGGCTGTATGTGCGCTACACCCAGGCAAGTGGGAAGGGAG 420
QY 726 CTGGGCAACCGGACCTGTGAAGCATCCGCCATGGGCCCAACGTCACCTGTGCGTGCCCAACATT 785
DB 421 CTGGGCAACCGGACCTGTGAAGCATCCGCCATGGGCCCAACGTCACCTGTGCGTGCCCAACATT 480
QY 786 GCTGCCATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCAATCCG 845
DB 481 GCTGCCATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCAATCCG 540
QY 846 GGGCTGGGCTATGCTGAGATTGCCAGGCTGACGACCTCCCTGGAGCCCTTCTTTGACTCT 905
DB 541 GGGCTGGGCTATGCTGAGATTGCCAGGCTGACGACCTCCCTGGAGCCCTTCTTTGACTCT 600
QY 906 CTGTTAAAGCAGACCCACCTTCCCAACCTCTTCTCCCTGCACGCTTGTGGTCTGGCTTC 965
DB 601 CTGTTAAAGCAGACCCACCTTCCCAACCTCTTCTCCCTGCACCTTGTGGTCTGGCTTC 660
QY 966 CCCCTCAACCACTGTGAAGTGTGGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC 1025
DB 661 CCCCTCAACCACTGTGAAGTGTGGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC 720
QY 1026 GACCACCTCGCTACACAGGCGAGTCTGTGTATACACCCATCCCGGGGAGTGGTATTAT 1085
DB 721 GACCACCTCGCTACACAGGCGAGTCTGTGTATACACCCATCCCGGGGAGTGGTATTAT 780
QY 1086 GAGGTGATCATTTGTGCGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 1145
DB 781 GAGGTGATCATTTGTGCGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
QY 1146 TACAACATATGACAAAGCATTTGGACAGTGGGACACCAACCACTTCGTTTGGCCCAAGAAA 1205
DB 841 TACAACATATGACAAAGCATTTGGACAGTGGGACACCAACCACTTCGTTTGGCCCAAGAAA 900
QY 1206 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGCGAGCCCTCCACGGGAGAAAGTTCCCTGAT 1265
DB 901 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGCGAGCCCTCCACGGGAGAAAGTTCCCTGAT 960
QY 1266 GGTTCCTGGCTAGGAGAGAGCTGTGTGTGCGCAAGCAGCACCACCCCTTGGAAACATT 1325
DB 961 GGTTCCTGGCTAGGAGAGAGCTGTGTGTGCGCAAGCAGCACCACCCCTTGGAAACATT 1020
QY 1326 TTCCCAAGTCATCTCACTCTACCTAATGCGTGAGGTACCAACCACTCCTTCGGCATCACC 1385
DB 1021 TTCCCAAGTCATCTCACTCTACCTAATGCGTGAGGTACCAACCACTCCTTCGGCATCACC 1080
QY 1386 ATCCTTCGGCAGCAATACCTCGGGCAGTGGAAGATGTGGCCACGTCCCAAGACCACTGT 1445
DB 1081 ATCCTTCGGCAGCAATACCTCGGGCAGTGGAAGATGTGGCCACGTCCCAAGACCACTGT 1140
QY 1446 TACAAGTTTGCCATCTCAGTCATCCACGGGCACTGTTATGGAGCTGTTATCATGGAG 1505
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QY 1506 GGCTTCACGTTGCTTTGATCGGGCCCGAAAACGAATGGCTTTGCTGTGAGCGCTTGC 1565
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QY 1626 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1685
DB 1321 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1380
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DB 1381 GTCATGGCTGCCATCTCGGCCCTCTTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
QY 1746 CGCTGCCTCGGCTGCGCTGGCCAGCAGCATGATGACTTTTGCTGTGATGACATCTCCCTGCTG 1805
DB 1441 CGCTGCCTCGGCTGCGCTGGCCAGCAGCATGATGACTTTTGCTGTGATGACATCTCCCTGCTG 1500
QY 1806 AAGTAGGAGGCGCATGGGAGAGATAGAGATCCCTGGACCAACACCTCCGTTGGTTCA 1865
DB 1501 AAGTAGGAGGCGCATGGGAGAGATAGAGATCCCTGGACCAACACCTCCGTTGGTTCA 1560
QY 1866 CTTTGGTCAACAAGTAGGAGACACAGATGGCACCCTGTGGCCAGAGCACTCTCAGGACCCCTCC 1925
DB 1561 CTTTGGTCAACAAGTAGGAGACACAGATGGCACCCTGTGGCCAGAGCACTCTCAGGACCCCTCC 1620
QY 1926 CCACCCACCAATGCCCTCTGCCCTTGATGGAGAAAGGCTGGCAAGGTGGTGGTCCAG 1985
DB 1621 CCACCCACCAATGCCCTCTGCCCTTGATGGAGAAAGGCTGGCAAGGTGGTGGTCCAG 1680
QY 1986 GGACTGTACTCTGTAGGAAACAGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2045
DB 1681 GGACTGTACTCTGTAGGAAACAGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1740
QY 2046 CTTGTTACCTCAAAATTTAAGTCGGGAAATTCCTGCTGTGTTGAAACTTCAGCCCTGAAACCT 2105
DB 1741 CTTGTTACCTCAAAATTTAAGTCGGGAAATTCCTGCTGTGTTGAAACTTCAGCCCTGAAACCT 1800
QY 2106 TTGTTCCACCATTCCTTTAAATTCCTCAACCCAAAGTATTCCTTTCTTTAGTTTCAGAA 2165
DB 1801 TTGTTCCACCATTCCTTTAAATTCCTCAACCCAAAGTATTCCTTTCTTTAGTTTCAGAA 1860
QY 2166 GTACTGGCATCAACGAGGTTTACCTTGGCGTGTCTCCCTGTGGTACCCTGGCAGACAAG 2225
DB 1861 GTACTGGCATCAACGAGGTTTACCTTGGCGTGTCTCCCTGTGGTACCCTGGCAGACAAG 1920
QY 2226 AGACCAAGCTTGTTCCTCTGCTGCCAAAGTCAGTAGGAGAGATGCACAGTTTGTCTATT 2285
DB 1921 AGACCAAGCTTGTTCCTCTGCTGCCAAAGTCAGTAGGAGAGATGCACAGTTTGTCTATT 1980
QY 2286 TGCTTTAGAGACAGGACTGTATAAACAAGCTTAACATTGGTGCAAGATTTGCCCTCTTGA 2345
DB 1981 TGCTTTAGAGACAGGACTGTATAAACAAGCTTAACATTGGTGCAAGATTTGCCCTCTTGA 2040
QY 2346 ATT 2348
DB 2041 ATT 2043
```

RESULT 11
ABL49914
ID ABL49914 standard; DNA; 2070 BP.

XX ABL49914;

XX AC ABL49914;

DT 31-MAY-2002 (first entry)

XX Human aspartyl protease nucleotide sequence SEQ ID NO:1.

DE Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;

XX aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;

XX Alzheimer's disease; gene; ds.

OS Homo sapiens.

XX WO200206306-A2.

XX 24-JAN-2002.

XX 19-JUL-2001; 2001WO-US23035.

XX 19-JUL-2000; 2000US-219795P.

XX 12-MAR-2001; 2001US-275251P.

XX


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XX 04-JAN-2001.
XX 27-JUN-2000; 2000WO-US17661.
XX
PR 28-JUN-1999; 99US-0141363.
PR 30-NOV-1999; 99US-0168060.
PR 25-JAN-2000; 2000US-0177836.
PR 27-JUN-2000; 2000US-0178368.
PR 08-JUN-2000; 2000US-0210292.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
XX Tang JJN, Lin X, Koelsch G;
PI WPI; 2001-102885/11.
XX
DR Purified recombinant catalytically active memapsin 2, used to screen
PT inhibitors of it, which are used to treat and prevent Alzheimer's
PT disease -
XX
XX Example 1; Page 71-72; 86pp; English.
XX
CC The present invention relates to a purified recombinant
CC catalytically active memapsin 2. The invention may be used for
CC isolating inhibitors which are used to treat or prevent
CC Alzheimer's disease. The invention may also be used to screen
CC for individuals more genetically prone to develop Alzheimer's
CC disease.
XX
XX Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;
SQ
Query Match 85.3%; Score 2004; DB 22; Length 3252;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GCGGGAGTGTCTGCCACGCCACCCAGCAGCGGATCCGGCTGCCCTGCCAGCGGC 60
QY 405 CTGGGGGGCCCCCTGGGGCTGCGGCTGCCCGGGAGACCGACGAGCCCGGAGGAG 464
DB 61 CTGGGGGGCCCCCTGGGGCTGCGGCTGCCCGGGAGACCGACGAGCCCGGAGGAG 120
QY 465 CCGCGCGGAGGGGAGCTTTGTGGAGATGCTGGACACCTGAGGGGCAAGTGGGGCAG 524
DB 121 CCGCGCGGAGGGGAGCTTTGTGGAGATGCTGGACACCTGAGGGGCAAGTGGGGCAG 180
QY 525 GGCTACTACGTGGAGATGACCGTGGGAGCGCCCGCCGAGACGCTCAACATCCTGGTGGAT 584
DB 181 GGCTACTACGTGGAGATGACCGTGGGAGCGCCCGCCGAGACGCTCAACATCCTGGTGGAT 240
QY 585 ACAGGCAGCAGTAACCTTGGCAGTGGGTGCTGCCCGCCGAGACGCTTCCCTGGTACTAC 644
DB 241 ACAGGCAGCAGTAACCTTGGCAGTGGGTGCTGCCCGCCGAGACGCTTCCCTGGTACTAC 300
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DB 301 CAGAGCAGCTGTCAGCACATACCGGACCTCCGGAGGAGTGTGTATGTCCTACACC 360
QY 705 CAGGGCAAGTGGGAAGGGAGCTGGGCACCGACCTGTGAAGCATGCCCATGGCCCCAAC 764
DB 361 CAGGGCAAGTGGGAAGGGAGCTGGGCACCGACCTGTGAAGCATGCCCATGGCCCCAAC 420
QY 765 GTCAGTGTGGTGGCAACATTTGTCATGTCATCACTGAATCAGACAAGTTCCTATCAACGGC 824
DB 421 GTCAGTGTGGTGGCAACATTTGTCATGTCATCACTGAATCAGACAAGTTCCTATCAACGGC 480
QY 825 TCCAACCTGGGAAGGACATCCTGGGGCTGGCCTATGCTAGATGTCAGGCTGAGACTCC 884
DB 481 TCCAACCTGGGAAGGACATCCTGGGGCTGGCCTATGCTAGATGTCAGGCTGAGACTCC 540
QY 885 CTGGAGCCTTTCTTGACTCTCTGGTAAAGCAGACCCACCGTTCCCAACCTCTTCTCCCTG 944
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DB 601 CAGCTTTGTGGTGTGCTGGCTTCCCCCTCAACAGCTCTCAAGTGTGGCTCTGTGGAGGG 660
QY 1005 AGCATGATCATTTGGAGGTATCGACCACTCGCTGTACACAGCAGCTCTCTGGTATACACC 1064
DB 661 AGCATGATCATTTGGAGGTATCGACCACTCGCTGTACACAGCAGCTCTCTGGTATACACC 720
QY 1065 ATCCGGGGGAGTGGTATTATGAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGAT 1124
DB 721 ATCCGGGGGAGTGGTATTATGAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGAT 780
QY 1125 CTGAAATGACATGCAAGGAGTACAACATATGACAAGAGCATTTGGGACAGTGGCACACC 1184
DB 781 CTGAAATGACATGCAAGGAGTACAACATATGACAAGAGCATTTGGGACAGTGGCACACC 840
QY 1185 AACCTTCGTTTGGCCCAAGAAAGTGTTTGAAGCTGACGTCAAAATCCATCAAGGCAGCCTCC 1244
DB 841 AACCTTCGTTTGGCCCAAGAAAGTGTTTGAAGCTGACGTCAAAATCCATCAAGGCAGCCTCC 900
QY 1245 TCCACGGAGAAAGTTCCCTGATGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGCAAGCA 1304
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DB 1021 AACAGTCCCTTCCGATCAGCATCTTCCGACGACAAATACCTTGGCCGAGTGAAGATGTG 1080
QY 1425 GCCAGTCCCAAGACGACTGTTTACAAGTTTGGCCATCTCACAGTCTATCCACGGGCACTGTT 1484
DB 1081 GCCAGTCCCAAGACGACTGTTTACAAGTTTGGCCATCTCACAGTCTATCCACGGGCACTGTT 1140
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DB 1141 ATGGGAGCTGTTATCATGAGGGGCTTCTAGCTTGTCTTGTATCGGGCCCGGAAACGAATT 1200
QY 1545 GGCTTTCTGTACGCGCTTGCATGTGCAGATGATGATGATGATGATGATGATGATGATGATGAT 1604
DB 1201 GGCTTTCTGTACGCGCTTGCATGTGCAGATGATGATGATGATGATGATGATGATGATGATGAT 1260
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DB 1261 CCTTTTCTACCTTGGACATGGAAGACTGTGGCTTACAACATTTCCACAGACAGATGAGTCA 1320
QY 1665 ACCCTCATGACCATAGCCTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1724
DB 1321 ACCCTCATGACCATAGCCTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1725 TGCTCATGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1784
DB 1381 TGCTCATGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1785 GCTCATGACATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1844
DB 1441 GCTCATGACATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1845 GGACACACCTCCCTGGTTCACCTTGGTTCACAGTAGAGACAGATGGCACCTGTGGC 1904
DB 1501 GGACACACCTCCCTGGTTCACCTTGGTTCACAGTAGAGACAGATGGCACCTGTGGC 1560
QY 1905 CAGAGCAGCTCAGGACCTCCACACCCACCAATGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1964
DB 1561 CAGAGCAGCTCAGGACCTCCACACCCACCAATGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1965 GGCTGGCAAGTGGGTTCACCTGTAGGAAACAGAAAAAGAGAAAGAAAG 2024
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Db 781 CTGAAATGGAGTCTCAAGGAGTACAACATATGACAAGAGCATTTGGACAGTGGCAACCACC 840
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Qy 2325 GGTGCAAAAGATTGGCTCTTTGAATT 2348
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Search completed: March 1, 2003, 22:17:24
Job time : 354.5 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2003, 13:38:25 ; Search time 4002 Seconds
(without alignments)
17074.810 Million cell updates/sec

Title: US-09-723-722A-42
Perfect score: 2348
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg.*
3: gb_in.*
4: gb_om.*
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6: gb_pat.*
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8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2342.8	99.8	2526	9	AF190725	AF190725 Homo sapi
2	2341.2	99.7	5878	9	AF201468	AF201468 Homo sapi
3	2331.8	99.3	5814	9	AB032975	AB032975 Homo sapi
4	2181.2	92.9	5757	6	AX364933	AX364933 Sequence
5	2041.4	86.9	2070	9	AF200343	AF200343 Homo sapi
6	2039.8	86.9	2070	6	AX105385	AX105385 Sequence
7	2039.8	86.9	2070	6	AX378015	AX378015 Sequence
8	2024	86.2	2541	6	AF178469	AF178469 Sequence
9	2024	86.2	2541	6	AX002655	AX002655 Sequence
10	2024	86.2	2541	6	E50816	E50816 Aspartate p
11	2004	85.3	3252	6	AX062111	AX062111 Sequence
12	2004	85.3	3252	6	AX063201	AX063201 Sequence
13	2004	85.3	3252	6	AX472368	AX472368 Sequence
14	2004	85.3	3252	9	AF200193	AF200193 Homo sapi
15	1881	80.1	1977	6	AX105387	AX105387 Sequence
16	1881	80.1	1977	6	AX378017	AX378017 Sequence
17	1835.4	78.2	2370	6	AF178470	AF178470 Sequence
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25	1506	64.1	1506	9	AF204943	AF204943 Homo sapi
26	1380	58.8	1465	9	AB050436	AB050436 Homo sapi
27	1355.8	57.7	1362	6	AX105411	AX105411 Sequence
28	1355.8	57.7	1380	6	AX105413	AX105413 Sequence
29	1344.4	57.3	1431	9	AF338816	AF338816 Homo sapi
30	1298	55.3	1506	6	AR202196	AR202196 Sequence
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38	1180	50.3	1278	6	AX105409	AX105409 Sequence
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C 41	781.2	33.3	134278	9	AP001822	AP001822 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS
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cnds.
ACCESSION AF190725
VERSION AF190725.1 GI:6118538
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2526)
AUTHORS Vassar,R., Bennett,B.D., Babu-Khan,S., Kahn,S., Mendiaz,E.A., Denis,P., Teplow,D.B., Ross,S., Amarante,P., Loeloff,R., Luo,Y.,

Fisher, S., Fuller, J., Edenson, S., Lile, J., Jarosinski, M.A.,
Biere, A.L., Curran, E., Burgess, T., Louis, J.C., Collins, F.,
Trenor, J., Rogers, G. and Citron, M.
Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
the transmembrane aspartic protease_BACE

Science 286 (5440), 735-741 (1999)
20002972
10531052

REFERENCE

2 (bases 1 to 2526)

Bennett, B.D., Vassar, R. and Citron, M.

Direct Submission

Submitted (29-SEP-1999) Neuroscience, Amgen Inc., One Amgen Center

Dr., Thousand Oaks, CA 91320-1799, USA

JOURNAL

Location/Qualifiers

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1. .2526

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454. .1959

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534 a 781 c 715 g 456 t

BASE COUNT

ORIGIN

Query Match 99.8%; Score 2342.8; DB 9; Length 2526;
Best Local Similarity 99.8%; Pred. No. 0;
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QY 61 CSGTGCGGATGTAGCGGCTCCGATCCAGCCTCTCCCTGCTCCCGTCTCTCGCGAT 120
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RESULT 3
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LOCUS Homo sapiens mRNA for KIAA149 protein, partial cds.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Hirose, M., Nagase, T., Ishikawa, K., Kikuno, R., Nomura, N. and Ohara, O.

TITLE Characterization of cDNA clones selected by the GeneMark analysis
from-size-fractionated cDNA libraries from human brain
JOURNAL DNA Res 6 (5): 329-336 (1999)
MEDLINE 20039618
REFERENCE 2 (bases 1 to 5814)
AUTHORS Ohara, O., Nagase, T. and Kikuno, R.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail: cdna@kazusa.or.jp)
URL: http://www.kazusa.or.jp/huge/, Tel: +81-438-52-3913,
Fax: +81-438-52-3914
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AUTHORS Novel nucleic acid and amino acid sequences
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JOURNAL Compugen Ltd. (IL)
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 1. (bases 1 to 2070)
 B. AUTHORS Van R. Binkowski, M.J., Shuck, M.E., Miao, H., Tory, M.C.,
 Buhl, A., Mahey, A.W., Brashier, J.R., Stratan, N.C., Mathews, W.R.,
 Carter, D.B., Tomasselli, A.G., Parodi, L.A., Heinrikson, R.L. and
 Currey, M.M.
 TITLE Membrane-anchored aspartyl protease with Alzheimer's disease
 beta-secretase activity
 JOURNAL Nature 402 (6761), 533-537 (1999)
 MEDLINE 20057170
 PUBMED 10591213
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 2. (bases 1 to 2070)
 Binkowski, M.J., Shuck, M.E., Slightom, J.L. and Drong, R.F.
 AUTHORS Direct Submission
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RESULT 6
AX105385
LOCUS AX105385 2070 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 3 from Patent WO0123533.
ACCESSION AX105385
VERSION AX105385.1 GI:13921511
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2070)
AUTHORS Gurney,M. and Bienkowski,M.J.
TITLE Alzheimer's disease secretase, app substrates therefor, and uses therefor

JOURNAL Patent: WO 0123533-A 3 05-APR-2001;
Pharmacia & Upjohn Company (US)
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Location/Qualifiers
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BASE COUNT 476 a 583 c 562 g 449 t
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Query Match 86.98; Score 2039.8; DB 6; Length 2070;
Best Local Similarity 99.9%; Pred. No. 0;
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QY 2346 ATT 2348
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RESULT 7
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LOCUS AX378015 2070 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 1 from Patent WO0206306.
ACCESSION AX378015
VERSION AX378015.1 GI:19574050
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Yan, R., Tomasselli, A. G., Gurney, M. E., Emmons, T. L., Bienkowski, M. J.
and Heintz, R. L.
TITLE Substrates and assays for _g(b)-secretase activity
JOURNAL Patent: WO 0206306-A 1 24-JAN-2002;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES
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Best Local Similarity 99.9%; Pred. No. 0;
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ACCESSION AX002655
VERSION AX002655.1 GI:7242133
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified
REFERENCE 1 (bases 1 to 2541)
AUTHORS Murphy, K. and Chapman, C.G.
TITLE Aspartic proteinase 2 (ASP2)
JOURNAL Patent: EP 0855444-A 1 29-JUL-1998;
SMITHKLINE BEECHAM PLC (GB); SMITHKLINE BEECHAM CORP (US)
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Q	y	1266	GGTTTTCTGGCTAGGAGAGCAGCTGTGTGTCTGGCAAGCAGGACACACCCCTTTGGAAACATT	1325
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DEFINITION	Aspartate proteinase ASP2.		
ACCESSION	E50816		
VERSION	E50816.1 GI:13023199		
KEYWORDS	JP 2000060579-A/1.		
SOURCE	unidentified.		
ORGANISM	unidentified.		
REFERENCE	1 (bases 1 to 2541)		
AUTHORS	David,J.P., Conrad,G.C., Kay,M. and Trudy,S.S.		
TITLE	Aspartate proteinase ASP2		
JOURNAL	Patent: JP 2000060579-A 1 29-FEB-2000;		
COMMENT	SMITHKLINE-BEECHAM CORP		
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	PI DAVID J POWER, CONRAD G CHAPPUMAN, KAY MAFI, TRUDY S SMITH PC		
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	A61K39/395, A61K48/00,		
	PC A61P25/28, A61P35/00, A61P43/00, C07K16/40, C12N1/15, C12N1/19, PC		
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LOCUS AX062111 3252 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 1 from Patent WO0100665.
ACCESSION AX062111
VERSION AX062111.1 GI:12540032

SOURCE
human.

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3252)
 AUTHORS Tang, J. J., Hong, L. and Ghosh, A. K.
 TITLE Inhibitors of membrane protein 2 and use thereof
 JOURNAL Patent WO 01/00665, A1, 2001, 6 JAN. 2001, 144
 OklaHoma-Medical-Research-Foundation-(US) ; THE BOARD OF TRUSTEES
 OF THE UNIVERSITY OF ILLINOIS (US)

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Query Match 85.3%; Score 2004; DB 6; Length 3252;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps

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RESULT 12
AX063201 LOCUS AX063201 3252 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 1 from Patent WO0100663.
ACCESSION AX063201
VERSION AX063201.1 GI:12541045
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3252)
AUTHORS Tang, J. J., Lin, X. and Koelsch, G.
TITLE Catalytically active recombinant memapsin and methods of use there
of
JOURNAL Patent: WO 0100663-A 1 04-JAN-2001;
Oklahoma Medical Research Foundation (US)
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BASE COUNT 804 a 863 c 811 g 771 t 3 others
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Query Match 85.3%; Score 2004; DB 6; Length 3252;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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VERSION AX472368.1 GI:22207364
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DEFINITION Sequence 5 from Patent WO0123533.
ACCESSION AX105387
VERSION AX105387.1 GI:13921512
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 1977)
AUTHORS Gurney,M. and Bienkowski,M.J.
TITLE Alzheimer's disease secretase, app substrates therefor, and uses therefor
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Qy 1086 GAGGTATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 1145
Db 706 GAGGTATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 765
Qy 1146 TACAACCTATGACAAGAGCATTGTGGACAGTGGCACCAACCACTTCGTTGCCCAAGAAA 1205
Db 766 TACAACCTATGACAAGAGCATTGTGGACAGTGGCACCAACCACTTCGTTGCCCAAGAAA 825
Qy 1206 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCCTCTCCACGGAGAGTTCCTTGAT 1265
Db 826 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCCTCTCCACGGAGAGTTCCTTGAT 885
Qy 1266 GGTTCCTGGCTAGGAGAGCAGCTGTGCTGGCAAGCAGGACCAACCCCTTTGGAACATT 1325
Db 886 GGTTCCTGGCTAGGAGAGCAGCTGTGCTGGCAAGCAGGACCAACCCCTTTGGAACATT 945
Qy 1326 TTCCCAAGTCACTCTACCTAATGGGTGAGGTTACCAACAGTCCCTTCCGCATCAACC 1385
Db 946 TTCCCAAGTCACTCTACCTAATGGGTGAGGTTACCAACAGTCCCTTCCGCATCAACC 1005
Qy 1386 ATCCTTCCGAGCAATACCTCGGCGCAGTGAAGATGTGGCCACAGTCCCAAGACGACTGT 1445
Db 1006 ATCCTTCCGAGCAATACCTCGGCGCAGTGAAGATGTGGCCACAGTCCCAAGACGACTGT 1065
Qy 1446 TACAAGTTTCCATCTCACAGTCAATCCACGGCAGTGTATGGAGCTGTTATCATGGAG 1505
Db 1066 TACAAGTTTCCATCTCACAGTCAATCCACGGCAGTGTATGGAGCTGTTATCATGGAG 1125
Qy 1506 GGCTTCTACGTTGCTTTGATGGGCGCCGAAAACGAATTTGGCTTTGCTGTCAGCGTTGC 1565
Db 1126 GGCTTCTACGTTGCTTTGATGGGCGCCGAAAACGAATTTGGCTTTGCTGTCAGCGTTGC 1185
Qy 1566 CATGTGCACATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTGTACCTTTGGACATG 1625
Db 1186 CATGTGCACATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTGTACCTTTGGACATG 1245
Qy 1626 GAAGACTGTGGCTACAACTTCCACAGACAGTGAAGTCAACCCCTCATGACCATAGCCTAT 1685
Db 1246 GAAGACTGTGGCTACAACTTCCACAGACAGTGAAGTCAACCCCTCATGACCATAGCCTAT 1305
Qy 1686 GTCATGGCTGCCATCTCGCCCTCTTCATGCTGCCACTCTGCTCATGCTGTGTCAGTGG 1745
Db 1306 GTCATGGCTGCCATCTCGCCCTCTTCATGCTGCCACTCTGCTCATGCTGTGTCAGTGG 1365
Qy 1746 CGGTGCTCGCTGCCCTGCCCGCAGCAGCATGATGACTTTGTGATGACATCTCCCTGCTG 1805
Db 1366 CGGTGCTCGCTGCCCTGCCCGCAGCAGCATGATGACTTTGTGATGACATCTCCCTGCTG 1425
Qy 1806 AAGTGAAGAGGCCCATGGGAGAGATAGATTTCCCTGGACACACCTCCGTTGTTCA 1865
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Search completed: March 2, 2003, 00:31:06

Job time : 4029 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 4, 2003, 10:00:56 ; Search time 17 Seconds
(without alignments)
789.227 Million cell updates/sec

Title: US-09-723-722A-43

Perfect score: 2419

Sequence: 1 ETDEPEPEGRGSGFVEMVD.....CLRLCRLQHQDDFADDISLIK 456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2.6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2.6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2.6/ptodata/1/iaa/6B_COMB.pep.*

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6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2419	100.0	501	US-09-548-372D-4	Sequence 4, Appli
2	2419	100.0	501	US-09-548-367D-4	Sequence 4, Appli
3	2413	99.8	501	US-09-009-191-2	Sequence 2, Appli
4	2390	98.8	501	US-09-713-158-2	Sequence 2, Appli
5	2390	98.8	501	US-09-548-372D-8	Sequence 8, Appli
6	2390	98.8	501	US-09-548-367D-8	Sequence 8, Appli
7	2320	95.9	774	US-09-009-191-4	Sequence 4, Appli
8	2264.5	93.6	476	US-09-548-372D-6	Sequence 6, Appli
9	2264.5	93.6	476	US-09-548-367D-6	Sequence 6, Appli
10	2238.5	92.5	476	US-09-548-372D-73	Sequence 73, Appli
11	2238.5	92.5	476	US-09-548-367D-73	Sequence 73, Appli
12	2160	89.3	453	US-09-548-372D-30	Sequence 30, Appli
13	2160	89.3	453	US-09-548-367D-30	Sequence 30, Appli
14	2160	89.3	459	US-09-548-372D-32	Sequence 32, Appli
15	2160	89.3	459	US-09-548-367D-32	Sequence 32, Appli
16	2155	89.1	433	US-09-548-372D-26	Sequence 26, Appli
17	2155	89.1	433	US-09-548-367D-26	Sequence 26, Appli
18	2135	89.1	446	US-09-548-372D-22	Sequence 22, Appli
19	2135	89.1	446	US-09-548-367D-22	Sequence 22, Appli
20	2155	89.1	459	US-09-548-372D-24	Sequence 24, Appli
21	2155	89.1	459	US-09-548-367D-24	Sequence 24, Appli
22	2090.5	86.4	425	US-09-548-372D-28	Sequence 28, Appli
23	2090.5	86.4	425	US-09-548-367D-28	Sequence 28, Appli
24	2005.5	82.9	428	US-09-548-372D-51	Sequence 51, Appli
25	2005.5	82.9	428	US-09-548-367D-51	Sequence 51, Appli
26	2005.5	82.9	434	US-09-548-372D-53	Sequence 53, Appli
27	2005.5	82.9	434	US-09-548-367D-53	Sequence 53, Appli

RESULT 1

US-09-548-372D-4

; Sequence 4, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE

; FILE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/62801

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 4

; LENGTH: 501

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-548-372D-4

Query Match 100.0%; Score 2419; DB 4; Length 501;

Best Local Similarity 100.0%; Pred. No. 1.1e-251;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ETDEPEPEGRGSGFVEMVDNLKSGQGYVEMTVGSPPTLNLVDTGSSNFAVGAAP	60
Db	46	ETDEPEPEGRGSGFVEMVDNLKSGQGYVEMTVGSPPTLNLVDTGSSNFAVGAAP	105
Qy	61	HPFLHRYQRLSSTYRDLKRGVYVPTQGWEGELGTLVSIHPGNVTVRANAAITE	120
Db	106	HPFLHRYQRLSSTYRDLKRGVYVPTQGWEGELGTLVSIHPGNVTVRANAAITE	165
Qy	121	SDKFFINGSNWEGTLGLAYAEIARPDSDLSLVKQTHVHPNLFSLQLCGAGFPLNQS	180
Db	166	SDKFFINGSNWEGTLGLAYAEIARPDSDLSLVKQTHVHPNLFSLQLCGAGFPLNQS	225
Qy	181	EVLASVGSMTLIGGDHSLTYTGSLSWYTPIRREWYVEYIIVRVEINGODLKMDCKEYNNDK	240
Db	226	EVLASVGSMTLIGGDHSLTYTGSLSWYTPIRREWYVEYIIVRVEINGODLKMDCKEYNNDK	285
Qy	241	SIVDSGTTNLRPLPKKVEFAAVKSIKAAASSTKFPDGFGLGVLGVQWAGTTPWNIFFVIS	300
Db	286	SIVDSGTTNLRPLPKKVEFAAVKSIKAAASSTKFPDGFGLGVLGVQWAGTTPWNIFFVIS	345

ALIGNMENTS

QY 301 LYLMEVNTNSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 346 LYLMEVNTNSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 405
QY 361 FDRARRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQDDESTLMTIAYVMAI 420
DB 406 FDRARRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQDDESTLMTIAYVMAI 465
QY 421 CALFMLPLCLMWQWRCRLRQOHHDDFADDISLLK 456
DB 466 CALFMLPLCLMWQWRCRLRQOHHDDFADDISLLK 501

RESULT 2

US-09-548-367D-4
; Sequence 4, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-4

Query Match 100.0%; Score 2419; DB 4; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.le-251;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETDEEPEEPPGRGGSFVEMVDNLRGKSGGYVYVMTVGGSPQTLNLLVDTGSSNFAVGAAP 60
DB 46 ETDEEPEEPPGRGGSFVEMVDNLRGKSGGYVYVMTVGGSPQTLNLLVDTGSSNFAVGAAP 105
QY 61 HPFLHRYYQRLSSTYRDLRKGVVYPTTQGWEGELGTDLSVPHGPNVTVRANIAAITE 120
DB 106 HPFLHRYYQRLSSTYRDLRKGVVYPTTQGWEGELGTDLSVPHGPNVTVRANIAAITE 165
QY 121 SKDFFINGSNWEGILGLAYAEIARPPDLSLVKQTHVPHNLSLQLCGAGFPNQS 180
DB 166 SKDFFINGSNWEGILGLAYAEIARPPDLSLVKQTHVPHNLSLQLCGAGFPNQS 225
QY 181 EVLASVGGSMIIGDHSYLTGSLWYTPIRREWYVEVILVRVEINGODLKMCKEYNDK 240
DB 226 EVLASVGGSMIIGDHSYLTGSLWYTPIRREWYVEVILVRVEINGODLKMCKEYNDK 285
QY 241 SIVDSGTTNLRPLPKKVFEEAAVKSIAASSTEFKPDGFWLGEQLVCWQAGTTPWNIFPVIS 300
DB 286 SIVDSGTTNLRPLPKKVFEEAAVKSIAASSTEFKPDGFWLGEQLVCWQAGTTPWNIFPVIS 345
QY 301 LYLMEVNTNSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 346 LYLMEVNTNSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 405
QY 361 FDRARRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQDDESTLMTIAYVMAI 420
DB 406 FDRARRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQDDESTLMTIAYVMAI 465

QY 421 CALFMLPLCLMWQWRCRLRQOHHDDFADDISLLK 456
DB 466 CALFMLPLCLMWQWRCRLRQOHHDDFADDISLLK 501

RESULT 3

US-09-009-191-2
; Sequence 2, Application US/09009191
; Patent No. 6315689
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID
; APPLICANT: CHAPMAN, CONRAD
; APPLICANT: MURPHY, KAY
; APPLICANT: SMITH, TRUDI
; TITLE OF INVENTION: ASP2
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,191
; FILING DATE: 20-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9701684.4
; FILING-DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 845169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-009-191-2

Query Match 99.8%; Score 2413; DB 4; Length 501;
Best Local Similarity 99.8%; Pred. No. 4.8e-251;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETDEEPEEPPGRGGSFVEMVDNLRGKSGGYVYVMTVGGSPQTLNLLVDTGSSNFAVGAAP 60
DB 46 ETDEEPEEPPGRGGSFVEMVDNLRGKSGGYVYVMTVGGSPQTLNLLVDTGSSNFAVGAAP 105
QY 61 HPFLHRYYQRLSSTYRDLRKGVVYPTTQGWEGELGTDLSVPHGPNVTVRANIAAITE 120
DB 106 HPFLHRYYQRLSSTYRDLRKGVVYPTTQGWEGELGTDLSVPHGPNVTVRANIAAITE 165
QY 121 SKDFFINGSNWEGILGLAYAEIARPPDLSLVKQTHVPHNLSLQLCGAGFPNQS 180
DB 166 SKDFFINGSNWEGILGLAYAEIARPPDLSLVKQTHVPHNLSLQLCGAGFPNQS 225
QY 181 EVLASVGGSMIIGDHSYLTGSLWYTPIRREWYVEVILVRVEINGODLKMCKEYNDK 240
DB 226 EVLASVGGSMIIGDHSYLTGSLWYTPIRREWYVEVILVRVEINGODLKMCKEYNDK 285
QY 241 SIVDSGTTNLRPLPKKVFEEAAVKSIAASSTEFKPDGFWLGEQLVCWQAGTTPWNIFPVIS 300

;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;; FILE OF INVENTION: THEREOF
;; FILE REFERENCE: 29915/6280H
;; CURRENT APPLICATION NUMBER: US/09/548,367D
;; CURRENT FILING DATE: 2000-04-12
;; PRIOR APPLICATION NUMBER: US 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: US 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: US 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 8
;; LENGTH: 501
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-548-367D-8

Query Match 98.8%; Score 2390; DB 4; Length 501;
Best Local Similarity 98.2%; Pred. No. 1.5e-248;
Matches 448; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 ETDEEPEEPRGRGSGFYEMVDNLKSGGQGYVEMTVGSPQTLNLLVDTGSSNFAVGAAP 60
DB 46 ETDEEPEEPRGRGSGFYEMVDNLKSGGQGYVEMTVGSPQTLNLLVDTGSSNFAVGAAP 105
QY 61 HPELHRYQRLSSYTRDLKRGVYPTGKGWEGELGTLVSPHGPNTVVRANIAAITE 120
DB 106 HPELHRYQRLSSYTRDLKRGVYPTGKGWEGELGTLVSPHGPNTVVRANIAAITE 165
QY 121 SOKFFFTNGWEGILGAYAEIARPDSDLEPFDSLKQTHVPHNLSLQLCGAGFPLNQS 180
DB 166 SOKFFFTNGWEGILGAYAEIARPDSDLEPFDSLKQTHVPHNLSLQLCGAGFPLNQT 225
QY 181 EVLASVGGSMITGGIDHSLYTSLSLWTPTRREWYVEIIVRVEINGQDLKMDCKEYNYOK 240
DB 226 EALASVGGSMITGGIDHSLYTSLSLWTPTRREWYVEIIVRVEINGQDLKMDCKEYNYOK 285
QY 241 SIVDSGTTNLRPKKVFEEAAVSKAASSTKFPDGLVQWAGTTPWNIFFVLS 300
DB 286 SIVDSGTTNLRPKKVFEEAAVSKAASSTKFPDGLVQWAGTTPWNIFFVLS 345
QY 301 LYLMGEVTTNQSFRTITLPOQYLRPVEDVATSDQDCYKFAISQSSGTGTVMGAVIMEGFYV 360
DB 346 LYLMGEVTTNQSFRTITLPOQYLRPVEDVATSDQDCYKFAISQSSGTGTVMGAVIMEGFYV 405
QY 361 FDRARRKRGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
DB 406 FDRARRKRGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465
QY 421 CALFMLPLCLMVCOMRCLRCRQHHDDFADDISLLK 456
DB 466 CALFMLPLCLMVCOMRCLRCRQHHDDFADDISLLK 501

RESULT 7

US-09-009-191-4
; Sequence 4, Application US/09009191
; Patent No. 6319689
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID
; APPLICANT: CHAPMAN, CONRAD
; APPLICANT: MURPHY, KAY
; APPLICANT: SMITH, TRUDI
; TITLE OF INVENTION: ASP2
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE

;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19482
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/009,191
;; FILING DATE: 20-JAN-1998
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: UK 9701684.4
;; FILING DATE: 28-JAN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: PRESTIA, PAUL F
;; REGISTRATION NUMBER: 23,031
;; REFERENCE/DOCKET NUMBER: GH-70368
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-407-0700
;; TELEFAX: 610-407-0701
;; TELEX: 846169
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 774 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-009-191-4

Query Match 95.9%; Score 2320; DB 4; Length 774;
Best Local Similarity 98.9%; Pred. No. 1e-240;
Matches 439; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 13 GSFVEMVDNLKSGGQGYVEMTVGSPQTLNLLVDTGSSNFAVGAAPPHLHRYQRL 72
DB 1 GSFVEMVDNLKSGGQGYVEMTVGSPQTLNLLVDTGSSNFAVGAAPPHLHRYQRL 60
QY 73 SSTYRDLRGVVPYTOGKWEGLGTLVSIPIHGPNTVVRANIAAITEADKFFINGSNME 132
DB 61 SSTYRDLRGVVPYTOGKWEGLGTLVSIPIHGPNTVVRANIAAITEADKFFINGSNME 120
QY 133 GILGLAYAEIARPDSDLEPFDSLKQTHVPHNLSLQLCGAGFPLNQSEVLASVGGSMII 192
DB 121 GILGLAYAEIARPDSDLEPFDSLKQTHVPHNLSLQLCGAGFPLNQSEVLASVGGSMII 180
QY 193 GGTIDHSLYTSLSLWTPTRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 252
DB 181 GGTIDHSLYTSLSLWTPTRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 240
QY 253 PKVFEAAVSKSKAASSTKFPDGLVQWAGTTPWNIFFVLSILYLMGEVTTNQSF 312
DB 241 PKVFEAAVSKSKAASSTKFPDGLVQWAGTTPWNIFFVLSILYLMGEVTTNQSF 300
QY 313 RITILPOQYLRPVEDVATSDQDCYKFAISQSSGTGTVMGAVIMEGFYVDFDRARRKRGFAV 372
DB 301 RITILPOQYLRPVEDVATSDQDCYKFAISQSSGTGTVMGAVIMEGFYVDFDRARRKRGFAV 360
QY 373 SACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAICALFMLPLCLMV 432
DB 361 SACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAICALFMLPLCLMV 420
QY 433 COMRCLRCRQHHDDFADDISLLK 456
DB 421 COMRCLRCRQHHDDFADDISLLK 444

RESULT 8

US-09-548-372D-6
; Application US/09548372D
; Sequence 6, Patent No. 6420534

Db 286 SIVDSGTTNLRPLPKKVFEEAAVSIKAASTKFPDGFNLGELQVLCVQAGTTPWNIFFVIS 345
QY 301 LYLMEVNTNQSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVV 360
Db 346 LYLMEVNTNQSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVV 405
QY 361 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465
QY 421 CALFMLPLCLMVQWRCRLRCLRQHQHDDFADDISLLK 456
Db 466 CALFMLPLCLMVQWRCRLRCLRQHQHDDFADDISLLK 501
RESULT 4
US-09-713-158-2
; Sequence 2, Application US/09713158
; Patent No. 6361975
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; APPLICANT: LI, XIAOTONG
; APPLICANT: POWELL, DAVID J.
; APPLICANT: CHRISTIE, GARY
; TITLE OF INVENTION: MOUSE ASPARTIC SECRETASE-2 (MASP-2)
; FILE REFERENCE: GP-70660
; CURRENT APPLICATION NUMBER: US/09/713,158
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 60/165,800
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-713-158-2
Query Match 98.8%; Score 2390; DB 4; Length 501;
Best Local Similarity 98.2%; Pred. No. 1.5e-248;
Matches 448; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 ETDEEPEPGRGSGFVEMVDNLKSGQGYVYVEMTVGSPPTNLILVDTGSSNFVAVGAAP 60
Db 46 ETDEEPEPGRGSGFVEMVDNLKSGQGYVYVEMTVGSPPTNLILVDTGSSNFVAVGAAP 105
QY 61 HPFLHRYQRLSSTYRDLRKGVYVPTQGWEGELGTLVSIPIHGPNTVVRANIAATE 120
Db 106 HPFLHRYQRLSSTYRDLRKGVYVPTQGWEGELGTLVSIPIHGPNTVVRANIAATE 165
QY 121 SDKFFINGSNWEGILGLAYAEIARPDSDLEPFDSLVKQTHVFNPLFSLQCCGAGFPLNQS 180
Db 166 SDKFFINGSNWEGILGLAYAEIARPDSDLEPFDSLVKQTHVFNPLFSLQCCGAGFPLNQS 225
QY 181 EVLASVGGSMIIGGDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDK 240
Db 226 EALASVGGSMIIGGDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDK 285
QY 241 SIVDSGTTNLRPLPKKVFEEAAVSIKAASTKFPDGFNLGELQVLCVQAGTTPWNIFFVIS 300
Db 286 SIVDSGTTNLRPLPKKVFEEAAVSIKAASTKFPDGFNLGELQVLCVQAGTTPWNIFFVIS 345
QY 301 LYLMEVNTNQSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVV 360
Db 346 LYLMEVNTNQSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVV 405
QY 421 CALFMLPLCLMVQWRCRLRCLRQHQHDDFADDISLLK 456
Db 466 CALFMLPLCLMVQWRCRLRCLRQHQHDDFADDISLLK 501

2/10/1999

Db 466 CALFMLPLCLMVQWRCRLRCLRQHQHDDFADDISLLK 501
RESULT 5
US-09-548-372D-8
; Sequence 8, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-548-372D-8
Query Match 98.8%; Score 2390; DB 4; Length 501;
Best Local Similarity 98.2%; Pred. No. 1.5e-248;
Matches 448; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 ETDEEPEPGRGSGFVEMVDNLKSGQGYVYVEMTVGSPPTNLILVDTGSSNFVAVGAAP 60
Db 46 ETDEEPEPGRGSGFVEMVDNLKSGQGYVYVEMTVGSPPTNLILVDTGSSNFVAVGAAP 105
QY 61 HPFLHRYQRLSSTYRDLRKGVYVPTQGWEGELGTLVSIPIHGPNTVVRANIAATE 120
Db 106 HPFLHRYQRLSSTYRDLRKGVYVPTQGWEGELGTLVSIPIHGPNTVVRANIAATE 165
QY 121 SDKFFINGSNWEGILGLAYAEIARPDSDLEPFDSLVKQTHVFNPLFSLQCCGAGFPLNQS 180
Db 166 SDKFFINGSNWEGILGLAYAEIARPDSDLEPFDSLVKQTHVFNPLFSLQCCGAGFPLNQS 225
QY 181 EVLASVGGSMIIGGDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDK 240
Db 226 EALASVGGSMIIGGDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDK 285
QY 241 SIVDSGTTNLRPLPKKVFEEAAVSIKAASTKFPDGFNLGELQVLCVQAGTTPWNIFFVIS 300
Db 286 SIVDSGTTNLRPLPKKVFEEAAVSIKAASTKFPDGFNLGELQVLCVQAGTTPWNIFFVIS 345
QY 301 LYLMEVNTNQSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVV 360
Db 346 LYLMEVNTNQSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVV 405
QY 361 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465
QY 421 CALFMLPLCLMVQWRCRLRCLRQHQHDDFADDISLLK 456
Db 466 CALFMLPLCLMVQWRCRLRCLRQHQHDDFADDISLLK 501
RESULT 6
US-09-548-367D-8
; Sequence 8, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.

GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 476
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-372D-6

Query Match 93.6%; Score 2264.5; DB 4; Length 476;
Best Local Similarity 94.5%; Pred. No. 4.4e-235;
Matches 431; Conservative 0; Mismatches 0; Indels 25; Gaps 1;

QY 1 ETDEEPEEPCRRGSGFVEMVDNLGRKSGQGYVYVEMTSGSPQTNLNLVDTGSSNFVGAAP 60
DB 46 ETDEEPEEPCRRGSGFVEMVDNLGRKSGQGYVYVEMTSGSPQTNLNLVDTGSSNFVGAAP 105
QY 61 HPFLHRYQRLSSTYRDLRKGYVYPYTOGKWEGLGTLVSIHPGPNVTVRANIAAITE 120
DB 106 HPFLHRYQRLSSTYRDLRKGYVYPYTOGKWEGLGTLVSIHPGPNVTVRANIAAITE 165
QY 121 SKKFFINGSNWEGILGLAYAEIARPDPSLEPPFDSLKQTHVPLNLSQLCGAGFPLNQS 180
DB 166 SKKFFINGSNWEGILGLAYAEIARPDPSLEPPFDSLKQTHVPLNLSQLCGAGFPLNQS 200
QY 181 EVLASVGGSMIIGGDHSLYTGSLWYTPIRREWYEVYIIVRVEINGODLKMDCKEYNDK 240
DB 201 EVLASVGGSMIIGGDHSLYTGSLWYTPIRREWYEVYIIVRVEINGODLKMDCKEYNDK 260
QY 241 SIIVDSGTTNLRPKKVFEEAAVKSIAKASSTKFPDGFNLGEQLVVCWQAGTTPWNIFPVIS 300
DB 261 SIIVDSGTTNLRPKKVFEEAAVKSIAKASSTKFPDGFNLGEQLVVCWQAGTTPWNIFPVIS 320
QY 301 LYLMGEVNTQSFRTITLPOQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 321 LYLMGEVNTQSFRTITLPOQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 380
QY 361 FDRARRKRGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
DB 381 FDRARRKRGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 440
QY 421 CALFMPLCLMWQWRCRLCRLRQHQHDDFADDISLLK 456
DB 441 CALFMPLCLMWQWRCRLCRLRQHQHDDFADDISLLK 476

RESULT 9
US-09-548-372D-6
Sequence 6, Application US/09548367D
Patent No. 6440698
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/6280H
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 476
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-367D-6

Query Match 93.6%; Score 2264.5; DB 4; Length 476;
Best Local Similarity 94.5%; Pred. No. 4.4e-235;
Matches 431; Conservative 0; Mismatches 0; Indels 25; Gaps 1;

QY 1 ETDEEPEEPCRRGSGFVEMVDNLGRKSGQGYVYVEMTSGSPQTNLNLVDTGSSNFVGAAP 60
DB 46 ETDEEPEEPCRRGSGFVEMVDNLGRKSGQGYVYVEMTSGSPQTNLNLVDTGSSNFVGAAP 105
QY 61 HPFLHRYQRLSSTYRDLRKGYVYPYTOGKWEGLGTLVSIHPGPNVTVRANIAAITE 120
DB 106 HPFLHRYQRLSSTYRDLRKGYVYPYTOGKWEGLGTLVSIHPGPNVTVRANIAAITE 165
QY 121 SKKFFINGSNWEGILGLAYAEIARPDPSLEPPFDSLKQTHVPLNLSQLCGAGFPLNQS 180
DB 166 SKKFFINGSNWEGILGLAYAEIARPDPSLEPPFDSLKQTHVPLNLSQLCGAGFPLNQS 200
QY 181 EVLASVGGSMIIGGDHSLYTGSLWYTPIRREWYEVYIIVRVEINGODLKMDCKEYNDK 240
DB 201 EVLASVGGSMIIGGDHSLYTGSLWYTPIRREWYEVYIIVRVEINGODLKMDCKEYNDK 260
QY 241 SIIVDSGTTNLRPKKVFEEAAVKSIAKASSTKFPDGFNLGEQLVVCWQAGTTPWNIFPVIS 300
DB 261 SIIVDSGTTNLRPKKVFEEAAVKSIAKASSTKFPDGFNLGEQLVVCWQAGTTPWNIFPVIS 320
QY 301 LYLMGEVNTQSFRTITLPOQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 321 LYLMGEVNTQSFRTITLPOQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 380
QY 361 FDRARRKRGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
DB 381 FDRARRKRGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 440
QY 421 CALFMPLCLMWQWRCRLCRLRQHQHDDFADDISLLK 456
DB 441 CALFMPLCLMWQWRCRLCRLRQHQHDDFADDISLLK 476

RESULT 10
US-09-548-372D-73
Sequence 73, Application US/09548372D
Patent No. 6420534
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
FILE REFERENCE: 29915/6280I
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 73

Db 166 S D K F F T N G S W E G I L G L A Y A E I A R P D S L E P P F D S L V K Q T H V P N L F S L Q L C G A G F P L N Q S 225
QY 181 E V L A S V G G S M I T G G I D H S L Y T G S L W T P I R R E W Y Y E V I I V R V E I N G O D L K M D C K E Y N D K 240
Db 226 E V L A S V G G S M I T G G I D H S L Y T G S L W T P I R R E W Y Y E V I I V R V E I N G O D L K M D C K E Y N D K 285
QY 241 S I V D S G T T N L R L P K P K V F E A A V K S I K A A S T E K P D G F W L G E Q L V C W Q A G T T P W N I P P V I S 300
Db 286 S I V D S G T T N L R L P K P K V F E A A V K S I K A A S T E K P D G F W L G E Q L V C W Q A G T T P W N I P P V I S 345
QY 301 L Y L M G E V T N O S R I T I L P Q O Y L R P V E D V A T S O D D C Y K F A I S Q S S T G T V M G A V I M E G F Y V V 360
Db 346 L Y L M G E V T N O S R I T I L P Q O Y L R P V E D V A T S O D D C Y K F A I S Q S S T G T V M G A V I M E G F Y V V 405
QY 361 F D R A R K R I G F A V S A C H V H D E F R T A A V E G P F V T L D M E D C G Y N I P Q T D E S 408
Db 406 F D R A R K R I G F A V S A C H V H D E F R T A A V E G P F V T L D M E D C G Y N I P Q T D E S 453
RESULT 13
US-09-548-367D-30
; Sequence 30, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-30

Query Match 89.3%; Score 2160; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 7.4e-224;
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 E T D E E P E E P G R R G S F V E M V D N L R K G S G Q Y Y V E M T V G S P P Q T L N I L V D T G S S N F A V G A A P 60
Db 46 E T D E E P E E P G R R G S F V E M V D N L R K G S G Q Y Y V E M T V G S P P Q T L N I L V D T G S S N F A V G A A P 105
QY 61 H P F L H R Y Y Q R L S S T Y R D L R K G Y V P Y T O G K W E G E L G T D L V S I P H G P N V T V R A N I A A I T E 120
Db 106 H P F L H R Y Y Q R L S S T Y R D L R K G Y V P Y T O G K W E G E L G T D L V S I P H G P N V T V R A N I A A I T E 165
QY 121 S D K F F T N G S W E G I L G L A Y A E I A R P D S L E P P F D S L V K Q T H V P N L F S L Q L C G A G F P L N Q S 180
Db 166 S D K F F T N G S W E G I L G L A Y A E I A R P D S L E P P F D S L V K Q T H V P N L F S L Q L C G A G F P L N Q S 225
QY 181 E V L A S V G G S M I T G G I D H S L Y T G S L W T P I R R E W Y Y E V I I V R V E I N G O D L K M D C K E Y N D K 240
Db 226 E V L A S V G G S M I T G G I D H S L Y T G S L W T P I R R E W Y Y E V I I V R V E I N G O D L K M D C K E Y N D K 285
QY 241 S I V D S G T T N L R L P K P K V F E A A V K S I K A A S T E K P D G F W L G E Q L V C W Q A G T T P W N I P P V I S 300
Db 286 S I V D S G T T N L R L P K P K V F E A A V K S I K A A S T E K P D G F W L G E Q L V C W Q A G T T P W N I P P V I S 345
QY 301 L Y L M G E V T N O S R I T I L P Q O Y L R P V E D V A T S O D D C Y K F A I S Q S S T G T V M G A V I M E G F Y V V 360
Db 346 S D K F F T N G S W E G I L G L A Y A E I A R P D S L E P P F D S L V K Q T H V P N L F S L Q L C G A G F P L N Q S 225
QY 181 E V L A S V G G S M I T G G I D H S L Y T G S L W T P I R R E W Y Y E V I I V R V E I N G O D L K M D C K E Y N D K 240
Db 226 E V L A S V G G S M I T G G I D H S L Y T G S L W T P I R R E W Y Y E V I I V R V E I N G O D L K M D C K E Y N D K 285
QY 241 S I V D S G T T N L R L P K P K V F E A A V K S I K A A S T E K P D G F W L G E Q L V C W Q A G T T P W N I P P V I S 300
Db 286 S I V D S G T T N L R L P K P K V F E A A V K S I K A A S T E K P D G F W L G E Q L V C W Q A G T T P W N I P P V I S 345
QY 301 L Y L M G E V T N O S R I T I L P Q O Y L R P V E D V A T S O D D C Y K F A I S Q S S T G T V M G A V I M E G F Y V V 360

Db 346 L Y L M G E V T N O S R I T I L P Q O Y L R P V E D V A T S O D D C Y K F A I S Q S S T G T V M G A V I M E G F Y V V 405
QY 361 F D R A R K R I G F A V S A C H V H D E F R T A A V E G P F V T L D M E D C G Y N I P Q T D E S 408
Db 406 F D R A R K R I G F A V S A C H V H D E F R T A A V E G P F V T L D M E D C G Y N I P Q T D E S 453
RESULT 14
US-09-548-372D-32
; Sequence 32, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-32

Query Match 89.3%; Score 2160; DB 4; Length 459;
Best Local Similarity 100.0%; Pred. No. 7.5e-224;
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 E T D E E P E E P G R R G S F V E M V D N L R K G S G Q Y Y V E M T V G S P P Q T L N I L V D T G S S N F A V G A A P 60
Db 46 E T D E E P E E P G R R G S F V E M V D N L R K G S G Q Y Y V E M T V G S P P Q T L N I L V D T G S S N F A V G A A P 105
QY 61 H P F L H R Y Y Q R L S S T Y R D L R K G Y V P Y T O G K W E G E L G T D L V S I P H G P N V T V R A N I A A I T E 120
Db 106 H P F L H R Y Y Q R L S S T Y R D L R K G Y V P Y T O G K W E G E L G T D L V S I P H G P N V T V R A N I A A I T E 165
QY 121 S D K F F T N G S W E G I L G L A Y A E I A R P D S L E P P F D S L V K Q T H V P N L F S L Q L C G A G F P L N Q S 180
Db 166 S D K F F T N G S W E G I L G L A Y A E I A R P D S L E P P F D S L V K Q T H V P N L F S L Q L C G A G F P L N Q S 225
QY 181 E V L A S V G G S M I T G G I D H S L Y T G S L W T P I R R E W Y Y E V I I V R V E I N G O D L K M D C K E Y N D K 240
Db 226 E V L A S V G G S M I T G G I D H S L Y T G S L W T P I R R E W Y Y E V I I V R V E I N G O D L K M D C K E Y N D K 285
QY 241 S I V D S G T T N L R L P K P K V F E A A V K S I K A A S T E K P D G F W L G E Q L V C W Q A G T T P W N I P P V I S 300
Db 286 S I V D S G T T N L R L P K P K V F E A A V K S I K A A S T E K P D G F W L G E Q L V C W Q A G T T P W N I P P V I S 345
QY 301 L Y L M G E V T N O S R I T I L P Q O Y L R P V E D V A T S O D D C Y K F A I S Q S S T G T V M G A V I M E G F Y V V 360
Db 346 L Y L M G E V T N O S R I T I L P Q O Y L R P V E D V A T S O D D C Y K F A I S Q S S T G T V M G A V I M E G F Y V V 405
QY 361 F D R A R K R I G F A V S A C H V H D E F R T A A V E G P F V T L D M E D C G Y N I P Q T D E S 408
Db 406 F D R A R K R I G F A V S A C H V H D E F R T A A V E G P F V T L D M E D C G Y N I P Q T D E S 453
RESULT 15
US-09-548-367D-32
; Sequence 32, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-32

Query Match 89.3%; Score 2160; DB 4; Length 459;
Best Local Similarity 100.0%; Pred. No. 7.5e-224;
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ETDEEPEEPCRRGGSFVEMVDNLRKSGQGYVVTGSPQTLNIIIVDTGSSNFAVGAAP	60
Db	46	ETDEEPEEPCRRGGSFVEMVDNLRKSGQGYVVTGSPQTLNIIIVDTGSSNFAVGAAP	105
Qy	61	HPFLHRYRQLSSTYRDLRKGVVYPTQKWEGLGTDLVSIHPGPNVTVRANIAATE	120
Db	106	HPFLHRYRQLSSTYRDLRKGVVYPTQKWEGLGTDLVSIHPGPNVTVRANIAATE	165
Qy	121	SKFFINGSNWEGILGLAYAEIARPDLSLEPFDLSLVKQTHVPNLFSLQCGAGPPLNOS	180
Db	166	SKFFINGSNWEGILGLAYAEIARPDLSLEPFDLSLVKQTHVPNLFSLQCGAGPPLNOS	225
Qy	181	EVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNDK	240
Db	226	EVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNDK	285
Qy	241	SIVDSGTTNLRPKKVFEEAAVKSIIKAASSTKFPDGFGLGQLVCWQAGTTPWNIFFPVIS	300
Db	286	SIVDSGTTNLRPKKVFEEAAVKSIIKAASSTKFPDGFGLGQLVCWQAGTTPWNIFFPVIS	345
Qy	301	LYLMGEVTHQSFRITILPQOYLRPVEDVATSDDCYKFAISQSSTGTVMGAVIMEGFYVV	360
Db	346	LYLMGEVTHQSFRITILPQOYLRPVEDVATSDDCYKFAISQSSTGTVMGAVIMEGFYVV	405
Qy	361	FDARRKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSE	408
Db	406	FDARRKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSE	453

Search completed: March 4, 2003, 10:01:52
Job time : 19 secs

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2003, 13:37:20 ; Search time 324.5 seconds
(without alignments)
16294.891 Million cell updates/sec

Title: US-09-723-722A-44
Perfect score: 2348
Sequence: 1 ccacgcggccctcacagc.....caagattgcctcttgatt 2348

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :			
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1:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*		
2:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*		
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4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*		
5:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*		
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12:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*		
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14:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*		
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19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*		
20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*		
21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*		
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*		
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*		
24:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2347.6	100.0	2348	21	AAA59551 DNA encoding a hum
2	2336.4	99.5	16080	21	AAA59553 DNA clone pCEK Cl.
3	2181.2	92.9	5757	24	ABL39774 Human NS cDNA sequ
4	2039.8	86.9	2070	21	AAA15662 Human aspartyl pro
5	2039.8	86.9	2070	22	AAD17865 Human aspartyl pro
6	2039.8	86.9	2070	22	AAD13021 Human aspartyl pro
7	2039.8	86.9	2070	22	AAA11517 Human cDNA encodin
8	2039.8	86.9	2070	22	AAA11702 DNA encoding human
9	2039.8	86.9	2070	22	AAD06739 Human aspartyl pro

10	2039.8	86.9	2070	24	ABL52457 Human Asp-2(a) nuc
11	2039.8	86.9	2070	24	ABL49914 Human aspartyl pro
12	2024	86.2	2541	19	AAV41696 Nucleotide sequenc
13	2004	85.3	3252	22	AAF31848 Human memapsin 2 c
14	2004	85.3	3252	22	AAF28101 Memapsin 2 DNA.. H
15	2004	85.3	3252	24	AAK88641 cDNA encoding huma
16	1881	80.1	1977	21	AAA15663 Human aspartyl pro
17	1881	80.1	1977	22	AAD17866 Human aspartyl pro
18	1881	80.1	1977	22	AAD13022 Human cDNA encodin
19	1881	80.1	1977	22	AAA11518 Human cDNA encodin
20	1881	80.1	1977	22	AAA11703 DNA encoding human
21	1881	80.1	1977	22	AAD06740 Human aspartyl pro
22	1881	80.1	1977	24	ABL52458 Human Asp-2(b) nuc
23	1881	80.1	1977	24	ABL49915 Human aspartyl pr
24	1835.4	78.2	2370	19	AAV41697 Partial nucleotide
25	1792	76.3	1979	22	AAK94824 Human full-length
26	1648	70.2	1747	20	AAK97602 Extended human sec
27	1550	66.0	2043	21	AAA15664 Murine aspartyl pr
28	1550	66.0	2043	22	AAD17867 Murine aspartyl pr
29	1550	66.0	2043	22	AAD13023 Murine aspartyl pr
30	1550	66.0	2043	22	AAA11519 Mouse cDNA encodin
31	1550	66.0	2043	22	AAA11704 DNA encoding mouse
32	1550	66.0	2043	22	AAD06741 Murine aspartyl pr
33	1511.2	64.4	2158	24	ABL52459 Mouse Asp-2(a) nuc
34	1511.2	64.4	2158	24	ABK63758 Rat sequence diffe
35	1504.4	64.1	2907	23	AAK82237 DNA encoding novel
36	1503	64.0	1503	21	AAA28278 Human cDNA encodin
37	1503	64.0	1503	21	AAA59550 DNA encoding a hum
38	1503	64.0	1527	24	ABA02406 FLAG-tagged human
39	1476.2	62.9	1911	22	AAD09485 Human aspartyl pro
40	1423	60.6	2914	23	AAA57398 DNA encoding novel
41	1355.8	57.7	1362	21	AAA15688 Modified human asp
42	1355.8	57.7	1362	22	AAD17878 Human-Asp 2(a) pro
43	1355.8	57.7	1362	22	AAD13034 Human-Asp2(a) delt
44	1355.8	57.7	1362	22	AAA11530 Human cDNA encodin
45	1355.8	57.7	1362	22	AAA11715 DNA encoding human

ALIGNMENTS

RESULT 1

AAA59551	ID	AAA59551 standard; DNA; 2348 BP.
XX	AC	AAA59551;
XX	DT	14-NOV-2000 (first entry)
XX	DE	DNA encoding a human beta-secretase enzyme.
XX	DE	Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
XX	KW	amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
XX	KW	inhibitor; ss.
XX	OS	Homo sapiens.
XX	PH	Key
XX	FT	CDS
XX	FT	Location/Qualifiers
XX	FT	306..1811
XX	FT	/*tag= a
XX	FT	/product= "beta-secretase"
XX	PN	WO200047618-A2.
XX	PD	17-AUG-2000.
XX	PF	10-FEB-2000; 2000WO-US03819.
XX	PR	10-FEB-1999; 99US-0119571.
XX	PR	15-JUN-1999; 99US-0139172.
XX	PA	(ELAN-) ELAN PHARM INC.
XX	XX	

PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;
 XX WPI: 2000-533011/48.
 DR P-PSDB: AAB07896.
 XX
 PT Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease -
 XX
 XX Disclosure; Fig 1B; 121pp; English.
 PS
 XX The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to
 CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
 CC disease-like pathology to test if they maintain or improve cognitive
 CC ability or reduce the plaque burden. The compounds are used for the
 CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
 CC present sequence encodes a human beta-secretase enzyme.
 XX
 SQ Sequence 2348 BP; 489 A; 713 C; 661 G; 484 T; 1 other;

Query Match 100.0%; Score 2347.6; DB 21; Length 2348;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCGGCGCCCTCACAGCCCGCGGAGCCGCGAGCCGCTGCCAGGCTGGCCGCGG 60
 DB 1 CCATGCGGCGCCCTCACAGCCCGCGGAGCCGCGGAGCCGCTGCCAGGCTGGCCGCGG 60

QY 61 CSFTGCCGATGAGCGGCTCGGATCCAGCCTCTCCCTCTGCTCCGCTGCTCGCGAT 120
 DB 61 CSFTGCCGATGAGCGGCTCGGATCCAGCCTCTCCCTCTGCTCCGCTGCTCGCGAT 120

QY 121 CTCCTCTGACCGCTCTCCACAGCCGAGCCCGGGGCTGGCCAGGCGCTGACAGGCCCT 180
 DB 121 CTCCTCTGACCGCTCTCCACAGCCGAGCCCGGGGCTGGCCAGGCGCTGACAGGCCCT 180

QY 181 GGCTCTCTGATGCCCCCAAGCTCCCTCTCTGAGAGCCACAGCACCACCCAGACTGG 240
 DB 181 GGCTCTCTGATGCCCCCAAGCTCCCTCTCTGAGAGCCACAGCACCACCCAGACTGG 240

QY 241 GGCAGCGCCGAGGACGAGCTGGGCGCCAGTGGAGCCGAGAGCCGCGGAGCCGCGG 300
 DB 241 GGCAGCGCCGAGGACGAGCTGGGCGCCAGTGGAGCCGAGAGCCGCGGAGCCGCGG 300

QY 301 CCACCTGGCCCAAGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 DB 301 CCACCTGGCCCAAGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

QY 361 CCCACGACCCAGCAGCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 DB 361 CCCACGACCCAGCAGCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

QY 421 TGGGGCTGCGGCTGCCCCGGGAGACCGAGAGAGCCGAGAGCCGCGGAGGGGCGCA 480
 DB 421 TGGGGCTGCGGCTGCCCCGGGAGACCGAGAGAGCCGAGAGCCGCGGAGGGGCGCA 480

QY 481 GCTTTGTGGAGATGTTGACAACTTGAAGGGCAAGTTCGGGGCAGGGCTACTACGTGGA 540
 DB 481 GCTTTGTGGAGATGTTGACAACTTGAAGGGCAAGTTCGGGGCAGGGCTACTACGTGGA 540

QY 541 TGACCTGGGAGAGCCCGGAGAGCGCTCAACATCTGTGGATACAGGAGAGAGTAACT 600
 DB 541 TGACCTGGGAGAGCCCGGAGAGCGCTCAACATCTGTGGATACAGGAGAGAGTAACT 600

QY 601 TTGCAGTGGGTGCTGCCCCCACCCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 601 TTGCAGTGGGTGCTGCCCCCACCCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

QY 1741 AGTGGCGCTGCCCTCCGCTGCTGCCAGCAGCATGATGATCTTGTGTGATGACATCTCC 1800

QY 661 GCACATACCGGAGCCTCGGGAAGGCTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAG 720
 DB 661 GCACATACCGGAGCCTCGGGAAGGCTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAG 720

QY 721 GGGAGCTGGGACCGACCTGTAAGCATCCCCCATGGCCCCAACGTCACCTGTGGTGCCA 780
 DB 721 GGGAGCTGGGACCGACCTGTAAGCATCCCCCATGGCCCCAACGTCACCTGTGGTGCCA 780

QY 781 ACATTGCTGCATCAGCAAGTCTTCAATCAAGCGCTCCAACCTGGAAGGCA 840
 DB 781 ACATTGCTGCATCAGCAAGTCTTCAATCAAGCGCTCCAACCTGGAAGGCA 840

QY 841 TCCTGGGCTGGCCTATGCTGAGATTGCCAGGCTTGCAGACTCCCTGGAGCCTTTCTTTG 900
 DB 841 TCCTGGGCTGGCCTATGCTGAGATTGCCAGGCTTGCAGACTCCCTGGAGCCTTTCTTTG 900

QY 901 ACTCTCTGTTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCGAGCTTTGTGGTCTG 960
 DB 901 ACTCTCTGTTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCGAGCTTTGTGGTCTG 960

QY 961 GCTTCCCTCTCAACGAGTCTGAAGTCTGCTGCGGAGGAGCATCATCTTGGAG 1020
 DB 961 GCTTCCCTCTCAACGAGTCTGAAGTCTGCTGCGGAGGAGCATCATCTTGGAG 1020

QY 1021 GTATCGACACTCGCTGTACACAGGAGTCTCTGTGTATACACCCATCCGCGGGAGTGGT 1080
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QY 1081 ATTATGAGGTGATCTTGTGGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCA 1140
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 DB 1141 AGGAGTACAACTATGACAAGAGCATTTGTGGACAGTGGCACCAACCACTCTCTTTGGCCCA 1200

QY 1201 AGAAAGTGTGTAAGCTGCAATCAATCAAGGAGGAGCTCTCCACAGGAGAAAGTTC 1260
 DB 1201 AGAAAGTGTGTAAGCTGCAATCAATCAAGGAGGAGCTCTCCACAGGAGAAAGTTC 1260

QY 1261 CTGATGTTTCTGCTAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 DB 1261 CTGATGTTTCTGCTAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320

QY 1321 ACATTTTCCAGTCTCTCACTCTACCTTAATGGGTGAGTTTACCAACCACTCTCTTCGCGCA 1380
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QY 1381 TCACCATCTCTCCGAGCAATACCTGCGGCGAGTGGAGATGTGGCCACGTCACCAAGAG 1440
 DB 1381 TCACCATCTCTCCGAGCAATACCTGCGGCGAGTGGAGATGTGGCCACGTCACCAAGAG 1440

QY 1441 ACTGTTACAAGTTTGGCATCTCACAGTCTATCCACGGGACTGTTATGGAGCTGTTATCA 1500
 DB 1441 ACTGTTACAAGTTTGGCATCTCACAGTCTATCCACGGGACTGTTATGGAGCTGTTATCA 1500

QY 1501 TGGAGGCTTCTAGCTTGTCTTTGATCGGGCGCCGAAAGAAATTTGCTTGTCTGTCAGCG 1560
 DB 1501 TGGAGGCTTCTAGCTTGTCTTTGATCGGGCGCCGAAAGAAATTTGCTTGTCTGTCAGCG 1560

QY 1561 CTTTGCCATGTGCAGATGAGTTTCAAGGAGGAGCGGTCGGAAGCCCTTTTGTCACTTGG 1620
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QY 1621 ACATGGAAGACTTGGGCTACAACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAG 1680
 DB 1621 ACATGGAAGACTTGGGCTACAACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAG 1680

QY 1681 CCTATGTCATGGCTGCGCCCTCTTTCATCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1740
 DB 1681 CCTATGTCATGGCTGCGCCCTCTTTCATCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1740

QY 1741 AGTGGCGCTGCCCTCCGCTGCTGCCAGCAGCATGATGATCTTGTGTGATGACATCTCC 1800

Db 1741 AGTGGCGCTCCCTCCGCTGCTGGCAGCAGCATGATGATCTTTGCTGATCACATCTCCC 1800
QY 1801 TGTGTAAGTCAGAGGCCATGGCAGAAATAGAGATTCCTCTGGACACACCTCGGTG 1860
Db 1801 TGTGTAAGTCAGAGGCCATGGCAGAAATAGAGATTCCTCTGGACACACCTCGGTG 1860
QY 1861 GTTCACTTTGGTGCACAGTAGAGACACAGATGGCAGCTGTGGCCAGAGCACCTCAGGAC 1920
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QY 1921 CTTCCGCCACCAATGCTCTGCTTGTATGGAGAGAAAGGCTGCGAAGTGGGT 1980
Db 1921 CTTCCGCCACCAATGCTCTGCTTGTATGGAGAGAAAGGCTGCGAAGTGGGT 1980
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QY 2161 CAGAAGTACTGGCATACACAGCAGGTACCTTGGCTGTGCTCTGCTGGTACCTGGCAG 2220
Db 2161 CAGAAGTACTGGCATACACAGCAGGTACCTTGGCTGTGCTCTGCTGGTACCTGGCAG 2220
QY 2221 AGAAGAGACCAAGCTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGATGCACAGTTTG 2280
Db 2221 AGAAGAGACCAAGCTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGATGCACAGTTTG 2280
QY 2281 CTATTTGCTTTAGACAGGAGCTGTATAACAAAGCCTAACATTTGGTGCAAAAGATTCGCT 2340
Db 2281 CTATTTGCTTTAGACAGGAGCTGTATAACAAAGCCTAACATTTGGTGCAAAAGATTCGCT 2340
QY 2341 CTTGAATT 2348
Db 2341 CTTGAATT 2348

RESULT 2
AAA59553
ID AAA59553 standard; DNA; 16080 BP.

AC AAA59553;

DT 14-NOV-2000 (first entry)

DE DNA clone pCEK C1.27 encoding a human beta-secretase enzyme.

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW inhibitor; ss.

XX Homo sapiens.

XX W0200047618-A2.

PN 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US03819.

PF 10-FEB-1999; 99US-0119571.

PR 15-JUN-1999; 99US-0139172.

XX (ELAN-) ELAN PHARM INC.

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

XX

WPI; 2000-533011/48.

XX Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease -

XX Disclosure; Fig 13A-E; 121pp; English.

XX The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to
CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
CC disease-like pathology to test if they maintain or improve cognitive
CC ability or reduce the plaque burden. The compounds are used for the
CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
CC present sequence encodes a human beta-secretase enzyme.

XX Sequence 16080 BP; 3627 A; 4556 C; 3962 G; 3913 T; 22 other;

Query Match 99.5%; Score 2336.4; DB 21; Length 16080;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2340; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCATGCCGGCCCTCACAGCCCGCGGAGCCGCGAGCCGCTGCCAGGCTGGCCGCCG 60

Db 1370 CCATGCCGGCCCTTCCAGCCCGCGGAGCCGCGCGCTGCCAGGCTGGCCGCCG 1429

QY 61 CSFTGCCGATGTAGCGGCTCCGGATCCAGCCCTCTCCCTGTCTCCCTGTCTCTGCGGAT 120

Db 1430 CCGTGCCGATGTAGCGGCTCCGGATCCAGCCCTCTCCCTGTCTCTGCGGAT 1489

QY 121 CTCCTGTAGCGCTCTCCAGAGCCCGGACCCGGGGGTGGCCAGGCGCCTTCAGAGCCCT 180

Db 1490 CTCCTGTAGCGCTCTCCAGAGCCCGGACCCGGGGGTGGCCAGGCGCCTTCAGAGCCCT 1549

QY 181 GGGCTCTGATGCCCCCAAGCTCCCTCTCTGAGAAGCCACACAGCCAGCTTGG 240

Db 1550 GGGCTCTGATGCCCCCAAGCTCCCTCTCTGAGAAGCCACACAGCCAGCTTGG 1609

QY 241 GGGCAGCGCCAGGAGCGAGCTGGGCCAGTGGCCAGTGGCCAGAGGCCCGGAGCCGGGC 300

Db 1610 GGGCAGCGCCAGGAGCGAGCTGGGCCAGTGGCCAGTGGCCAGAGGCCCGGAGCCGGGC 1669

QY 301 CCACCATGGCCCAAGCCCTGCCCTGTCTGTGTGGATGGGCGCGGAGTGTGCTG 360

Db 1670 CCACCATGGCCCAAGCCCTGCCCTGTCTGTGTGGATGGGCGCGGAGTGTGCTG 1729

QY 361 CCCACGGCACCCAGCAGCGCATCCGGCTGCCCTTGGCCAGCGGCTGGGGGCGCCGCC 420

Db 1730 CCCACGGCACCCAGCAGCGCATCCGGCTGCCCTTGGCCAGCGGCTGGGGGCGCCGCC 1789

QY 421 TGGGGCTGCGGCTGCCCGGGAGACCCAGCAAGAGCCCGAGAGCCCGCGGCGGAGGGCA 480

Db 1790 TGGGGCTGCGGCTGCCCGGGAGACCCAGCAAGAGCCCGAGAGCCCGCGGCGGAGGGCA 1849

QY 481 GCTTTGTGGAGATGGTGACAACTGAGGGGCAAGTGGGGCAGGGCTACTACGTGGAGA 540

Db 1850 GCTTTGTGGAGATGGTGACAACTGAGGGGCAAGTGGGGCAGGGCTACTACGTGGAGA 1909

QY 541 TGACCGTGGGCGAGCCCGCCAGACGCTCAACATCTGTGGATACAGGACAGTAACT 600

Db 1910 TGACCGTGGGCGAGCCCGCCAGACGCTCAACATCTGTGGATACAGGACAGTAACT 1969

QY 601 TTGCAGTGGGTGCTGCCCGCCACCCCTTCTGTGATCTACTACAGAGGCGAGCTGTCCA 660

Db 1970 TTGCAGTGGGTGCTGCCCGCCACCCCTTCTGTGATCTACTACAGAGGCGAGCTGTCCA 2029

QY 661 GCACATACCGGGACCTCCGGGAAGGCTGTATGTGCCCTACACCCAGGCGAAGTGGGAAG 720

Db 2030 GCACATACCGGGACCTCCGGGAAGGCTGTATGTGCCCTACACCCAGGCGAAGTGGGAAG 2089

QY 721 GGGAGCTGGGACCGAAGCTGTGAAGCATCCGCCATGGCCCCAACGTCACCTGTGCGTGCCA 780
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QY 781 ACATTTGCTGCCATCAGTGAATCAGACAAAGTTCCTTATCAACAGGCTCCAACTGGGAAGGCA 840
DB 2150 ACATTTGCTGCCATCAGTGAATCAGACAAAGTTCCTTATCAACAGGCTCCAACTGGGAAGGCA 2209
QY 841 TCCTGGGCTGGCCATGCTGAGATTTGCCAGGCTGACAGCTCCCTGGAGCCCTTTCTTTG 900
DB 2210 TCCTGGGCTGGCCATGCTGAGATTTGCCAGGCTGACAGCTCCCTGGAGCCCTTTCTTTG 2269
QY 901 ACTCTCTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGACGCTTTGTGGTGTG 960
DB 2270 ACTCTCTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGACGCTTTGTGGTGTG 2329
QY 961 GCTTCCCTCCCTCAACAGCTCTCAAGTCTGGGCTCTGTGGAGGGGAGCATGATCATTTGGAG 1020
DB 2330 GCTTCCCTCCCTCAACAGCTCTCAAGTCTGGGCTCTGTGGAGGGGAGCATGATCATTTGGAG 2389
QY 1021 GTATCGACCACTGCTGTACACAGGAGCTCTCTGGTATACACCCATCCGCGGGAGTGT 1080
DB 2390 GTATCGACCACTGCTGTACACAGGAGCTCTCTGGTATACACCCATCCGCGGGAGTGT 2449
QY 1081 ATTATGAGGTGATCATTTGTGGGGTGGAGATCAATGGAGGAGTCTGAAATGGACTGCA 1140
DB 2450 ATTATGAGGTGATCATTTGTGGGGTGGAGATCAATGGAGGAGTCTGAAATGGACTGCA 2509
QY 1141 AGGAGTACAATATGACAAAGAGCTTTGGACAGTGGGACAGTGGGACCAACCTTCGTTTGGCCA 1200
DB 2510 AGGAGTACAATATGACAAAGAGCTTTGGACAGTGGGACAGTGGGACCAACCTTCGTTTGGCCA 2569
QY 1201 AGAAGTGTTTGAAGCTGACGTCAAAATCCATCAAGGAGCCCTCCACGAGCAAGTTC 1260
DB 2570 AGAAGTGTTTGAAGCTGACGTCAAAATCCATCAAGGAGCCCTCCACGAGCAAGTTC 2629
QY 1261 CTGATGTTTCTGGCTAGGAGAGCAGTGTGTGTGGCAAGCAGGACCAACCCCTTGGGA 1320
DB 2630 CTGATGTTTCTGGCTAGGAGAGCAGTGTGTGTGGCAAGCAGGACCAACCCCTTGGGA 2689
QY 1321 ACATTTTCCAGTCTCATCTACCTTAATGGGTGAGTTTACCAACCACTCTTCGCA 1380
DB 2690 ACATTTTCCAGTCTCATCTACCTTAATGGGTGAGTTTACCAACCACTCTTCGCA 2749
QY 1381 TCACCATCTTCCGACGCAATACCTGCGGCGAGTGGAGAGTGTGGCCACCTCCCAAGAGC 1440
DB 2750 TCACCATCTTCCGACGCAATACCTGCGGCGAGTGGAGAGTGTGGCCACCTCCCAAGAGC 2809
QY 1441 ACTGTTACAAGTTTGGCATCTCACAGTCCACGCGCACTGTTATGGAGCTGTTATCA 1500
DB 2810 ACTGTTACAAGTTTGGCATCTCACAGTCCACGCGCACTGTTATGGAGCTGTTATCA 2869
QY 1501 TGGAGGCTTCTAGCTGTCTTTGATCGGGCCGAAACGAATTTGCTGTGTCAGCG 1560
DB 2870 TGGAGGCTTCTAGCTGTCTTTGATCGGGCCGAAACGAATTTGCTGTGTCAGCG 2929
QY 1561 CTTGGCCATGTGCAGATGAGTTTACAGGCGGAGCGGTGGAGGCGCTTTTGTACACCTTG 1620
DB 2930 CTTGGCCATGTGCAGATGAGTTTACAGGCGGAGCGGTGGAGGCGCTTTTGTACACCTTG 2989
QY 1621 ACATGGAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAG 1680
DB 2990 ACATGGAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAG 3049
QY 1681 CCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCCTCATGGTGTGTC 1740
DB 3050 CCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCCTCATGGTGTGTC 3109
QY 1741 AGTGGCGCTGCCCTCGGCTGCGTGGCCAGCAGCATGATGACTTTGCTGATGATCATCTCCC 1800
DB 3110 AGTGGCGCTGCCCTCGGCTGCGTGGCCAGCAGCATGATGACTTTGCTGATGATCATCTCCC 3169

QY 1801 TCCTGAAGTGAAGAGGCCCCATGGCGAGAAGATAGAGATTTCCCTTGGACCACACCTTCCGTG 1860
DB 3170 TCCTGAAGTGAAGAGGCCCCATGGCGAGAAGATAGAGATTTCCCTTGGACCACACCTTCCGTG 3229
QY 1861 GTTCACTTTTGGTACAAAGTAGGAGACACAGATGCGACCTGTGGCCAGAGCCTCAGGAC 1920
DB 3230 GTTCACTTTTGGTACAAAGTAGGAGACACAGATGCGACCTGTGGCCAGAGCCTCAGGAC 3289
QY 1921 CCTCCCCACCCCAAAATGCTTCTGCTTGTATGAGAAAGAAAGGCTGGCAAGTGGGT 1980
DB 3290 CCTCCCCACCCCAAAATGCTTCTGCTTGTATGAGAAAGAAAGGCTGGCAAGTGGGT 3349
QY 1981 TCCAGGAGCTGTACCTGTAGGAACAGAAAGAGAAAGAACAGACACTCTCTGCTGGCGGA 2040
DB 3350 TCCAGGAGCTGTACCTGTAGGAACAGAAAGAGAAAGAACAGACACTCTCTGCTGGCGGA 3409
QY 2041 ATACTCTTGGTCACTCAAAATTTAAGTTCGGGAAATTTCTGCTTGAACCTTCAGCCCTG 2100
DB 3410 ATACTCTTGGTCACTCAAAATTTAAGTTCGGGAAATTTCTGCTTGAACCTTCAGCCCTG 3469
QY 2101 AACCTTTTGTCCACCACTTCTTAAATTTCTCAACCCCAAAAGTATCTTCTTTTCTTAGTTT 2160
DB 3470 AACCTTTTGTCCACCACTTCTTAAATTTCTCAACCCCAAAAGTATCTTCTTTTCTTAGTTT 3529
QY 2161 CAGAAGTACTGTCATCACAGCAGGTTACCTTGGCGTGTGTCCCTGTGCTACCTGGCAG 2220
DB 3530 CAGAAGTACTGTCATCACAGCAGGTTACCTTGGCGTGTGTCCCTGTGCTACCTGGCAG 3589
QY 2221 AGAAGAGACCAAGCTTTGTTTCCCTGCTGGCCAAAGTCTAGTAGGAGAGATGCACAGTTT 2280
DB 3590 AGAAGAGACCAAGCTTTGTTTCCCTGCTGGCCAAAGTCTAGTAGGAGAGATGCACAGTTT 3649
QY 2281 CTATTTGCTTTAGAGACAGGACTGTATAAACAAGCCCTTAACATTTGGTGCAAGATTGCCCT 2340
DB 3650 CTATTTGCTTTAGAGACAGGACTGTATAAACAAGCCCTTAACATTTGGTGCAAGATTGCCCT 3709
QY 2341 CTTGAATT 2348
DB 3710 CTTGAATT 3717

RESULT 3

ABL39774
ID ABL39774 standard; cdna; 5757 BP.

XX ABL39774;

XX
XX
XX 10-MAY-2002 (first entry)

XX Human NS cDNA sequence SEQ ID NO:84.

XX Human: cytostatic; osteopathic; gynaecological; neuroprotective;
KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KW anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;
KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiac;
KW anticonvulsant; antidiabetic; tranquilizer; antidepressant; neuroleptic;
KW gastrointestinal; virucide; antitumor; cerebroprotective; nootropic;
KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KW ischaemia; asthma; immune disease; coagulation disease; hypertension;
KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KW gastric ulcer; Alzheimer's disease; gene; ss.

XX Homo sapiens.

XX OS

XX PN WO200206315-A2.

XX XX
XX PD 24-JAN-2002.

XX

PF 17-JUL-2001; 2001WO-1L00653.
XX
XX 18-JUL-2000; 2000IL-0137345.
PR 15-DEC-2000; 2000IL-0140354.
XX
XX (COMP-) COMPUGEN LTD.
XX
PI Mintz L, Freilich S, Bernstein J;
XX
XX WPI: 2002-155037/20.
DR P-PSDB; AB06120.
XX
XX One hundred and twenty eight novel nucleic acid sequences, useful for
PT treating and diagnosing e.g. cancer, asthma and Alzheimer's -
XX
XX Claim 1; Page 124-126; 290pp; English.
XX
XX ABL39691 to ABL39818 represent novel human nucleic acid sequences
CC encoding the proteins given in AB06037 to AB06164. The novel sequences
CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
CC anorectic, muscular, anti-HIV, antiinfertility, cardiovascular,
CC anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiac,
CC immunomodulator, anticonvulsant, antidiabetic, tranquiliser, antiulcer,
CC antidepressant, gastrointestinal, neuroleptic, cerebroprotective,
CC nootropic and contraceptive activities. The NS can be used in vaccines,
CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
CC antibodies from the present invention can be used for treating and
CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
CC disease, coagulation disease, ischaemia, hypertension, cardiovascular
CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety, immune
CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC Alzheimer's disease and as a contraceptive.
XX
XX Sequence 5757 BP; 1485 A; 1490 C; 1392 G; 1388 T; 2 other;

Query Match 92.9%; Score 2181.2; DB 24; Length 5757;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 2268; Conservative 1; Mismatches 4; Indels 75; Gaps 1;

QY 1 CCATGCGGCGCTCACAGCCCGCGGAGCCCGAGCCGCTGCCAGGCTGGCGCGCG 60
DB 150 CCATGCGGCGCTCCAGCCCGCGGAGCCCGCGCGCTGCCAGGCTGGCGCGCG 209
QY 61 CSGTGCCGATGTAGCGGCTCCGGATCCCGAGCTCTCCCTGCTCCCGCTGCGGAT 120
DB 210 CCGTGCCGATGTAGCGGCTCCGGATCCCGAGCTCTCCCTGCTCCCGCTGCGGAT 269
QY 121 CTCCTGACCGCTCCACAGCCCGAGCCCGGGGCTGCCAGGCGCTGCCAGGCGCT 180
DB 270 CTCCTGACCGCTCTCCACAGCCCGAGCCCGGGGCTGCCAGGCGCTGCCAGGCGCT 329
QY 181 GCGGCTCTGATGCCCGCAAGCTCCCTCTCTCTGAGAGCCACACAGCACCCAGACTTG 240
DB 330 GCGGCTCTGATGCCCGCAAGCTCCCTCTCTCTGAGAGCCACACAGCACCCAGACTTG 389
QY 241 GCGGAGCGCCAGGAGCGAGCTGGGCGAGTGGAGCCAGAGGCGCCGAGCGCGGCG 300
DB 390 GCGGAGCGCCAGGAGCGAGCTGGGCGAGTGGGAGCCAGAGGCGCCGAGCGCGGCG 449
QY 301 CCACCATGCCCGAGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 450 CCACCATGCCCGAGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 509
QY 361 CCCACGCGCCAGCAGCGGATCCGGCTGCCCTGCGCAGCGGCTGGGGGCGCGCGCC 420
DB 510 CCCACGCGCCAGCAGCGGATCCGGCTGCCCTGCGCAGCGGCTGGGGGCGCGCGCC 569
QY 421 TGGGGGTGGGGCTGCCCCCGGAGACCGACGAGAGAGCCCGAGGAGCCCGCGCGAGGCGCA 480

DB 570 TGGGGGTGGGGTGGCCCCGGGAGACCGAGAGCCCGAGAGCCCGCGCGGAGGGGCA 629
QY 481 GCCTTTGTGGAGATGTGGGACAACTGAGGGGCAAGTGGGGGAGGGCTACTAGCTGGAGA 540
DB 630 GCCTTTGTGGAGATGTGGGACAACTGAGGGGCAAGTGGGGGAGGGCTACTAGCTGGAGA 689
QY 541 TGACCGGTGGGACGCCCCCGGACAGAGCTCAACATCTCTGTGGATACAGGAGAGTAACT 600
DB 690 TGACCGGTGGGACGCCCCCGGACAGAGCTCAACATCTCTGTGGATACAGGAGAGTAACT 749
QY 601 TTGACGTGGGTGCTGCCCCCGGACAGAGCTCAACATCTCTGTGGATACAGGAGAGTAACT 660
DB 750 TTGACGTGGGTGCTGCCCCCGGACAGAGCTCAACATCTCTGTGGATACAGGAGAGTAACT 809
QY 661 GCACATACCGGGAGCTCCCGGAGGGTGTGTGTGGCTTACACCGAGGGCAAGTGGGAAG 720
DB 810 GCACATACCGGGAGCTCCCGGAGGGTGTGTGTGGCTTACACCGAGGGCAAGTGGGAAG 869
QY 721 GGGAGCTGGGACCGGACCTGGTAAGCATCCCATGGCCCAAGCTCACGTGCGGTGCCA 780
DB 870 GGGAGCTGGGACCGGACCTGGTAAGCATCCCATGGCCCAAGCTCACGTGCGGTGCCA 929
QY 781 ACATTTGCTGCCATCACTGAATCAGACAAGTTCCTCATCAACGGCTCCAACTGGGAAGCA 840
DB 930 ACATTTGCTGCCATCACTGAATCAGACAAGTTCCTCATCAACGGCTCCAACTGGGAAGCA 989
QY 841 TCCTGGGGTGGCTATGCTGAGATTCGCGAGGCTCAGGACTCCCTGGGAGGCTTTCTTTG 900
DB 990 TCCTGGGGTGGCTATGCTGAGATTCGCGAGTTCGCGAGTTCGCGAGGCTTTCTTTG 1020
QY 901 ACTCTCTGGTAAAGCAGAGACCCACGTTCCCAACCTCTCTCCCTGCGAGCTTTGGTGGCTG 960
DB 1021 -----GCTTTGGTGGCTG 1034
QY 961 GCTTCCCTCCATCAACAGTCTGAAGTGTGGCTCTCTGCGGAGGAGCATGATCATTTGGAG 1020
DB 1035 GCTTCCCTCCATCAACAGTCTGAAGTGTGGCTCTCTGCGGAGGAGCATGATCATTTGGAG 1094
QY 1021 GTATCCACCACTCGCTGTACACAGGAGTCTCTGGTATACACCATCCGCGGAGGAGTGGT 1080
DB 1095 GTATCCACCACTCGCTGTACACAGGAGTCTCTGGTATACACCATCCGCGGAGGAGTGGT 1154
QY 1081 ATTATGAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGAGCTGCA 1140
DB 1155 ATTATGAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGAGCTGCA 1214
QY 1141 AGGAGTACAACTATGACAAAGAGCATTTGGACAGTGGCACACCAACCTTTGTTTGGCCA 1200
DB 1215 AGGAGTACAACTATGACAAAGAGCATTTGGACAGTGGCACACCAACCTTTGTTTGGCCA 1274
QY 1201 AGAAGTGTGTTGAGCTGAGGAGAGCTGGTGTGCTGGCAAGGAGGACCAACCTTTGTTTGG 1260
DB 1275 AGAAGTGTGTTGAGCTGAGGAGAGCTGGTGTGCTGGCAAGGAGGACCAACCTTTGTTTGG 1334
QY 1261 CTGATGTTTCTGGCTAGGAGAGAGCTGGTGTGCTGGCAAGGAGGACCAACCTTTGTTTGG 1320
DB 1335 CTGATGTTTCTGGCTAGGAGAGAGCTGGTGTGCTGGCAAGGAGGACCAACCTTTGTTTGG 1394
QY 1321 ACATTTTCCAGTCACTCTACTCTACCTAATGGTGGAGTTACCAACAGTCTCTTTCCGCA 1380
DB 1395 ACATTTTCCAGTCACTCTACTCTACCTAATGGTGGAGTTACCAACAGTCTCTTTCCGCA 1454
QY 1381 TCACCATCTCTCCGAGCAATACCTCGGCGAGTGGAGAGTGGCCACAGCTCCCAAGAG 1440
DB 1455 TCACCATCTCTCCGAGCAATACCTCGGCGAGTGGAGAGTGGCCACAGCTCCCAAGAG 1514
QY 1441 ACTGTTACAAAGTTTGGCATCTCAGTCACTCCAGGCGACTGTTATGGGAGCTGTTATCA 1500
DB 1515 ACTGTTACAAAGTTTGGCATCTCAGTCACTCCAGGCGACTGTTATGGGAGCTGTTATCA 1574
QY 1501 TGSAGGCGCTTCTACGTTGCTTTTGTATCGGCGCCGAAACGAATTTGCTGCTGTCAGCG 1560
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QY 726 CTGGGACCGACCTGGTAAGCATCCCCCATGGCCCCAAGCTCACTGTGGTGGCAACATT 785
DB 421 CTGGGACCGACCTGGTAAGCATCCCCCATGGCCCCAAGCTCACTGTGGTGGCAACATT 480
QY 786 GCTGGCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCTCTG 845
DB 481 GCTGGCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCTCTG 540
QY 846 GGGCTGGCTATTGCTGAGATTGGCAGGCTGAGCATCTCCCTGGAGCTTTCTTTGACTCT 905
DB 541 GGGCTGGCTATTGCTGAGATTGGCAGGCTGAGCATCTCCCTGGAGCTTTCTTTGACTCT 600
QY 906 CTGGTAAAGCAGACCCACCGTTCCTCAACCTCTCTCCCTGCAGCTTTGTTGGTGGCTTC 965
DB 601 CTGGTAAAGCAGACCCACCGTTCCTCAACCTCTCTCCCTGCAGCTTTGTTGGTGGCTTC 660
QY 966 CCGCTCAACGAGTCTGAAGTGTGGCTCTGTGGAGGAGCATGATCATTTGGAGGTATC 1025
DB 661 CCGCTCAACGAGTCTGAAGTGTGGCTCTGTGGAGGAGCATGATCATTTGGAGGTATC 720
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DB 781 GAGGTGATCATTTGTGGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 840
QY 1146 TACAACATGACAAAGCATTTGGAGACATGGGACACCAACCATCTCGTTTGGCCCAAGAA 1205
DB 841 TACAACATGACAAAGCATTTGGAGACATGGGACACCAACCATCTCGTTTGGCCCAAGAA 900
QY 1206 GTGTTTGAAGCTGACGCTCAATCATCAAGGACGCTCTCCACGGAGAGTTCCCTGAT 1265
DB 901 GTGTTTGAAGCTGACGCTCAATCATCAAGGACGCTCTCCACGGAGAGTTCCCTGAT 960
QY 1266 GTTCTTGGCTAGGAGCAGCTGGTGTGCTGGCAAGCAGGACACCCCTTGGAAACATT 1325
DB 961 GTTCTTGGCTAGGAGCAGCTGGTGTGCTGGCAAGCAGGACACCCCTTGGAAACATT 1020
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DB 1081 ATCTTTCCGAGCAATACCTGCGGCAGTGGAAAGATGTGGCCACGCTCCCAAGACGACTGT 1140
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DB 1141 TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
QY 1506 GCGTCTACGTTCTTTGATCGGGCCGGAACGAAATGGCTTTGCTGTCACGCTTGC 1565
DB 1201 GCGTCTACGTTCTTTGATCGGGCCGGAACGAAATGGCTTTGCTGTCACGCTTGC 1260
QY 1566 CATGTGCACGATGAGTTTCAGGACGGCGGTGGAGGCGCTTTTGTCACTTTGGACATG 1625
DB 1261 CATGTGCACGATGAGTTTCAGGACGGCGGTGGAGGCGCTTTTGTCACTTTGGACATG 1320
QY 1626 GAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT 1685
DB 1321 GAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT 1380
QY 1686 GTCATGGCTGCCATCTGCGCCCTCTTTCATGCTGCCACTCTGCCCTCATGTTGTGTCAGTGG 1745
DB 1381 GTCATGGCTGCCATCTGCGCCCTCTTTCATGCTGCCACTCTGCCCTCATGTTGTGTCAGTGG 1440
QY 1746 CGCTGCTCGCTGCTGCGCCAGCAGCATGATGACTTTTCTGATGACATCTCCCTGCTG 1805
DB 1441 CGCTGCTCGCTGCTGCGCCAGCAGCATGATGACTTTTCTGATGACATCTCCCTGCTG 1500
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DB 1501 AAGTGAGGAGGCGCCATGGGCAGAAGATAGAGATTCCCTTGGACACACCTCCCTGGTTCA 1560
QY 1866 CTTTGTGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCAGCTCAGACCTCC 1925
DB 1561 CTTTGTGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCAGCTCAGACCTCC 1620
QY 1926 CACCCACCAAAATGCTCTGCTTGTATGGAGAAGAAAGCTTGGCAAGTGGTTCAG 1985
DB 1621 CACCCACCAAAATGCTCTGCTTGTATGGAGAAGAAAGCTTGGCAAGTGGTTCAG 1680
QY 1986 GGAAGTGTCTGTAGGAAACAGAAAGAGAAAGAACGACTCTGTGGCGGGAATACT 2045
DB 1681 GGAAGTGTCTGTAGGAAACAGAAAGAGAAAGAACGACTCTGTGGCGGGAATACT 1740
QY 2046 CTTGGTCACTCAAAATTAAGTCGGGAATTTCTGCTGCTTGAACCTTCAGCCCTGACCT 2105
DB 1741 CTTGGTCACTCAAAATTAAGTCGGGAATTTCTGCTGCTTGAACCTTCAGCCCTGACCT 1800
QY 2106 TTGTCCACCATTCCTTTAAATTTCTCAACCCAAAGATTTCTTCTTTTCTTTAGTTTCAGAA 2165
DB 1801 TTGTCCACCATTCCTTTAAATTTCTCAACCCAAAGATTTCTTCTTTTCTTTAGTTTCAGAA 1860
QY 2166 GTACTGGCATCACACGAGGTTACCTTGGCGTGTGCTCCCTGTGTTGCTGGCAGAGAAG 2225
DB 1861 GTACTGGCATCACACGAGGTTACCTTGGCGTGTGCTCCCTGTGTTGCTGGCAGAGAAG 1920
QY 2226 AGACCAAGCTTGTTCCTGCTGGCCAAAGTCACTAGGAGAGGATGCACAGTTTGTCTATT 2285
DB 1921 AGACCAAGCTTGTTCCTGCTGGCCAAAGTCACTAGGAGAGGATGCACAGTTTGTCTATT 1980
QY 2286 TGCTTTAGACACAGGACTGTATAAACAAGCTTAACATTTGGTCAAAAGATTGCTCTTTGA 2345
DB 1981 TGCTTTAGACACAGGACTGTATAAACAAGCTTAACATTTGGTCAAAAGATTGCTCTTTGA 2040
QY 2346 ATT 2348
DB 2041 ATT 2043
RESULT 5
AADI7865
ID AADI7865 standard; cDNA; 2070' BP.
XX
AC AADI7865;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human aspartyl protease 2(a) [hu-Asp2(a)] cDNA.
XX
KW Human; aspartyl protease 2(a); Asp2(a); amyloid precursor protein; APP;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nontropic; neuroprotective;
KW chromosome 11q23.3-24.1; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
DB CDS 1..1506
FT /*tag= a
FT /product= "Human aspartyl protease 2(a)"
FT sig_peptide 1..63
FT /*tag= b
FT mat_peptide 64..1503
FT /*tag= c
FT /product= "Mature human aspartyl protease 2(a)"
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-0023315.
XX

PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX (PHAA) PHARMACTA & UPJOHN CO.
PA
XX Bienkowski MJ, Gurney M;
XX
XX WPI; 2001-444208/48.
DR P-PSDB; AA010629.
XX
XX Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
XX Example 2; Fig 2; 187pp; English.
XX
XX The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC Asp1 proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding
CC long form of human Asp2 protein, designated as Asp2(a). Asp2 gene is
CC localised on chromosome 11q23.3-24.1.
XX
XX Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;
SQ

Query Match 86.9%; Score 2039.8; DB 22; Length 2070;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 306 ATGGCCCAAGCCCTGCGCTCTGCTGTGGATGGGCGGGAGTGCTGCCCTGCCAC 365
DB 1 ATGGCCCAAGCCCTGCGCTCTGCTGTGGATGGGCGGGAGTGCTGCCCTGCCAC 60
QY 366 GGCACCCAGCAGCATCCGCTGCGCTGCGCAGGGGCTGGGGGGCGCCCTGGGG 425
DB 61 GGCACCCAGCAGCATCCGCTGCGCTGCGCAGGGGCTGGGGGGCGCCCTGGGG 120
QY 426 CTGGGCTGCGCCCGGAGACCGACCAAGACCGCCGAGGCGCGGGGCGGCGCTTT 485
DB 121 CTGGGCTGCGCCCGGAGACCGACCAAGACCGCCGAGGCGCGGGGCGGCGCTTT 180
QY 486 GTGGAGATGTGGACAACTGAGGGGCAAGTCGGGCGAGGCTACTACGTGGAGATGACC 545
DB 181 GTGGAGATGTGGACAACTGAGGGGCAAGTCGGGCGAGGCTACTACGTGGAGATGACC 240
QY 546 GTGGGACCCCGCCGACAGCTCAACATCCTGGTGGATACAGCAGCAGTAACTTGCA 605
DB 241 GTGGGACCCCGCCGACAGCTCAACATCCTGGTGGATACAGCAGCAGTAACTTGCA 300
QY 606 GTGGGCTGCTGCCCGCCACCCCTTCCCTGCTGCTACTACAGAGGCGAGCTGCCAGCACA 665
DB 301 GTGGGCTGCTGCCCGCCACCCCTTCCCTGCTGCTACTACAGAGGCGAGCTGCCAGCACA 360
QY 666 TACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGCGAAGTGGGAAGGGAG 725
DB 361 TACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGCGAAGTGGGAAGGGAG 420
QY 726 CTGGGACCCAGCTGGTAAAGATCCCCATGGCCCCCAAGCTCACTGTGCGTGCACATT 785
DB

DB 421 CTGGGACCCAGCTGGTAAAGCATCCCCCATGGCCCCCAAGCTCACTGTGCGTGCCAAACAATT 480
QY 786 GCTGCCATCACTGAATCAGCAAGTTCTTTCATCAACGGCTCCCAACTGGGAAGGATCCCTG 845
DB 481 GCTGCCATCACTGAATCAGCAAGTTCTTTCATCAACGGCTCCCAACTGGGAAGGATCCCTG 540
QY 846 GGGTGGCCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCCTTTCTTTGACATCT 905
DB 541 GGGTGGCCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCCTTTCTTTGACATCT 600
QY 906 CTGGTAAAGCAGACCCAGCTTCCCAACCTTCTTCTCCCTGCAGCTTTGTGGTGGCTGC 965
DB 601 CTGGTAAAGCAGACCCAGCTTCCCAACCTTCTTCTCCCTGCAGCTTTGTGGTGGCTGC 660
QY 966 CCCTCAACCAAGTCTGAAGTGTGCTGCTGGAGGAGCATGATCATTTGGAGGTATC 1025
DB 661 CCCTCAACCAAGTCTGAAGTGTGCTGCTGGAGGAGCATGATCATTTGGAGGTATC 720
QY 1026 GACCACTCGCTGTACACAGGAGTCTCTGGTATACACCCATCCCGGGGAGTGGTATTTAT 1085
DB 721 GACCACTCGCTGTACACAGGAGTCTCTGGTATACACCCATCCCGGGGAGTGGTATTTAT 780
QY 1086 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGATCTGAAAAATGGACTGCAAGGAG 1145
DB 781 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGATCTGAAAAATGGACTGCAAGGAG 840
QY 1146 TACAACATATGACAAGAGCATTTGTGGACAGTGGCACCACCAACCTTCTTTGCCCAAGAAA 1205
DB 841 TACAACATATGACAAGAGCATTTGTGGACAGTGGCACCACCAACCTTCTTTGCCCAAGAAA 900
QY 1206 GTGTTTGAAGTGGAGTCAAAATCCATCAAGGAGCCTCTTCCAGGAGAAAGTTCCCTGAT 1265
DB 901 GTGTTTGAAGTGGAGTCAAAATCCATCAAGGAGCCTCTTCCAGGAGAAAGTTCCCTGAT 960
QY 1266 GGTGTTCTGGCTAGGAGAGCAGCTGTGCTGCGAAGCAGGACCAACCTTCTTGAACATT 1325
DB 961 GGTGTTCTGGCTAGGAGAGCAGCTGTGCTGCGAAGCAGGACCAACCTTCTTGAACATT 1020
QY 1326 TTCCAGTCACTCTCACTTACCTAATGGGTGAGGTTTACCAACCAAGTCTTCCCGATACC 1385
DB 1021 TTCCAGTCACTCTCACTTACCTAATGGGTGAGGTTTACCAACCAAGTCTTCCCGATACC 1080
QY 1386 ATGCTTCCGAGAGCAATACCTGCGGCGAGTGGAGATGTGGCCAGGTCCCAAGAGACATGT 1445
DB 1081 ATGCTTCCGAGAGCAATACCTGCGGCGAGTGGAGATGTGGCCAGGTCCCAAGAGACATGT 1140
QY 1446 TACAAGTTTGCATCTCACTCACTCCAGCGGCACTGTTATGGAGCTGTTATCATGGAG 1505
DB 1141 TACAAGTTTGCATCTCACTCACTCCAGCGGCACTGTTATGGAGCTGTTATCATGGAG 1200
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DB 1201 GGTCTTCACTGCTTGTGATCGGGCCGAAACGAAATTTGGCTTGTGTCAGGCGTTGC 1260
QY 1566 CATGTGACGATGAGTTTCAAGGAGGCGGCTGGAGAGGCCCTTTTGTACACCTTGGACATG 1625
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QY 1686 GTCATGGCTGCCATCTGCGCCCTTTCATGCTGCCACTCTGCTCATATGGTGTGTCAGTGG 1745
DB 1381 GTCATGGCTGCCATCTGCGCCCTTTCATGCTGCCACTCTGCTCATATGGTGTGTCAGTGG 1440
QY 1746 CGCTGCTCCCTGCTGCTGGGCGAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1805
DB 1441 CGCTGCTCCCTGCTGCTGGGCGAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
QY 1806 AAGTGAGGAGGCCCATGGGCAAGATAGAGATTTCCCTTGACACCAACCTCCGTGGTTCA 1865
DB 1501 AAGTGAGGAGGCCCATGGGCAAGATAGAGATTTCCCTTGACACCAACCTCCGTGGTTCA 1560


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QY 1866 CTTTGGTCAACAGTAGGAGACAGATGGCACCTGTGGCCAGAGCAGCCTCAGGACCTCC 1925
DB 1561 CTTTGGTCAACAGTAGGAGACAGATGGCACCTGTGGCCAGAGCAGCCTCAGGACCTCC 1620
QY 1926 CCACCCACCAATAGCCTCTGCTGCTGTATGGAGAGGAAAAGCCTGGCAGTGGTTCAG 1985
DB 1621 CCACCCACCAATAGCCTCTGCTGCTGTATGGAGAGGAAAAGCCTGGCAGTGGTTCAG 1680
QY 1986 GGACTGTACCTGTAGGAAACAGAGAAAGAGAAAGAACGACCTGCTGCTGGCGGAATACT 2045
DB 1681 GGACTGTACCTGTAGGAAACAGAGAAAGAGAAAGAACGACCTGCTGCTGGCGGAATACT 1740
QY 2046 CTTTGGTCAACCTAAATTTAAGTCGGGAAATTTCTGCTGCTTTGAAACTTCAGCCCTGAACCT 2105
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DB 1801 TTGTCCACCAATTCCTTTAAATTTCCNACCCAAAGATATCTCTTTTCTTAGTTTCAGAA 1860
QY 2166 GTACTGGCATCACAGCAGTTACCTTGGCGTGTGTCCTGTGTACCTGGCAGAGAAG 2225
DB 1861 GTACTGGCATCACAGCAGTTACCTTGGCGTGTGTCCTGTGTGTGTCCTGGCAGAGAAG 1920
QY 2226 AGACCAAGCTTGTTCCTGCTGCTGCGCAAAAGTCAGTAGGAGAGGATGCACAGTTTGTCTATT 2285
DB 1921 AGACCAAGCTTGTTCCTGCTGCTGCGCAAAAGTCAGTAGGAGAGGATGCACAGTTTGTCTATT 1980
QY 2286 TGCTTTAGACAGAGGACTGTATTAACAGCCCTAACATTTGGTGCAGAGATTGCTCTTGA 2345
DB 1981 TGCTTTAGACAGAGGACTGTATTAACAGCCCTAACATTTGGTGCAGAGATTGCTCTTGA 2040
QY 2346 ATT 2348
DB 2041 ATT 2043

RESULT 6
AAD13021
ID AAD13021 standard; cDNA; 2070 BP.
XX
AC AAD13021;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human aspartyl protease 2a (Hu-Asp2a) cDNA.
XX
KW Human; aspartyl protease 2a; Asp 2a; beta-amyloid precursor protein; APP;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW neuroprotective; antisense therapy; gene therapy;
KW chromosome 11q23.3-24.1; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 1..1506
FT /tag= a
FT /product= "Human aspartyl protease 2a (Hu-Asp2a)"
FT sig_peptide
FT 1..63
FT /tag= b
FT mat_peptide
FT 64..1503
FT /tag= c
FT /product= "Mature human aspartyl protease 2a (Hu-Asp2a)"
XX
PN W0200150829-A2.
XX
PD 19-JUL-2001.
XX
PE 09-MAY-2001; 2001WO-IB00799.
XX
PR 09-MAY-2001; 2001WO-IB00799.
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XX
: PA
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI: 2001-483072/52.
DR P-PSDB: AAE06859.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity
XX
PS Claim 98: Fig 2; 185pp: English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in vitro assays and in Northern and Southern
CC blots. The present cDNA sequence encodes human aspartyl protease 2
CC (Hu-Asp2), a 'long' form designated as (Hu-Asp2a). Hu-Asp 2 gene is
CC localised on chromosome 11q23.3-24.1.
XX
SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;
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Query Match 86.9%; Score 2039.8; DB 22; Length 2070;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 306 ATGCCCAAGCCCTGCCCTGCTGCTGTGGATGGCGCGGAGTGCTGCCCTGCCAC 365
DB 1 ATGCCCAAGCCCTGCCCTGCTGCTGTGGATGGCGCGGAGTGCTGCCCTGCCAC 60

QY 366 GGCACCCAGACAGCGCATCCGGCTGCCCTGCGCAGCGGCTGGGGGGCGCCCTGGGG 425
DB 61 GGCACCCAGACAGCGCATCCGGCTGCCCTGCGCAGCGGCTGGGGGGCGCCCTGGGG 120

QY 426 CTGGGCTGCCCGGGAGACGAGAGCCCGAGAGCCCGAGAGCCCGCGGAGGGGAGCTTT 485
DB 121 CTGGGCTGCCCGGGAGACGAGAGCCCGAGAGCCCGCGGAGGGGAGCTTT 180

QY 486 GTGGAGATGTTGGACAACCTGAGGGGCAAGTCCGGGGCAGGCTACTACGTGGAGATGACC 545
DB 181 GTGGAGATGTTGGACAACCTGAGGGGCAAGTCCGGGGCAGGCTACTACGTGGAGATGACC 240

QY 546 GTGGGAGCCCCCGCAGACGCTCAACATCTGTTGGATACAGCAGCAGTAACTTTGCA 605
DB 241 GTGGGAGCCCCCGCAGACGCTCAACATCTGTTGGATACAGCAGCAGTAACTTTGCA 300

QY 606 GTGGGTGCTGCCCCCCCCCTTCCCTGCATCGCTACTACCAGAGGAGCTGTCAGCACA 665
DB 301 GTGGGTGCTGCCCCCCCCCTTCCCTGCATCGCTACTACCAGAGGAGCTGTCAGCACA 360

QY 666 TACCGGACCTCCGGAAGGGTGTATGTGCCCTTACACCCAGGCAAGTGGGAAGGGAG 725
DB 361 TACCGGACCTCCGGAAGGGTGTATGTGCCCTTACACCCAGGCAAGTGGGAAGGGAG 420

QY 726 CTGGGCACCGACCTGGTAAAGCATCCCCCATGGCCCCCAACGCTCACTGTGCGTGCGCAACATT 785
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QY 486 GTGGAGATGCTGACAACTTGAGGGCAAGTCGGGGCAGGCTACTACGTGGAGATGACC 545
DB 181 GTGGAGATGCTGACAACTTGAGGGCAAGTCGGGGCAGGCTACTACGTGGAGATGACC 240
QY 546 GTGGGAGCCCCCGGACGCTCAACATCCTGGTGGATACAGGACGACGTAACATTTGCA 605
DB 241 GTGGGAGCCCCCGGACGCTCAACATCCTGGTGGATACAGGACGACGTAACATTTGCA 300
QY 606 GTGGGTGCTGCCCCCCCCACCCCTTCTGCTGCTACTACTACGAGGCGAGCTGCCAGACA 665
DB 301 GTGGGTGCTGCCCCCCCCACCCCTTCTGCTGCTACTACTACGAGGCGAGCTGCCAGACA 360
QY 666 TACCGGACCTCCGGAAAGGCTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGGAG 725
DB 361 TACCGGACCTCCGGAAAGGCTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGGAG 420
QY 726 CTGGGACCGACCTGTGTAGATGCGAGGCTGACGACTCCCTGGAGCCCTTTCTTTGACTCT 785
DB 421 CTGGGACCGACCTGTGTAGATGCGAGGCTGACGACTCCCTGGAGCCCTTTCTTTGACTCT 480
QY 786 GCTGCCATCACTGAATCAGACAAAGTTCTTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 845
DB 481 GCTGCCATCACTGAATCAGACAAAGTTCTTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
QY 846 GGGCTGGCCCTATGCTGAGATTGGCAGGCTGACGACTCCCTGGAGCCCTTTCTTTGACTCT 905
DB 541 GGGCTGGCCCTATGCTGAGATTGGCAGGCTGACGACTCCCTGGAGCCCTTTCTTTGACTCT 600
QY 906 CTGGTAAAGCAGACCCACGTTCCCAAGCTCTTCTCCCTGCGAGCTTTGTGTGGTGGCTTC 965
DB 601 CTGGTAAAGCAGACCCACGTTCCCAAGCTCTTCTCCCTGCGAGCTTTGTGTGGTGGCTTC 660
QY 966 CCCCTCAACAGCTGTAAGTGTGGCTGTGCTGGAGGAGCATGATCATTTGGAGGTATC 1025
DB 661 CCCCTCAACAGCTGTAAGTGTGGCTGTGCTGGAGGAGCATGATCATTTGGAGGTATC 720
QY 1026 GACCACTCGCTTACACAGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 1085
DB 721 GACCACTCGCTTACACAGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
QY 1086 GAGGTGATCAATGTGGGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 1145
DB 781 GAGGTGATCAATGTGGGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
QY 1146 TACAACATATGACAAAGAGCATTTGGACAGTGGCAGTGGCACCACCAACCTTCGTTTGGCCCAAGAAA 1205
DB 841 TACAACATATGACAAAGAGCATTTGGACAGTGGCAGTGGCACCACCAACCTTCGTTTGGCCCAAGAAA 900
QY 1206 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGCGAGCCCTCCACGGAGAAAGTTCCTGTAT 1265
DB 901 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGCGAGCCCTCCACGGAGAAAGTTCCTGTAT 960
QY 1266 GGTTCCTGGCTAGGAGAGCAGTGGTGTGCTGGCAAGCAGCACCACCCCTTTGGAAACATT 1325
DB 961 GGTTCCTGGCTAGGAGAGCAGTGGTGTGCTGGCAAGCAGCACCACCCCTTTGGAAACATT 1020
QY 1326 TTCCCACTCATCTACCTTACCTAATGGGTGAGGTTACCAACCAAGTCTTCCCGCATCACC 1385
DB 1021 TTCCCACTCATCTACCTTACCTAATGGGTGAGGTTACCAACCAAGTCTTCCCGCATCACC 1080
QY 1386 ATCTCTCCGAGCAATACCTCCGCGCCAGTGGAGATGTGGCCAGCTGCCAAGACGACTGT 1445
DB 1081 ATCTCTCCGAGCAATACCTCCGCGCCAGTGGAGATGTGGCCAGCTGCCAAGACGACTGT 1140
QY 1446 TACAAGTTTGGCCATCTCACAGTATCATCCAGCGGCACTGTTATGGAGCTGTATCATGGAG 1505
DB 1141 TACAAGTTTGGCCATCTCACAGTATCATCCAGCGGCACTGTTATGGAGCTGTATCATGGAG 1200
QY 1506 GGCTTCTACGTTTGTCTTTGATCGGGGCCCCGAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1565
DB 1201 GGCTTCTACGTTTGTCTTTGATCGGGGCCCCGAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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QY 1566 CATGTCACGATGAGTTTCAGGAGCGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1625
DB 1261 CATGTCACGATGAGTTTCAGGAGCGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320
QY 1626 GAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1685
DB 1321 GAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1380
QY 1686 GTCATGCTGCCATCTCGGCCCTTTCATGCTGCCACTCTGCCCTCATGCTGTGTCAGTGG 1745
DB 1381 GTCATGCTGCCATCTCGGCCCTTTCATGCTGCCACTCTGCCCTCATGCTGTGTCAGTGG 1440
QY 1746 CGTGTCCCTCGCTGCCCTCGCCAGCAGCATGATGACTTTTGTGATGACATCTCCCTGCTG 1805
DB 1441 CGTGTCCCTCGCTGCCCTCGCCAGCAGCATGATGACTTTTGTGATGACATCTCCCTGCTG 1500
QY 1806 AAGTGAGGAGGCCATGGGAGAGAATAGAGATTTCCCTGGACCACACCTCCCGTGGTTCA 1865
DB 1501 AAGTGAGGAGGCCATGGGAGAGAATAGAGATTTCCCTGGACCACACCTCCCGTGGTTCA 1560
QY 1866 CTTTGTGTCAAACTGAGGAGACAGATGGCACCTGTGCCAGAGCACCCTCAGGACCCCTCC 1925
DB 1561 CTTTGTGTCAAACTGAGGAGACAGATGGCACCTGTGCCAGAGCACCCTCAGGACCCCTCC 1620
QY 1926 CCACCCACCAATGCTCTGCTTGTATGGAGAGAAAGGCTGGCAAGGTGGGTTCCAG 1985
DB 1621 CCACCCACCAATGCTCTGCTTGTATGGAGAGAAAGGCTGGCAAGGTGGGTTCCAG 1680
QY 1986 GGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGAGCACTCTGTGGCGGGAATFACT 2045
DB 1681 GGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGAGCACTCTGTGGCGGGAATFACT 1740
QY 2046 CTTTGTGTCAAACTGAGGAGAAATTAAGTGGGAAATTCGCTCTTCAAACTTCAGCCCTGAACCT 2105
DB 1741 CTTTGTGTCAAACTGAGGAGAAATTAAGTGGGAAATTCGCTCTTCAAACTTCAGCCCTGAACCT 1800
QY 2106 TTGTCCACCAATTCCTTTAAATTCCTCAACCCAAAGATTTCTTCTTTCTTAGTTTCAGAA 2165
DB 1801 TTGTCCACCAATTCCTTTAAATTCCTCAACCCAAAGATTTCTTCTTTCTTAGTTTCAGAA 1860
QY 2166 GTACTGGCATCACACGAGGTTACCTTGGGCTGTGCTTGTGTACCCCTGGGAGAGAAAG 2225
DB 1861 GTACTGGCATCACACGAGGTTACCTTGGGCTGTGCTTGTGTACCCCTGGGAGAGAAAG 1920
QY 2226 AGACCAAGCTGTGTTCCCTGCTGCCAAAGTCACTAGGAGAGGATGCACAGTTTGTCTATT 2285
DB 1921 AGACCAAGCTGTGTTCCCTGCTGCCAAAGTCACTAGGAGAGGATGCACAGTTTGTCTATT 1980
QY 2286 TGCTTTAGACAGAGGACTGTATAAACAAGCCTAACATTTGGTGCAAGATTGCCCTCTTGA 2345
DB 1981 TGCTTTAGACAGAGGACTGTATAAACAAGCCTAACATTTGGTGCAAGATTGCCCTCTTGA 2040
QY 2346 ATT 2348
DB 2041 ATT 2043
RESULT 9
AAD06739
ID AAD06739 standard; cdna; 2070 BP.
XX
AC AAD06739;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human aspartyl protease 2a (Asp2a) cdna.
XX
KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp 2a;
XX beta-secretase; chromosome 11q23.3-24.1; ss.
XX
OS Homo sapiens.
XX
```

FH Key Location/Qualifiers
 FT 1..1506
 FT /*tag= a
 FT /product= "Human aspartyl protease 2a"
 FT 1..63
 FT /*tag= b
 FT 64..135
 FT /*tag= c
 FT /note= "Pre-pro-peptide"
 FT 136..171
 FT /*tag= d
 FT /note= "Pro-peptide"
 FT 172..1503
 FT /*tag= e
 FT /product= "Human mature aspartyl protease 2a"
 XX WO200123533-A2.
 XX 05-APR-2001.
 XX 22-SEP-2000; 2000WO-US26080.
 XX 23-SEP-1999; 99US-0155493.
 XX 23-SEP-1999; 99WO-US20881.
 XX 13-OCT-1999; 99US-0416901.
 XX 06-DEC-1999; 99US-0169232.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Gurney M, Bienkowski MJ;
 XX WPI; 2001-290516/30.
 XX P-PSDB; AAE02581.
 XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
 XX protein, useful for the treatment of Alzheimer's disease -
 XX Example 2; Page 126-127; 189pp; English.
 XX The present invention relates to enzymes for cleaving the alpha-
 XX secretase site of the amyloid precursor protein (APP) and methods of
 XX identifying those enzymes. The methods may be used to identify enzymes
 XX that may be used to cleave the alpha-secretase cleavage site of the APP
 XX protein. The enzymes may be used to treat or modulate the progress of
 XX Alzheimer's disease. The present sequence is human aspartyl protease
 XX (Asp) 2a cDNA. Asp 2a has beta-secretase protease activity. Asp2 gene
 XX is located on chromosome 11q23.3-24.1.
 XX Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;
 SQ
 Query Match 86.9%; Score 2039.8; DB 22; Length 2070;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2041; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 306 ATGGCCCAAGCCCTGGCTCTGCTGTGGATGGGCGGGAGTGTGCTGCCAC 365
 DB 1 ATGGCCCAAGCCCTGGCTCTGCTGTGGATGGGCGGGAGTGTGCTGCCAC 60
 QY 366 GGCACACAGCAGCATCCGCTGCCCTGCGCAGCGCTGGGGCGCCCTGGGG 425
 DB 61 GGCACACAGCAGCATCCGCTGCCCTGCGCAGCGCTGGGGCGCCCTGGGG 120
 QY 426 CTGCGGCTGCCGGGAGACCGAGACGCCGAGGAGCCCGCGGAGGGGCGAGCTTT 485
 DB 121 CTCGCGCTGCCGGGAGACCGAGAGCCCGAGGAGCCCGCGGAGGGGCGAGCTTT 180
 QY 486 GTGAGATGTGGACAACTCTGAGGGGCAAGTCGGGCGAGGGCTACTACGTGGAGATGACC 545
 DB 181 GTGAGATGTGGACAACTCTGAGGGCAAGTCGGGCGAGGGCTACTACGTGGAGATGACC 240
 QY 546 GTGGGAGCCCCCGGAGACGCTCAACATCTGTTGGATACAGGAGAGTAAGTTCGA 605
 DB 241 GTGGGAGCCCCCGGAGACGCTCAACATCTGTTGGATACAGGAGAGTAAGTTCGA 300

QY 606 GTGGGTGCTGCCCCCACCCTTCTCTGATCGCTACTACCAGAGCAGCTGTCTCAGCACA 665
 DB 301 GTGGGTGCTGCCCCCACCCTTCTCTGATCGCTACTACCAGAGCAGCTGTCTCAGCACA 360
 QY 666 TACCGGACCTCCGGAAGGGTGTGTATGTGGCTTACACCCAGGGAAGTGGGAAGGGAG 725
 DB 361 TACCGGACCTCCGGAAGGGTGTGTATGTGGCTTACACCCAGGGAAGTGGGAAGGGAG 420
 QY 726 CTGGGACCCAGCTGGTAAGCATCCCATCGCCCCCAAGCTTCTTCAACCGGTCCAACTGGGAAGGCATCTTG 785
 DB 421 CTGGGACCCAGCTGGTAAGCATCCCATCGCCCCCAAGCTTCTTCAACCGGTCCAACTGGGAAGGCATCTTG 480
 QY 786 GCTGCCATCATCTGAATCAGACAAGTTCTTCAACCGGTCCAACTGGGAAGGCATCTTG 845
 DB 481 GCTGCCATCATCTGAATCAGACAAGTTCTTCAACCGGTCCAACTGGGAAGGCATCTTG 540
 QY 846 GGGCTGGCTTATGCTGAGATTTGCCAGGCTTACGACTTCTTGGAGGCTTTTCTTTGACTCT 905
 DB 541 GGGCTGGCTTATGCTGAGATTTGCCAGGCTTACGACTTCTTGGAGGCTTTTCTTTGACTCT 600
 QY 906 CTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGCACCTTTTGTGTGCTGCTTC 965
 DB 601 CTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGCACCTTTTGTGTGCTGCTTC 660
 QY 966 CCCTTCAACCAAGTCTGAAGTCTGCGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC 1025
 DB 661 CCCTTCAACCAAGTCTGAAGTCTGCGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC 720
 QY 1026 GACCACCTGCTGTACAGAGCAGTCTCTGGTATACACCATCCGCGGGAGTGGTATAT 1085
 DB 721 GACCACCTGCTGTACAGAGCAGTCTCTGGTATACACCATCCGCGGGAGTGGTATAT 780
 QY 1086 GAGGTATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGAGCTGCAAGGAG 1145
 DB 781 GAGGTATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGAGCTGCAAGGAG 840
 QY 1146 TACAACATATGACAAGAGCATTTGTGGACAGTGGCACACCAACCTTCTGTTGCCAAGAAA 1205
 DB 841 TACAACATATGACAAGAGCATTTGTGGACAGTGGCACACCAACCTTCTGTTGCCAAGAAA 900
 QY 1206 GTGTTTGAAGCTGAGTCAAAATCCATCAAGCAGGCTCTCTCCAGGAGAAGTTCCTGTAT 1265
 DB 901 GTGTTTGAAGCTGAGTCAAAATCCATCAAGCAGGCTCTCTCCAGGAGAAGTTCCTGTAT 960
 QY 1266 GGTTCCTGGCTAGGAGACGACGTGCTGCTGGCAAGGAGGACCAACCTTCTGGAACATT 1325
 DB 961 GGTTCCTGGCTAGGAGACGACGTGCTGCTGGCAAGGAGGACCAACCTTCTGGAACATT 1020
 QY 1326 TTCCCAAGTCACTCTACCTAATGGGTGAGGTTTACCAACAGTCTCTTCCGCATCACC 1385
 DB 1021 TTCCCAAGTCACTCTACCTAATGGGTGAGGTTTACCAACAGTCTCTTCCGCATCACC 1080
 QY 1386 ATCCCTTCCGAGCAATACCTGCGGCGAGTGGAAAGATGTGGCAGCTGCCAAGACGACTGT 1445
 DB 1081 ATCCCTTCCGAGCAATACCTGCGGCGAGTGGAAAGATGTGGCAGCTGCCAAGACGACTGT 1140
 QY 1446 TACAAGTTTGGCACTCTCACAGTCACTCCAGGCGACTGTTATGGAGCTGTTATCATGGAG 1505
 DB 1141 TACAAGTTTGGCACTCTCACAGTCACTCCAGGCGACTGTTATGGAGCTGTTATCATGGAG 1200
 QY 1506 GGTTCCTACGTTGCTTTTGTATCGGGCGCGAAGAACTTGGCTTGTCTGTCAGCGCTTGC 1565
 DB 1201 GGTTCCTACGTTGCTTTTGTATCGGGCGCGAAGAACTTGGCTTGTCTGTCAGCGCTTGC 1260
 QY 1566 CATGTCCAGATGAGTTTCAGGACGCGAGTGGGAAGGCCCTTTTGTCACTTTGGACATG 1625
 DB 1261 CATGTCCAGATGAGTTTCAGGACGCGAGTGGGAAGGCCCTTTTGTCACTTTGGACATG 1320
 QY 1626 GAAGACTGTGGCTTACAACATTTCCAGACAGATGAGTCAACCTCATGACCATAGCCTAT 1685
 DB 1321 GAAGACTGTGGCTTACAACATTTCCAGACAGATGAGTCAACCTCATGACCATAGCCTAT 1380


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Qy 1206 GTGTTTGAAGCTGCAGTCAATCAATCAATCAAGCAGCCTCTCCACGGAGAAGTTCCCTGAT 1265
Db 901 GTGTTTGAAGCTGCAGTCAATCAATCAATCAAGCAGCCTCTCCACGGAGAAGTTCCCTGAT 960
Qy 1266 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGTGGCAAGCAGCACCACCCCTTGGAAACATT 1325
Db 961 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGTGGCAAGCAGCACCACCCCTTGGAAACATT 1020
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Db 1021 TTCCCACTCATCTACCTACCTAATGGGTGAGGTACCAACCACTCTTCCCGATCACC 1080
Qy 1386 ATCTCTCCGAGCAATACCTGCGGCCAGTGAAGATGTGGCCACGTCCCAAGACGACTGT 1445
Db 1081 ATCTCTCCGAGCAATACCTGCGGCCAGTGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
Qy 1446 TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTATGGAGAGTGTATCATGGAG 1505
Db 1141 TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTATGGAGAGTGTATCATGGAG 1200
Qy 1506 GGCTTCTACGTTGCTTTGATCGGGCCCGGAAACGAATTGGCTTTGCTGTCAGGCGCTGC 1565
Db 1201 GGCTTCTACGTTGCTTTGATCGGGCCCGGAAACGAATTGGCTTTGCTGTCAGGCGCTGC 1260
Qy 1566 CATGTGCACGATGATTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACTTTGGACATG 1625
Db 1261 CATGTGCACGATGATTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACTTTGGACATG 1320
Qy 1626 GAAGACTGTGGCTACAACTATCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1685
Db 1321 GAAGACTGTGGCTACAACTATCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1380
Qy 1686 GTCATGCGTGCCTATCTGGCCCTCTTTCATGCTGCACTCTGCCATCATGGTGTGTCAGTGG 1745
Db 1381 GTCATGCGTGCCTATCTGGCCCTCTTTCATGCTGCACTCTGCCATCATGGTGTGTCAGTGG 1440
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Db 1441 CGCTGCGCTCGCTCGCTCGCCACAGCAGCATGATGACTTTTGTGATGACATCTCCCTGCTG 1500
Qy 1806 AAGTGAGAGGCCCATGGGCAAGATAGAGATTCCCT -GGACCACACCTCCGTGGTTC 1864
Db 1501 AAGTGAGAGGCCCATGGGCAAGATAGAGATTCCCTGGGAGCAGCACCCTCCGTGGTTC 1560
Qy 1865 ACTTTGCTCACAAGTAGGAGACAGATGCCACCTGTGGCAGAGCAGCCTCAGGACCCCTC 1924
Db 1561 ACTTTGCTCACAAGTAGGAGACAGATGGCACCTGTGGCAGAGCAGCCTCAGGACCCCTC 1620
Qy 1925 CCCACCACCAATTCCTCTGCTTGATGGAGAGGAAAGGCTGGCAAGGTGGGTTC 1984
Db 1621 CCCACCACCAATTCCTCTGCTTGATGGAGAGGAAAGGCTGGCAAGGTGGGTTC 1680
Qy 1985 GGGACTGTACCTGTAGGAACAGAAAAGAGAAAGAACAGACATCTGCTGGCGGGAATAC 2044
Db 1681 GGGACTGTACCTGTAGGAACAGAAAAGAGAAAGAACAGACATCTGCTGGCGGGAATAC 1740
Qy 2045 TCTTGGTCACTCAAAATTAAGTCGGGAAATTCCTGCTTGAACATTCAGCCCTGAACC 2104
Db 1741 TCTTGGTCACTCAAAATTAAGTCGGGAAATTCCTGCTTGAACATTCAGCCCTGAACC 1800
Qy 2105 TTTGTCCACCATTCCTTTAAATTTCCAAACCAAGATATTCTTCTTTTAGTTTTCAGA 2164
Db 1801 TTTGTCCACCATTCCTTTAAATTTCCAAACCAAGATATTCTTCTTTTAGTTTTCAGA 1860
Qy 2165 AGTACTGGCATCACACGAGATTACCTTTGGCGTGTGTCCTCTGTTGGTACCCCTGGCAGAGAA 2224
Db 1861 AGTACTGGCATCACACGAGATTACCTTTGGCGTGTGTCCTCTGTTGGTACCCCTGGCAGAGAA 1920
Qy 2225 GAGACCAAGCTTTCTTCCCTGCTGGCCAAAGTTCAGTAGGAGAGATGCACAGATTTGCTAT 2284
Db 1921 GAGACCAAGCTTTCTTCCCTGCTGGCCAAAGTTCAGTAGGAGAGATGCACAGATTTGCTAT 1980
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Qy 2285 TTGCTTTAGACACAGGACTGTATATAACAGCCTTAACATTGGTGCAAGAGATTGGCTCTTG 2344
Db 1981 TTGCTTTAGACACAGGACTGTATATAACAGCCTTAACATTGGTGCAAGAGATTGGCTCTTG 2040
Qy 2345 AATT 2348
Db 2041 AATT 2044
RESULT 13
AAF31848
ID AAF31848 standard; cDNA; 3252 BP.
XX AAF31848;
XX AC
XX AC
DT 12-APR-2001 (first entry)
XX Human memapsin 2 cDNA.
DE Human; memapsin 2; nootropic; neuroprotective; amyloid precursor protein;
KW APP; memapsin 2 inhibitor; Alzheimer's disease; ds.
XX Homo sapiens.
OS WO200100665-A2.
PN 04-JAN-2001.
PD 27-JUN-2000; 2000WO-US17742.
XX 28-JUN-1999; 99US-0141363.
PR 30-NOV-1999; 99US-0168060.
PR 25-JAN-2000; 2000US-0177836.
PR 27-JAN-2000; 2000US-0178388.
PR 08-JUN-2000; 2000US-0210292.
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA (UNII ) UNIV ILLINOIS FOUND.
XX Tang JJN, Hong L, Ghosh AK;
XX WPI; 2001-137933/14.
DR P-PSDB; AAB66572.
XX Novel memapsin 2 inhibitors which bind to active site of memapsin 2
PT having 2 catalytic aspartic residues and substrate binding cleft, used
PT to treat Alzheimer's disease by blocking amyloid precursor.protein
PT cleavage
XX
PS Example 1; Page 70-71; 86pp; English.
XX The present sequence is given in a specification relating to an inhibitor
CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
CC active site, which is defined by the presence of two catalytic aspartic
CC residues and a substrate binding cleft. The inhibitor is useful for
CC the treatment and diagnosis of Alzheimer's disease. It is useful in
CC screens for individuals with a genetic predisposition to Alzheimer's
CC disease. The inhibitor is useful as a reagent for specifically binding to
CC memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2
CC isolation, purification and characterisation.
XX
SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;
Query Match 85.3%; Score 2004; DB 22; Length 3252;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 345 GCGGAGTGCTGCTGCTGCCACCGGACCCAGCAGCAGCCTCCGCTGCCGACGGC 404
Db 1 GCGGAGTGCTGCTGCTGCCACCGGACCCAGCAGCAGCCTCCGCTGCCGACGGC 60
Qy 405 CTGGGGGGCGCCCTCCCTGGGCTCGGCTGCCCGGGGAGACCGAGAGCCCGAGGAG 464
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Db 61 CTGGGGGGCCCCCTGGGGCTGCCGCTGCCCGGGAGACCGAGAGAGAGG 120
QY 465 CCCGCCGGAGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGCAAGTCGGGGCAG 524
Db 121 CCCGCCGGAGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGCAAGTCGGGGCAG 180
QY 525 GGCTACTACGTGGAGATGACCGTGGCAGGCCCCCGGAGAGCGCTCAACATCCTGGTGAT 584
Db 181 GGCTACTACGTGGAGATGACCGTGGCAGGCCCCCGGAGAGCGCTCAACATCCTGGTGAT 240
QY 585 ACAGGCAGCAAGTCTTGCAGTGGGTGCTGCCCGCCACCCCTCCCTGCATCGCTACTAC 644
Db 241 ACAGGCAGCAAGTCTTGCAGTGGGTGCTGCCCGCCACCCCTCCCTGCATCGCTACTAC 300
QY 645 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGTGTGTATGTGCCCTACACC 704
Db 301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGTGTGTATGTGCCCTACACC 360
QY 705 CAGGCAAGTGGGAAGGGAGCTGGGCACCGAGCTGGTAAGCATCCGCCATGGGCCCAAC 764
Db 361 CAGGCAAGTGGGAAGGGAGCTGGGCACCGAGCTGGTAAGCATCCGCCATGGGCCCAAC 420
QY 765 GTCACTGTGCGTGCACAACATTCCTGCATCACTGAATCAGACAAGTTCTTCATCAACGGC 824
Db 421 GTCACTGTGCGTGCACAACATTCCTGCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480
QY 825 TCCAACTGGGAAGGATCCTGGGGTGGCCTATGCTGAGATGGCCAGGCGTACGACTCC 884
Db 481 TCCAACTGGGAAGGATCCTGGGGTGGCCTATGCTGAGATGGCCAGGCGTACGACTCC 540
QY 885 CTGAGCCCTTTCTTTGACTCTCTGCTAAAGCAGACCCACCTTCCCAACCTCTTCTCCCTG 944
Db 541 CTGAGCCCTTTCTTTGACTCTCTGCTAAAGCAGACCCACCTTCCCAACCTCTTCTCCCTG 600
QY 945 CAGCTTTGTGCTGCTGCTTCCCTCAACCACTGCTGAAGTGTGGGCTCTGTGGAGGG 1004
Db 601 CAGCTTTGTGCTGCTGCTTCCCTCAACCACTGCTGAAGTGTGGGCTCTGTGGAGGG 660
QY 1005 AGCATGATCATTGGAGGTATCGACACTCGCTGTACAGCGAGTCTCTGGTATACACC 1064
Db 661 AGCATGATCATTGGAGGTATCGACACTCGCTGTACAGCGAGTCTCTGGTATACACC 720
QY 1065 ATCCGGGGAGTGTATTATCAGGTGATCATGTGCGGGTGGAGATCAATGGACAGAT 1124
Db 721 ATCCGGGGAGTGTATTATCAGGTGATCATGTGCGGGTGGAGATCAATGGACAGAT 780
QY 1125 CTGAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTTGGACAGTGGCCACC 1184
Db 781 CTGAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTTGGACAGTGGCCACC 840
QY 1185 AACCTTCGTTTGGCCCAAGAAAGTGTGTAAGCTGCAAGTCAAAATCCATCAAGGCGCTCC 1244
Db 841 AACCTTCGTTTGGCCCAAGAAAGTGTGTAAGCTGCAAGTCAAAATCCATCAAGGCGCTCC 900
QY 1245 TCCACGAGAAAGTTCCTTCATGCTTCTGCTAGGAGAGCAGCTGCTGCTGCGCAAGCA 1304
Db 901 TCCACGAGAAAGTTCCTTCATGCTTCTGCTAGGAGAGCAGCTGCTGCTGCGCAAGCA 960
QY 1305 GGCAACACCCCTTGGAAACATTTCCACAGTCATCTCACTTAACCTAATGGGTGAGTTTACC 1364
Db 961 GGCAACACCCCTTGGAAACATTTCCACAGTCATCTCACTTAACCTAATGGGTGAGTTTACC 1020
QY 1365 AACCAAGTCTCCGATCACCATCTCCGAGCAATACCTGCGGCGAGTGGAAAGATGTG 1424
Db 1021 AACCAAGTCTCCGATCACCATCTCCGAGCAATACCTGCGGCGAGTGGAAAGATGTG 1080
QY 1425 GCCAGTCCCAAGAGGACTGTACAAAGTTTGCATCTCACAGTCATCCAGGGCAGCTGT 1484
Db 1081 GCCAGTCCCAAGAGGACTGTACAAAGTTTGCATCTCACAGTCATCCAGGGCAGCTGT 1140
QY 1485 ATGGAGCTGTATTATCATGGAGGCTTCTACGTTGTCTTTGATCGGGCCCCGAAACGAATT 1544
Db 1141 ATGGAGCTGTATTATCATGGAGGCTTCTACGTTGTCTTTGATCGGGCCCCGAAACGAATT 1200

QY 1545 GGCTTTGCTGTACGCGCTTGCCATGTGCAGATGAGTTTCAGGACGGCAGCGGTGGAAGGC 1604
Db 1201 GGCTTTGCTGTACGCGCTTGCCATGTGCAGATGAGTTTCAGGACGGCAGCGGTGGAAGGC 1260
QY 1605 CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCACAGACAGATGAGTCA 1664
Db 1261 CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCACAGACAGATGAGTCA 1320
QY 1665 ACCCTCATGACCATAGCCTATGTGCTGCGCATCTGGCCCTCTTTCATGCTGCCACTC 1724
Db 1321 ACCCTCATGACCATAGCCTATGTGCTGCGCATCTGGCCCTCTTTCATGCTGCCACTC 1380
QY 1725 TGCTCATGTGTGTACGTGGCGCTGCCCTCCGCTGCGCTGCGCAGCAGCATGATGACTTT 1784
Db 1381 TGCTCATGTGTGTACGTGGCGCTGCCCTCCGCTGCGCTGCGCAGCAGCATGATGACTTT 1440
QY 1785 GCTGATGACATCTCCCTGCTGAAGTGAAGGAGGCCCCATGGCAGAAATAGAGATTCCCT 1844
Db 1441 GCTGATGACATCTCCCTGCTGAAGTGAAGGAGGCCCCATGGCAGAAATAGAGATTCCCT 1500
QY 1845 GGACCACACCTCCGCTGGTTTCACTTTGGTCAAGTAGGAGACACAGATGCCACCTGTGCG 1904
Db 1501 GGACCACACCTCCGCTGGTTTCACTTTGGTCAAGTAGGAGACACAGATGCCACCTGTGCG 1560
QY 1905 CAGAGCACCTCAGGACCTCCGCCACCCACCAATGCTCTGCTTGTATGGAGAAAGAAA 1964
Db 1561 CAGAGCACCTCAGGACCTCCGCCACCCACCAATGCTCTGCTTGTATGGAGAAAGAAA 1620
QY 1965 GGCTGGCAAGTGGTTCCAGGACTGTACCTGTAGGAAACAGAAAAGAGAAAGAG 2024
Db 1621 GGCTGGCAAGTGGTTCCAGGACTGTACCTGTAGGAAACAGAAAAGAGAAAGAG 1680
QY 2025 CACTCTGCTGCGGGAATACTCTTGGTCACTCAAAATTTAAGTCGGGAAATTTCTGCTCT 2084
Db 1681 CACTCTGCTGCGGGAATACTCTTGGTCACTCAAAATTTAAGTCGGGAAATTTCTGCTCT 1740
QY 2085 TGAACCTTCAAGCTTGAACCTTTGTCCACCATTTCCCTTTAAATTTCTCAACCCAAAGTATT 2144
Db 1741 TGAACCTTCAAGCTTGAACCTTTGTCCACCATTTCTTTAAATTTCTCAACCCAAAGTATT 1800
QY 2145 CTCTCTTTCTTAGTTTCAGAACTACTGGCATCACAGCAGGTTACCTTGGGCTGTGCTCC 2204
Db 1801 CTCTCTTTCTTAGTTTCAGAACTACTGGCATCACAGCAGGTTACCTTGGGCTGTGCTCC 1860
QY 2205 TGTGGTACCTTGGCAGAGAAGACCAAGCTTTGTTTCCCTGCTGGCCAAAGTCAAGTACGA 2264
Db 1861 TGTGGTACCTTGGCAGAGAAGACCAAGCTTTGTTTCCCTGCTGGCCAAAGTCAAGTACGA 1920
QY 2265 GAGATGCACAGTTTGTCTATTGCTTTAGAGACAGGAGCTGTATTAACAAGCCCTAACATT 2324
Db 1921 GAGATGCACAGTTTGTCTATTGCTTTAGAGACAGGAGCTGTATTAACAAGCCCTAACATT 1980
QY 2325 GGTGCAAGATTGCTCTTTGAATT 2348
Db 1981 GGTGCAAGATTGCTCTTTGAATT 2004

RESULT 14

AAF28101

ID AAF28101 standard; DNA; 3252 BP.

XX AAF28101;

XX AC

XX XX

DT 02-APR-2001 (first entry)

XX Memapsin 2 DNA.

DE Memapsin 2.

XX Memapsin 2; catalyst; Alzheimer's; ds.

XX Homo sapiens.

XX OS

XX WO200100663-A2.

PN

XX 04-JAN-2001.
XX 27-JUN-2000; 2000WO-US17661.
XX 28-JUN-1999; 99US-0141363.
PR 30-NOV-1999; 99US-0168060.
PR 25-JAN-2000; 2000US-017836.
PR 27-JAN-2000; 2000US-0178368.
PR 08-JUN-2000; 2000US-0210292.
XX {OKLA-} OKLAHOMA MEDICAL RES FOUND.
PA Tang JJN, Lin X, Koelsch G;
XX WPI; 2001-102885/11.
XX Purified recombinant catalytically active memapsin 2, used to screen
PT inhibitors of it, which are used to treat and prevent Alzheimer's
PT disease -
XX Example 1; Page 71-72; 86pp; English.
XX The present invention relates to a purified recombinant
CC catalytically active memapsin 2. The invention may be used for
CC isolating inhibitors which are used to treat or prevent
CC Alzheimer's disease. The invention may also be used to screen
CC for individuals more genetically prone to develop Alzheimer's
CC disease.
XX Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;
SQ
Query Match 85.3%; Score 2004; DB 22; Length 3252;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 345 GCGGGAGTGTGCTGCGCCACGCGGACCCAGCAGCGGCATCGGGCTGCCCTGCGCAGCGGC 404
DB 1 GCGGGAGTGTGCTGCGCCACGCGGACCCAGCAGCGGCATCGGGCTGCCCTGCGCAGCGGC 60
QY 405 CTGGGGGGCGCCCTTGGGGCTGCGGCTGCGCGGGAGAGCCGACGAGCCGCGAGGAG 464
DB 61 CTGGGGGGCGCCCTTGGGGCTGCGGCTGCGCGGGAGAGCCGACGAGCCGCGAGGAG 120
QY 465 CCCGCCGAGGGGACGCTTGTGGAGATGGTGACACCTGAGGGGCAAGTCGGGGCAG 524
DB 121 CCCGCCGAGGGGACGCTTGTGGAGATGGTGACACCTGAGGGGCAAGTCGGGGCAG 180
QY 525 GGCTACTAGTGGAGATGACGCTGGGGGAGCCCGCCGAGAGCGCTCAACATCCTGGTGGAT 584
DB 181 GGCTACTAGTGGAGATGACGCTGGGGGAGCCCGCCGAGAGCGCTCAACATCCTGGTGGAT 240
QY 585 ACAGGCAGCAGTAACTTTGAGTGGGTGCTGCGCCCGCCCGCCCGCTTCTTGCATCGCTACTAC 644
DB 241 ACAGGCAGCAGTAACTTTGAGTGGGTGCTGCGCCCGCCCGCCCGCTTCTTGCATCGCTACTAC 300
QY 645 CAGAGGCAGCTGTCCAGCACATACCGGACCTCCGGAAGGTGTGTATGTGCCCTACACC 704
DB 301 CAGAGGCAGCTGTCCAGCACATACCGGACCTCCGGAAGGTGTGTATGTGCCCTACACC 360
QY 705 CAGGGCAAGTGGGAAGGGAGCTGGGACCGACCTGTGTAAGCATCCCGCCAGCCCCAAC 764
DB 361 CAGGGCAAGTGGGAAGGGAGCTGGGACCGACCTGTGTAAGCATCCCGCCAGCCCCAAC 420
QY 765 GTCAGTGTGGTGGCAACATTTGCGCATCACTGAATCAGACAAAGTTCTTCATCAAGCGC 824
DB 421 GTCAGTGTGGTGGCAACATTTGCGCATCACTGAATCAGACAAAGTTCTTCATCAAGCGC 480
QY 825 TCCAACTGGGAAGGCATCCTGGGGCTGGCCCTATGCTGAGATTGGCAGGCGCTGACGACTCC 884
DB 481 TCCAACTGGGAAGGCATCCTGGGGCTGGCCCTATGCTGAGATTGGCAGGCGCTGACGACTCC 540
QY 885 CTGAGGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACCGTTCCCAACCTCTTCTCCCTG 944

DB 541 CTGGAGCCTTTCTTTGACTCTCTGTTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600
QY 945 CAGCTTTGTGGTGTGGTTCCTCCCTCAACACGAGTCTGAAGTGTGGCTCTGTGGAGGG 1004
DB 601 CAGCTTTGTGGTGTGGTTCCTCCCTCAACACGAGTCTGAAGTGTGGCTCTGTGGAGGG 660
QY 1005 AGCATGATCATTGGAGGTATCGAGCACTCGCTGTACAGCAGCTCTCTGGTATACACCC 1064
DB 661 AGCATGATCATTGGAGGTATCGAGCACTCGCTGTACAGCAGCTCTCTGGTATACACCC 720
QY 1065 ATCCGCGGGAGTGGTATTATGAGGTGATCATTTGCGGGTGGAGATCAATGGACAGAG 1124
DB 721 ATCCGCGGGAGTGGTATTATGAGGTGATCATTTGCGGGTGGAGATCAATGGACAGAG 780
QY 1125 CTGAAAATGGACTCAAGGAGTACAACATATGACAAAGACATTTGGACAGTGGCACACC 1184
DB 781 CTGAAAATGGACTCAAGGAGTACAACATATGACAAAGACATTTGGGACAGTGGCACACC 840
QY 1185 AACCTTCGTTTGGCCCAAGAAAGTGTGTAAGCTCAGTCAAAATCCATCAAGCGACCTCC 1244
DB 841 AACCTTCGTTTGGCCCAAGAAAGTGTGTAAGCTCAGTCAAAATCCATCAAGCGACCTCC 900
QY 1245 TCCACGAGAGAGTTCCCTGATGGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 1304
DB 901 TCCACGAGAGAGTTCCCTGATGGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960
QY 1305 GGCACACCCCTTGGAAACATTTCCAGTATCTACCTCTACCTTAATGGGTGAGTTACC 1364
DB 961 GGCACACCCCTTGGAAACATTTCCAGTATCTACCTCTACCTTAATGGGTGAGTTACC 1020
QY 1365 AACCACTTCCTCCGATCACCATCTTCCGACGAAATACCTGCGGCCAGTGGAGATGTG 1424
DB 1021 AACCACTTCCTCCGATCACCATCTTCCGACGAAATACCTGCGGCCAGTGGAGATGTG 1080
QY 1425 GCCACGTCCTCCCAAGAGCAGCTGTTTACAAGTTTCCCATCTCACAGTCAATCCACGGCAGCTGT 1484
DB 1081 GCCACGTCCTCCCAAGAGCAGCTGTTTACAAGTTTCCCATCTCACAGTCAATCCACGGCAGCTGT 1140
QY 1485 ATGGAGCTGTATCATGGAGGGCTTCTACGTTGCTTTGATCGGGCCCGAAACGAAT 1544
DB 1141 ATGGAGCTGTATCATGGAGGGCTTCTACGTTGCTTTGATCGGGCCCGAAACGAAT 1200
QY 1545 GGCCTTGTCTGTCAGCGCTTGCATGTGCACGATGAGTTCAGGACGGCAGCGTGGAAAGC 1604
DB 1201 GGCCTTGTCTGTCAGCGCTTGCATGTGCACGATGAGTTCAGGACGGCAGCGTGGAAAGC 1260
QY 1605 CCTTTTGTACCTTGGACATGGAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCA 1664
DB 1261 CCTTTTGTACCTTGGACATGGAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCA 1320
QY 1665 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTCGCCCTCTTCCATGCTGCCACTC 1724
DB 1321 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTCGCCCTCTTCCATGCTGCCACTC 1380
QY 1725 TGCCTCATGCTGTGTCAGTGGCGCTGCTCCGCTGCCCTGCCCGCAGCAGCATGATGACTTT 1784
DB 1381 TGCCTCATGCTGTGTCAGTGGCGCTGCTCCGCTGCCCTGCCCGCAGCAGCATGATGACTTT 1440
QY 1785 GCTGATGACATCTCCTGCTGAAAGTGGAGGGCCCATGGGAGAGATAGAGATTCCCT 1844
DB 1441 GCTGATGACATCTCCTGCTGAAAGTGGAGGGCCCATGGGAGAGATAGAGATTCCCT 1500
QY 1845 GGACACACCTCCCTGGTGTGCTTGGTTCACAACTAGGAGACACAGATGGCACCTGTGGC 1904
DB 1501 GGACACACCTCCCTGGTGTGCTTGGTTCACAACTAGGAGACACAGATGGCACCTGTGGC 1560
QY 1905 CAGAGCAGCTCAGGACCCCTCCCGCCACCAATGCCCTCTGCTTGTGATGGAGAGAGAAA 1964
DB 1561 CAGAGCAGCTCAGGACCCCTCCCGCCACCAATGCCCTCTGCTTGTGATGGAGAGAGAAA 1620
QY 1965 GGCTGGCAAGTGGGTTCAGGAGCTGTACCTGTAGGAAACAGAGAGAGAGAGAG 2024

Db 1621 GCCTGGCAAGTGGTTCAGGAGCTGTACCTCTAGGAACACAGAAAAGAGAAAGAG 1680
QY 2025 CACTCTGCTGGCGGAATACTCTTGGTCACCTCAAAATTTAAGTCGGGAAATTCCTGCT 2084
Db 1681 CACTCTGCTGGCGGAATACTCTTGGTCACCTCAAAATTTAAGTCGGGAAATTCCTGCT 1740
QY 2085 TGAACCTTCAGCCCGAATCTTGGTCACCATTCCTTTAAATTCGAAACCCAAAGTATT 2144
Db 1741 TGAACCTTCAGCCCGAATCTTGGTCACCATTCCTTTAAATTCGAAACCCAAAGTATT 1800
QY 2145 CTCTCTTTCTTAGTTTCAGAACTACTGGCATCACAGCAGTTACCTTGGCGTGTGCC 2204
Db 1801 CTCTCTTTCTTAGTTTCAGAACTACTGGCATCACAGCAGTTACCTTGGCGTGTGCC 1860
QY 2205 TGTGTTACCTTCGGCAGAGAGACCAAGCTTGTTCCTCTGCTGGCCAAAGTCAGTAGGA 2264
Db 1861 TGTGTTACCTTCGGCAGAGAGACCAAGCTTGTTCCTCTGCTGGCCAAAGTCAGTAGGA 1920
QY 2265 GAGGATGCACAGTTGCTATTGCTTTAGAGCAGGAGCTGTATAACAGCCCTAACATT 2324
Db 1921 GAGGATGCACAGTTGCTATTGCTTTAGAGCAGGAGCTGTATAACAGCCCTAACATT 1980
QY 2325 GGTCAAAGATTGCTCTTGAATT 2348
Db 1981 GGTCAAAGATTGCTCTTGAATT 2004

RESULT 15

ABR88641

ID ABR88641 standard; cDNA; 3252 BP.

AC ABR88641;

XX

DT 07-OCT-2002 (first entry)

DE cDNA encoding human memapsin 2.

XX

KW Human; memapsin 2; beta secretase; aspartic protease; APP;
KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;
KW neuroprotective; nontropic; expressed sequence tag; EST; gene; ss.
XX

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1467

FT /*tag= a

FT /partial

FT /product= "Memapsin 2"

FT /note= "This sequence lacks a start codon"

XX

PN US2002049303-A1.

XX

PD 25-APR-2002.

XX

PF 28-FEB-2001; 2001US-0796264.

XX

PR 28-JUN-1999; 99US-141363P.

XX

PR 30-NOV-1999; 99US-168060P.

XX

PR 25-JAN-2000; 2000US-177836P.

XX

PR 27-JAN-2000; 2000US-178368P.

XX

PR 27-JUN-2000; 2000US-0604608.

XX

PA (TANG/) TANG J J N.

XX

PA (LINK/) LIN X.

XX

PA (KOEL/) KOELSCH G.

XX

PA (HONG/) HONG L.

XX

PI Tang JJN, Lin X, Koelsch G, Hong L;

XX

DR WPI; 2002-507280/54.

XX

DR P-PSDB; AAU99488.

XX

PT New recombinant catalytically active memapsin 2, useful to screen for

PT inhibitors of memapsin 2 which can be used to prevent and treat
PT Alzheimer's disease -
XX
PS Example 1; Page 20-21; 44pp; English.
XX
CC The present invention relates to methods for the production of
CC purified, recombinant catalytically active, memapsin 2 (beta
CC secretase). Memapsin 2, a member of the aspartic protease family,
CC cleaves beta-amyloid precursor protein (APP) found in amyloid plaques.
CC The recombinant memapsin 2 is useful for identifying inhibitors of
CC memapsin 2 in the design of drugs for the treatment and/or prevention
CC of Alzheimer's disease. The recombinant memapsin 2 can be used to
CC immunise against Alzheimer's disease. The present sequence encodes
CC human memapsin 2.
XX
SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

Query Match 85.3%; Score 2004; DB 24; Length 3252;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 GCGGAGTGTCTGCCACGCGCACCCAGCAGGATCCGGCTGCCCTCGGACGCGC 404
Db 1 GCGGAGTGTCTGCCACGCGCACCCAGCAGGATCCGGCTGCCCTCGGACGCGC 60
QY 405 CTGGGGGCGCCCCCTGGGCTGCGGCTGCCCGGAGACCGACGAGCCCCGAGGAG 464
Db 61 CTGGGGGCGCCCCCTGGGCTGCGGCTGCCCGGAGACCGACGAGCCCCGAGGAG 120
QY 465 CCGGCGGAGGGGCGAGCTTTCTGGAGATGGTGGACAACTGAGGGGCAAGTCGGGGGAG 524
Db 121 CCGGCGGAGGGGCGAGCTTTCTGGAGATGGTGGACAACTGAGGGGCAAGTCGGGGGAG 180
QY 525 GGCTACTACGTGGAGATGACCGTGGCAGCCCCCGCAGACGCTCAACATCTGCTGGAT 584
Db 181 GGCTACTACGTGGAGATGACCGTGGCAGCCCCCGCAGACGCTCAACATCTGCTGGAT 240
QY 585 ACAGGACGAGTAACCTTTTGCAGTGGTGTGCCCGCCACCCCTTCCTGCATCGCTACTAC 644
Db 241 ACAGGACGAGTAACCTTTTGCAGTGGTGTGCCCGCCACCCCTTCCTGCATCGCTACTAC 300
QY 645 CAGAGGAGCTGTCCAGCACATACCGGGAGCTCCGGAAGGTGTGTATGTCCTACAC 704
Db 301 CAGAGGAGCTGTCCAGCACATACCGGGAGCTCCGGAAGGTGTGTATGTCCTACAC 360
QY 705 CAGGCAAGTGGGAAGGGAGCTGGCAGCGACCTGTGAAGCATCCCGCCATGGCCCCAAC 764
Db 361 CAGGCAAGTGGGAAGGGAGCTGGCAGCGACCTGTGAAGCATCCCGCCATGGCCCCAAC 420
QY 765 GTCAGTGTGCTGCCAACATTTGCTGCCATCAGTGAATCAGACAAAGTTCTTCATCAACGCG 824
Db 421 GTCAGTGTGCTGCCAACATTTGCTGCCATCAGTGAATCAGACAAAGTTCTTCATCAACGCG 480
QY 825 TCCAACTGGGAAGGAGCTCTGGGGCTGGGCTATGCTGAGATTTGCCAGGCTGAGACATCC 884
Db 481 TCCAACTGGGAAGGAGCTCTGGGGCTGGGCTATGCTGAGATTTGCCAGGCTGAGACATCC 540
QY 885 CTGGAGCTTTCTTTGACTCTCTGTGTAAGAGCAGACCCACGCTTCCCAACCTCTCTTCCCTG 944
Db 541 CTGGAGCTTTCTTTGACTCTCTGTGTAAGAGCAGACCCACGCTTCCCAACCTCTCTTCCCTG 600
QY 945 CAGCTTTGTGCTGGCTTCCCGCTCAACACGATCTCAAGTGTGCTGGCTCTGTGGAGGG 1004
Db 601 CAGCTTTGTGCTGGCTTCCCGCTCAACACGATCTCAAGTGTGCTGGCTCTGTGGAGGG 660
QY 1005 AGCATGATCATTGGAGGTATCGACCATCTGCTGTACACAGGAGCTCTCTGGTATACACCC 1064
Db 661 AGCATGATCATTGGAGGTATCGACCATCTGCTGTACACAGGAGCTCTCTGGTATACACCC 720
QY 1065 ATCCGCGGGAGTGTATTATGAGGTGATCATTTGTCGGGTGGAGATCAATGGACAGGAT 1124
Db 721 ATCCGCGGGAGTGTATTATGAGGTGATCATTTGTCGGGTGGAGATCAATGGACAGGAT 780

QY 1125 CTGAAATGACTGCAAGGAGTACAACTATGACAAGAGCATTTGGACAGTGGCAACC 1184
DB 781 CTGAAATGACTGCAAGGAGTACAACTATGACAAGAGCATTTGGACAGTGGCAACC 840
QY 1185 AACCTTCGTTGGCCCAAGAAAGTGTGAGCTGCAAGTCAAAATCCATCAAGGAGGCTCC 1244
DB 841 AACCTTCGTTGGCCCAAGAAAGTGTGAGCTGCAAGTCAAAATCCATCAAGGAGGCTCC 900
QY 1245 TCCACGAGGAAGTTCCTTGATGGTTTCTGCTAGGAGAGCAGCTGGTGTCTGCGCAAGCA 1304
DB 901 TCCACGAGGAAGTTCCTTGATGGTTTCTGCTAGGAGAGCAGCTGGTGTCTGCGCAAGCA 960
QY 1305 GGCACACCCCTTGGAAACATTTTCCAGTCATCTACTCTACCTAATGGGTGAGGTTACC 1364
DB 961 GGCACACCCCTTGGAAACATTTTCCAGTCATCTACTCTACCTAATGGGTGAGGTTACC 1020
QY 1365 AACCACTCCTTCGGCATCACCATCCTTCGCGAGCAATACCTGCGGCCAGTGGGAAGATGG 1424
DB 1021 AACCACTCCTTCGGCATCACCATCCTTCGCGAGCAATACCTGCGGCCAGTGGGAAGATGG 1080
QY 1425 GCCACGTCCCAAGCACACTGTTACAAAGTTTGCCATCTCACAGTCATCCACGGGCAGTGT 1484
DB 1081 GCCACGTCCCAAGCACACTGTTACAAAGTTTGCCATCTCACAGTCATCCACGGGCAGTGT 1140
QY 1485 ATGGAGCTGTTATCATGGAGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1544
DB 1141 ATGGAGCTGTTATCATGGAGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1200
QY 1545 GGCCTTGTGTCAGCGCTTGCATGTGCAGAGTGTTCAGGACGGCAGCGGTGGGAAGC 1604
DB 1201 GGCCTTGTGTCAGCGCTTGCATGTGCAGAGTGTTCAGGACGGCAGCGGTGGGAAGC 1260
QY 1605 CTTTTTGTCACTTGGACATGGAAGACTTGGCTACAACATTCACAGACAGATGACTCA 1664
DB 1261 CTTTTTGTCACTTGGACATGGAAGACTTGGCTACAACATTCACAGACAGATGACTCA 1320
QY 1665 ACCCTCATGACCATAGCCTATGTATGGCTGCCATCTGCGCCCTCTTCAATGCTGCCACTC 1724
DB 1321 ACCCTCATGACCATAGCCTATGTATGGCTGCCATCTGCGCCCTCTTCAATGCTGCCACTC 1380
QY 1725 TGGCTCATGGTGTGTCAGTGGCGCTGCCCTCCGCTGCCCTGCGCCAGCAGCATGACTTT 1784
DB 1381 TGGCTCATGGTGTGTCAGTGGCGCTGCCCTCCGCTGCCCTGCGCCAGCAGCATGACTTT 1440
QY 1785 GCTGATGACATCTCCCTGCTGGAAGTGGAGGCCCCATGGGCAAGATAGAGATTCCCT 1844
DB 1441 GCTGATGACATCTCCCTGCTGGAAGTGGAGGCCCCATGGGCAAGATAGAGATTCCCT 1500
QY 1845 GGACACACCTCCGTTGGTTCACTTTGGTCAAAAGTAGGAGACACAGATGCCACCTGTGC 1904
DB 1501 GGACACACCTCCGTTGGTTCACTTTGGTCAAAAGTAGGAGACACAGATGCCACCTGTGC 1560
QY 1905 CAGAGCACCTCAGGACCTCCGCCACCAATGGCTCTGCTGCTGATGGAGAAGGAAA 1964
DB 1561 CAGAGCACCTCAGGACCTCCGCCACCAATGGCTCTGCTGCTGATGGAGAAGGAAA 1620
QY 1965 GGCCTGCAAGGTGGGTTCCAGGAGCTGTACCTGTAGSAAACAGAAAGAGAAAGAG 2024
DB 1621 GGCCTGCAAGGTGGGTTCCAGGAGCTGTACCTGTAGSAAACAGAAAGAGAAAGAG 1680
QY 2025 CACTCTGCTGGCGGGAATACTCTTGTGTCACCTCAAAATTTAAAGTCGGGAAATCTGCTGCT 2084
DB 1681 CACTCTGCTGGCGGGAATACTCTTGTGTCACCTCAAAATTTAAAGTCGGGAAATCTGCTGCT 1740
QY 2085 TGAACCTTCAGCCCTGAACCTTTGTCCACCAATTCCTTTAAATTTCCAAACCCAAAGTATT 2144
DB 1741 TGAACCTTCAGCCCTGAACCTTTGTCCACCAATTCCTTTAAATTTCCAAACCCAAAGTATT 1800
QY 2145 CTTCTTTTCTTAGTTTTCAGAAAGTACTGGCATCACAGCAGGTTACCTTGGCGTGTGCC 2204
DB 1801 CTTCTTTTCTTAGTTTTCAGAAAGTACTGGCATCACAGCAGGTTACCTTGGCGTGTGCC 1860
QY 2205 TGTGGTACCCTTGGCAGAGAAGAGAACCAAGCTTTGTTCCCTGTGCTGGCCAAAGTCAGTAGGA 2264

DB 1861 TGTGGTACCCTGCGAGAGAAGAGACCAAGCTTGTTCCTTGTGGCCAAAGTCAGTAGGA 1920
QY 2265 GAGGATGCACAGTTTGTCTATTTGCTTTAGAGACAGGAGCTGTATAACAAGCCTTAACATT 2324
DB 1921 GAGGATGCACAGTTTGTCTATTTGCTTTAGAGACAGGAGCTGTATAACAAGCCTTAACATT 1980
QY 2325 GGTGCAAAAGATTGCCCTCTTGAATT 2348
DB 1981 GGTGCAAAAGATTGCCCTCTTGAATT 2004

Search completed: March 1, 2003, 22:17:53
Job time : 353.5 secs

Qy	606	GTGGGTGCTGCCCCACACCCCTTCCTGCAATCGCTACTACGAGGCGAGCTGTCCAGCACA	665
Db	301	GTGGGTGCTGCCCCACACCCCTTCCTGCAATCGCTACTACGAGGCGAGCTGTCCAGCACA	360
Qy	666	TACCGGGACCTCCGGAAGGCTGTATGTGCCCTACACCCAGGCGAAGTGGGAAGGGGAG	725
Db	361	TACCGGGACCTCCGGAAGGCTGTATGTGCCCTACACCCAGGCGAAGTGGGAAGGGGAG	420
Qy	726	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGCGTGCGCAACATT	785
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGCGTGCGCAACATT	480
Qy	786	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTTG	845
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTTG	540
Qy	846	GGCTGGCCCTATGCTGTAGATTGCCAGGCTGAGGACTCCTCGGAGCCTTCTTTTGACTCT	905
Db	541	GGCTGGCCCTATGCTGTAGATTGCCAGGCTGAGGACTCCTCGGAGCCTTCTTTTGACTCT	600
Qy	906	CTGGTAAAGCAGACCCACGTTCCCAACCTTCTCCTCGCAGCTTTGGTGTGCTGCTTC	965
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTTCTCCTCGCAGCTTTGGTGTGCTGCTTC	660
Qy	966	CCCCTCACCAAGCTGTGAAGTGTGGCCTCTGTCTGGAGGAGCATGATCATTTGGAGGTATC	1025
Db	661	CCCCTCACCAAGCTGTGAAGTGTGGCCTCTGTCTGGAGGAGCATGATCATTTGGAGGTATC	720
Qy	1026	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	1085
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	1086	GAGGTGATCATTTGCGGGTGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	1145
Db	781	GAGGTGATCATTTGCGGGTGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	1146	TACAACATATGACAAGAGCATTTGGACAGTGGCACCAACCTTCGTTTGGCCCAAGAAA	1205
Db	841	TACAACATATGACAAGAGCATTTGGACAGTGGCACCAACCTTCGTTTGGCCCAAGAAA	900
Qy	1206	GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGCAGCCTCTCCACGGAGAAAGTTCCCTGAT	1265
Db	901	GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGCAGCCTCTCCACGGAGAAAGTTCCCTGAT	960
Qy	1266	GGTTTCTGGCTAGGAGAGCAGCTGGTGTCTGGCAAGCAGGCACACCCCTTGGAAACATT	1325
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTCTGGCAAGCAGGCACACCCCTTGGAAACATT	1020
Qy	1326	TTCCCAAGTCAATCTACTCTACCTAATGGGTGAGGTTTACCAACAGCTCCTTCCGCATCACC	1385
Db	1021	TTCCCAAGTCAATCTACTCTACCTAATGGGTGAGGTTTACCAACAGCTCCTTCCGCATCACC	1080
Qy	1386	ATCCTTCGCGACCAATACCTCGGGCCAGTGGAAAGATGTGGCCACAGTCCCAAGAGGACTGT	1445
Db	1081	ATCCTTCGCGACCAATACCTCGGGCCAGTGGAAAGATGTGGCCACAGTCCCAAGAGGACTGT	1140
Qy	1446	TACAAGTTTGGCATCTCAGATCATCCAGGGCAGCTGTTATGGAGCTGTTATCATGGAG	1505
Db	1141	TACAAGTTTGGCATCTCAGATCATCCAGGGCAGCTGTTATGGAGCTGTTATCATGGAG	1200
Qy	1506	GGCTTCTACGTTTGTCTTGTATCGGGCCGAAAACGAATTTGGCTTGTCTGTCAAGGCTTGC	1565
Db	1201	GGCTTCTACGTTTGTCTTGTATCGGGCCGAAAACGAATTTGGCTTGTCTGTCAAGGCTTGC	1260
Qy	1566	CATGTGCACGATGAGTTCAGGACGCGGTGGAAAGGCCCTTTTGTCACTTTGGACATG	1625
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Qy	1626	GAAGACTGTGGCTACAAACATTCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT	1685
Db	1321	GAAGACTGTGGCTACAAACATTCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT	1380

RESULT 2

RESULTS 2
IIS-09-548-367D-303-09-348-307D-3
: Sequence 3. Application US/095483367D: sequence 3, Appl. No. 644,069.8
: Patent No. 644,069.8

: FACILE NO. 0440698
 : GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/2088

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 6

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF

; SOFTWARE: Pat

; SEQ ID NO 3

; ORGANISM: Homo sapiens									
Us-09-548-367D-3									
Query Match 86.9% Score 2041.4; DB 4; Length 2070;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2042; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	306	ATGGCCCAAGCCCTGCCCTGCTCCTGCTGTGGATGGCGGGGAGTGTCTGCTGCCAC	365						
Db	1	ATGGCCCAAGCCCTGCCCTGCTCCTGCTGTGGATGGCGGGAGTGTCTGCCTGCCAC	60						
Qy	366	GGCACCCAGCAGGATCCGCTGCTGCTGCGAGCGCTGGGGGGGCCCCCTGGGG	425						
Db	61	GGCACCCAGCAGGATCCGCTGCTGCTGCGAGCGCTGGGGGGGCCCCCTGGGG	120						
Qy	426	CTGGGCTGCCCGGGAGACGACGACGAGCCGAGGAGCGCGCGGAGGCGAGCTTT	485						
Db	121	CTGGGCTGCCCGGGAGACGACGAGGCGCGAGGAGCGCGCGGAGGCGAGCTTT	180						
Qy	486	GTGGAGATGTGGACAACCTTGAAGGGCAAGTCGGGGCAGGGCTACTAGTGGAGATGACC	545						
Db	181	GTGGAGATGTGGACAACCTTGAAGGGCAAGTCGGGGCAGGGCTACTAGTGGAGATGACC	240						
Qy	546	GTGGGACGCCCCCGCAGACGCTCAACATCTCTGTGGTGGATACAGGACGAGTAACCTTGA	605						
Db	241	GTGGGACGCCCCCGCAGACGCTCAACATCTCTGTGGTGGATACAGGACGAGTAACCTTGA	300						
Qy	606	GTGGGTGCTGCCCGCCACCCCTTCTGTCATCGCTACTACGAGGCGAGCTGTCCAGCACA	665						
Db	301	GTGGGTGCTGCCCGCCACCCCTTCTGTCATCGCTACTACGAGGCGAGCTGTCCAGCACA	360						
Qy	666	TACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	725						
Db	361	TACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420						
Qy	726	CTGGGACCGACTGGTGAAGCATCCCCCATGGCCCCAAGCTGCTGCTGCCAACATTT	785						
Db	421	CTGGGACCGACTGGTGAAGCATCCCCCATGGCCCCAAGCTGCTGCTGCCAACATTT	480						
Qy	786	GCTGCATCACTGAATCAGACAAGTTCTTCAACAGGCTCCAAGTGGGAAGGCAATCTGT	845						
Db	481	GCTGCATCACTGAATCAGACAAGTTCTTCAACAGGCTCCAAGTGGGAAGGCAATCTGT	540						
Qy	846	GGGCTGGCTATGTGAGATTGCCAGGCTGACGACTCCCTGGAGCCCTTTCTTGACTCT	905						
Db	541	GGGCTGGCTATGTGAGATTGCCAGGCTGACGACTCCCTGGAGCCCTTTCTTGACTCT	600						
Qy	906	CTGGTAAAGCAGACCCAGTTCCCAACCTCTTCTCCCTGCGAGCTTTGTGGCTGGCTTC	965						
Db	601	CTGGTAAAGCAGACCCAGTTCCCAACCTCTTCTCCCTGCGAGCTTTGTGGCTGGCTTC	660						
Qy	966	CCCCTCAACCACTGTGAAGTCTGGCCCTCTGCGAGGAGCATGATCATTTGGAGGTATC	1025						
Db	661	CCCCTCAACCACTGTGAAGTCTGGCCCTCTGCGAGGAGCATGATCATTTGGAGGTATC	720						
Qy	1026	GACCACCTCGCTGTACACAGGAGTCTCTGGTATACACCATCCCGGGGAGTGGTATTAT	1085						
Db	721	GACCACCTCGCTGTACACAGGAGTCTCTGGTATACACCATCCCGGGGAGTGGTATTAT	780						
Qy	1086	GAGTGATCATTTGTGGGGTGGAGATCAATGACAGGATCTGAAATGGACTGCAAGGAG	1145						
Db	781	GAGTGATCATTTGTGGGGTGGAGATCAATGACAGGATCTGAAATGGACTGCAAGGAG	840						
Qy	1146	TACAACTATGACAGAGCATTTGTGACAGTGGCACCCACCAACCTTCGTTGCCCAAGAAA	1205						
Db	841	TACAACTATGACAGAGCATTTGTGACAGTGGCACCCACCAACCTTCGTTGCCCAAGAAA	900						
Qy	1206	GTGTTTGAAGCTGAGTCAAAATCCATCAAGGAGGCTCTCCACGAGGAAGTTCCCTGAT	1265						
Db	901	GTGTTTGAAGCTGAGTCAAAATCCATCAAGGAGGCTCTCCACGAGGAAGTTCCCTGAT	960						
Qy	1266	GGTTTCTGGCTAGGAGACGCTGGTGTGCTGGCAAGCAGCACACCCTTTGGAACATTT	1325						

RESULT 3

US-09-009-191-1

: Sequence 1, Application US/09009191

: Patent No. 6319689

: GENERAL INFORMATION:

: APPLICANT: POWELL, DAVID

: APPLICANT: CHAPMAN, CONRAD

: APPLICANT: MURPHY, KAY

: APPLICANT: SMITH, TRUDI

: TITLE OF INVENTION: ASP2

: NUMBER OF SEQUENCES: 6

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: RATNER & PRESTIA

: STREET: P.O. BOX 980

: CITY: VALLEY FORGE

: STATE: PA

: COUNTRY: USA

: ZIP: 19482

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Diskette

: COMPUTER: IBM Compatible

: OPERATING SYSTEM: DOS

: SOFTWARE: FASTSEQ for Windows Version 2.0

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/009,191

: FILING DATE: 20-JAN-1998

: CLASSIFICATION:

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: UK 9701684.4

: FILING DATE: 28-JAN-1997

: ATTORNEY/AGENT INFORMATION:

: NAME: PRESTIA, PAUL F

: REGISTRATION NUMBER: 23,031

: REFERENCE/DOCKET NUMBER: GH-70368

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 610-407-0700

: TELEFAX: 610-407-0701

: TELEX: 846169

: INFORMATION FOR SEQ ID NO: 1:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 2541 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA

US-09-009-191-1

Query Match 86.2%; Score 2024; DB 4; Length 2541;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2038; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY	306	ATGCCCAAGCCCTCCCTGGCTCTGCTGTGATGGCGGGGAGTGCTGCTGCCAC	365
Db	1	ATGCCCAAGCCCTCCCTGGCTCTGCTGTGATGGCGGGGAGTGCTGCTGCCAC	60
QY	366	GGCACCCAGCAGCGGATCGGCTGCCCTGCGCAGCGGCTGGGGGGCGCCCTGGGG	425
Db	61	GGCACCCAGCAGCGGATCGGCTGCCCTGCGCAGCGGCTGGGGGGCGCCCTGGGG	120
QY	426	CTGGCGCTGCCCGGGAGACCACGAAGACCCGAGGAGCCCGCGGAGGGGAGCTTT	485
Db	121	CTGGCGCTGCCCGGGAGACCACGAAGACCCGAGGAGCCCGCGGAGGGGAGCTTT	180
QY	486	GTGAGATGGTGACAACCTGAGGGCAAGTCGGGGCAGGCTACTAGTGGAGATGACC	545
Db	181	GTGAGATGGTGACAACCTGAGGGCAAGTCGGGGCAGGCTACTAGTGGAGATGACC	240
QY	546	GTGGCAGCCCCCGGAGACGCTCAACATCCTGGTGATACAGGACGAGTAACCTTGA	605
Db	241	GTGGCAGCCCCCGGAGACGCTCAACATCCTGGTGATACAGGACGAGTAACCTTGA	300

QY	606	GTGGTGCTGCCCCCACCACCCCTTCTGTCATCGTCTACTACAGAGCAGCTGTCCAGCACA	665
Db	301	GTGGTGCTGCCCCCACCACCCCTTCTGTCATCGTCTACTACAGAGCAGCTGTCCAGCACA	360
QY	666	TACCGGAGCTCCGGAAGGCTGTATGTGCCCTACACCCAGGCAAGTGGAAAGGGAG	725
Db	361	TACCGGAGCTCCGGAAGGCTGTATGTAGCCCTTACACCCAGGCAAGTGGAAAGGGAG	420
QY	726	CTGGSCACCGACCTGTGAAGCATCCCCCATGGCCCCCAAGGTCACCTGTGCGTCCCAACATT	785
Db	421	CTGGSCACCGACCTGTGAAGCATCCCCCATGGCCCCCAAGGTCACCTGTGCGTCCCAACATT	480
QY	786	GCTGCCATCACTGAATCAGACAAAGTTCTTTCATCAACGGCTCCAACTGGGAAGGCAATCCTG	845
Db	481	GCTGCCATCACTGAATCAGACAAAGTTCTTTCATCAACGGCTCCAACTGGGAAGGCAATCCTG	540
QY	846	GGGCTGGGCTATGCTGAGATTGCCAGGCTGACGACCTCCCTGGAGCCCTTCTTTGACATCT	905
Db	541	GGGCTGGGCTATGCTGAGATTGCCAGGCTGACGACCTCCCTGGAGCCCTTCTTTGACATCT	600
QY	906	CTGTTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAAGCTTTTGTGGTCTGGCTTTC	965
Db	601	CTGTTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAAGCTTTTGTGGTCTGGCTTTC	660
QY	966	CCCTCAACACGCTCTGAAGTGTGGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC	1025
Db	661	CCCTCAACACGCTCTGAAGTGTGGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC	720
QY	1026	GACCACTGCTGTACACAGGCTCTGCTGGTATACACCCATCCCGGGGAGTGGTATTTAT	1085
Db	721	GACCACTGCTGTACACAGGCTCTGCTGGTATACACCCATCCCGGGGAGTGGTATTTAT	780
QY	1086	GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACCTGCAAGGAG	1145
Db	781	GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACCTGCAAGGAG	840
QY	1146	TACAACTATGACAAGAGCATTTGGAGAGTGGACAGTGGACCAACCACTTTCGTTGCCCAAGAA	1205
Db	841	TACAACTATGACAAGAGCATTTGGAGAGTGGACAGTGGACCAACCACTTTCGTTGCCCAAGAA	900
QY	1206	GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCCCTCTCCACGGGAGGTTCCCTGAT	1265
Db	901	GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCCCTCTCCACGGGAGGTTCCCTGAT	960
QY	1266	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGAAGCAGCACCACCCCTTGGAAACATT	1325
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGAAGCAGCACCACCCCTTGGAAACATT	1020
QY	1326	TTCCCACTCATCTCACTCTACCTTAATGGGTGAGGTTACCAACAGTCTTCCGCAATCAC	1385
Db	1021	TTCCCACTCATCTCACTCTACCTTAATGGGTGAGGTTACCAACAGTCTTCCGCAATCAC	1080
QY	1386	ATCCTTCCGACCAATACCTCGGCGCAGTGGGAAGATGGCCACGTCCTCCCAAGACGACTGT	1445
Db	1081	ATCCTTCCGACCAATACCTCGGCGCAGTGGGAAGATGGCCACGTCCTCCCAAGACGACTGT	1140
QY	1446	TACAAGTTTGGCATCTCAGATCATCCACGGGCACTGTATGGGAGCTGTTATCATGGAG	1505
Db	1141	TACAAGTTTGGCATCTCAGATCATCCACGGGCACTGTATGGGAGCTGTTATCATGGAG	1200
QY	1506	GGCTTCTACGTTGTCTTTGATCGGGCCGAAAACGAATGGCTTTGCTGTCAGCGCTTGC	1565
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCGAAAACGAATGGCTTTGCTGTCAGCGCTTGC	1260
QY	1566	CATGTGCAGGATGAGTTCAGGAGCGGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1625
Db	1261	CATGTGCAGGATGAGTTCAGGAGCGGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
QY	1626	GAAGACTCTGGCTACAACATTTCCACAGACAGATGAGTCAACCCCTCATCACCATAGCTAT	1685
Db	1321	GAAGACTCTGGCTACAACATTTCCACAGACAGATGAGTCAACCCCTCATCACCATAGCTAT	1380
QY	1686	GTCATGGCTGCCATCTGCGGCCCTCTTTCATGCTGCCACTCTGCCCTCATGGTGTGATGG	1745

Db 1381 GTCATGGCTGCCATCTCGGCCCTTTTCATGCTGCCACTCTGCCCTCATGGTGTGTCAGTGG 1440
Qy 1746 CGCTGCCCTCGCTGCGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1805
Db 1441 CGCTGCCCTCGCTGCGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
Qy 1806 AAGTGAGAGGCCCATGGGAGAGATAGAGATTCCCT-GGACCACACCTCCGTTGGTTC 1864
Db 1501 AAGTGAGAGGCCCATGGGAGAGATAGAGATTCCCTGGGACCACACCTCCGTTGGTTC 1560
Qy 1865 ACTTTGCTCACAGTAGAGACAGATGGCACTGTGGCCAGAGACCTCAGGACCCCTC 1924
Db 1561 ACTTTGCTCACAGTAGAGACAGATGGCACTGTGGCCAGAGACCTCAGGACCCCTC 1620
Qy 1925 CCCACCCACCAATGCTCTGCTTTGATGGAGAGGAAAGGCTGGCAAGTGGTTCCA 1984
Db 1621 CCCACCCACCAATGCTCTGCTTTGATGGAGAGGAAAGGCTGGCAAGTGGTTCCA 1680
Qy 1985 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAAGAACACTCTGCTGGCGGGAATAC 2044
Db 1681 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAAGAACACTCTGCTGGCGGGAATAC 1740
Qy 2045 TCTTGGTCACTCAAAATTAAGTCGGGAAATCTGCTGTGAATCTCAGCCCTGAACC 2104
Db 1741 TCTTGGTCACTCAAAATTAAGTCGGGAAATCTGCTGTGAATCTCAGCCCTGAACC 1800
Qy 2105 TTTGTCACCATCTCTTAATTTCAATCTCAACCCAAAGTATCTCTTTTCTAGTTTCAGA 2164
Db 1801 TTTGTCACCATCTCTTAATTTCAATCTCAACCCAAAGTATCTCTTTTCTAGTTTCAGA 1860
Qy 2165 AGTACTGGCATCACACGAGGTTTACCTTGGCGTGTGTCCTGTGGTACCTTGGCAGAGAA 2224
Db 1861 AGTACTGGCATCACACGAGGTTTACCTTGGCGTGTGTCCTGTGGTACCTTGGCAGAGAA 1920
Qy 2225 GAGACCAAGCTTTTCCCTGCTGGCCAAAGTCACTAGTAGGAGAGATGACAGTTTGTAT 2284
Db 1921 GAGACCAAGCTTTTCCCTGCTGGCCAAAGTCACTAGTAGGAGAGATGACAGTTTGTAT 1980
Qy 2285 TTGCTTTAGAGACAGGACTGTATAACACAGCCCTAAGCTTGGTCAAGATTTGCTCTTG 2344
Db 1981 TTGCTTTAGAGACAGGACTGTATAACACAGCCCTAAGCTTGGTCAAGATTTGCTCTTG 2040
Qy 2345 AATT 2348
Db 2041 AATT 2044

RESULT 4

US-09-548-372D-5
; Sequence 5, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548.372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-548-372D-5
Query Match 80.1%; Score 1881; DB 4; Length 1977;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1966; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 306 ATGCCCAAGCCCTGCCCTTCTGCTGTGGATGGCGGGAGTGTCTGCTGCCAC 365
Db 1 ATGCCCAAGCCCTGCCCTTCTGCTGTGGATGGCGGGAGTGTCTGCTGCCAC 60
Qy 366 GGCACCAGCAGCATCCGCTTCCCTTGGCAGCGCTTGGGGGGGGGGGGGGGGGG 425
Db 61 GGCACCAGCAGCATCCGCTTCCCTTGGCAGCGCTTGGGGGGGGGGGGGGGGGG 120
Qy 426 CTGCGGCTGCCCGGGAGCAGCAGAGAGCCGAGAGCCGCGGAGCGGAGGCGAGCTTT 485
Db 121 CTGCGGCTGCCCGGGAGCAGCAGAGAGCCGAGAGCCGCGGAGCGGAGGCGAGCTTT 180
Qy 486 GTGAGATGTGGACAACTGAGGGGCAAGTGGGGGAGGCTTACTAGTGGAGATGACC 545
Db 181 GTGAGATGTGGACAACTGAGGGGCAAGTGGGGGAGGCTTACTAGTGGAGATGACC 240
Qy 546 GTGGGCGACCCCGCGCAGACGCTCAACATCTCTGCTACTACAGAGGCGAGCTGTCCAGCACA 605
Db 241 GTGGGCGACCCCGCGCAGACGCTCAACATCTCTGCTGGGATACAGGCGAGTAACTTTGCA 300
Qy 606 GTGGGTGCTGCCCGCCCGCCCTTCTGCTACTACTACAGAGGCGAGCTGTCCAGCACA 665
Db 301 GTGGGTGCTGCCCGCCCGCCCTTCTGCTACTACTACAGAGGCGAGCTGTCCAGCACA 360
Qy 666 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTTACACCCAGGCGAGTGGGGAAGGGAG 725
Db 361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTTACACCCAGGCGAGTGGGGAAGGGAG 420
Qy 726 CTGGGCGACCGACCTGGTAAAGCATCCCCCATGGCCCAACGCTCACTGTCGTCGCCAAT 785
Db 421 CTGGGCGACCGACCTGGTAAAGCATCCCCCATGGCCCAACGCTCACTGTCGTCGCCAAT 480
Qy 786 GCTGCCATCACTGAATCAGACAAAGTTTTCATCAACGGCTCCAACTGGGAAGGCACTCTG 845
Db 481 GCTGCCATCACTGAATCAGACAAAGTTTTCATCAACGGCTCCAACTGGGAAGGCACTCTG 540
Qy 846 GGGTGGCTTATGTGTAGATTGCCAGGCGCTGACGACTCCCTTGGAGCCCTTCTTTGACTCT 905
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Qy 906 CTGGTAAAGCAGACCCAGCTTCCCAACCTCTCTCCCTGCGAGCTTGTGGTCTGCTGCTC 965
Db 567 -----GCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
Qy 966 CCCCTCAACACAGTCTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1025
Db 586 CCCCTCAACACAGTCTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
Qy 1026 GACCACTGCTGTACAGGAGTGTCTGCTGTATACACCCATCCCGGGGAGTGGTATTAT 1085
Db 646 GACCACTGCTGTACAGGAGTGTCTGCTGTATACACCCATCCCGGGGAGTGGTATTAT 705
Qy 1086 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGACACTGCAAGGAG 1145
Db 706 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGACACTGCAAGGAG 765
Qy 1146 TACAACTATGACAGAGCATTTGTGGACAGTGGCAGCACCACCAAGCTTCTGTTTGGCCCAAGAA 1205
Db 766 TACAACTATGACAGAGCATTTGTGGACAGTGGCAGCACCACCAAGCTTCTGTTTGGCCCAAGAA 825
Qy 1206 GTTTTGAAGTGTGAGTCAAAATCCATCAAGGAGGCTCTCTCCACGAGAGTTCCTGTAT 1265
Db 826 GTTTTGAAGTGTGAGTCAAAATCCATCAAGGAGGCTCTCTCCACGAGAGTTCCTGTAT 885
Qy 1266 GTTTTCTGCTAGGAGAGCAGCTGTGTGCTGGCAGGAGGAGCACCACCTTGGGACATT 1325
Db 886 GTTTTCTGCTAGGAGAGCAGCTGTGTGCTGGCAGGAGGAGCACCACCTTGGGACATT 945

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Db 1486 CTTTGGTACAAAGTAGGACACAGATGGCACCTGTGGCCAGACCTTCAGGACCCCTCC 1545
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Db 1606 GGAAGTACCTGTAGGAAACAGAAAGAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1665
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Db 1726 TTGTCCACCATCTCTTAAATCTCCAAACCCCAAGATATCTCTTCTTCTAGTTTCAGAA 1785
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Db 1786 GTACTGGCATCACAGCGAGGTACCTTGGCGGTGTGTCCTGTGTGATACCTCCGACAGAG 1845
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QY 2226 AGACCAAGCTTTTCCCTGCTGGCCAAAGTCAAGTAGGAGAGGATGCACAGTTTGTCTATT 2285
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Db 1846 AGACCAAGCTTTTCCCTGCTGGCCAAAGTCAAGTAGGAGAGGATGCACAGTTTGTCTATT 1905
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QY 2286 TGCTTTAGAGACAGGACTGTATAACACAGCCCTAAACATTTGGTGCAGAGATTGCCCTCTTGA 2345
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Db 1906 TGCTTTAGAGACAGGACTGTATAACACAGCCCTAAACATTTGGTGCAGAGATTGCCCTCTTGA 1965
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QY 2346 A 2346
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Db 1966 A 1966
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RESULT 5

US-09-548-367D-5

: Sequence 5, Application US/09548367D

: Patent No. 6440698

: GENERAL INFORMATION:

: APPLICANT: GURNEY ET AL.

: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND

: TITLE OF INVENTION: THEREOF

: FILE REFERENCE: 29915/6280H

: CURRENT APPLICATION NUMBER: US/09/548,367D

: CURRENT FILING DATE: 2000-04-12

: PRIOR APPLICATION NUMBER: US 60/155,493

: PRIOR FILING DATE: 1999-09-23

: PRIOR APPLICATION NUMBER: US 09/404,133

: PRIOR FILING DATE: 1999-09-23

: PRIOR APPLICATION NUMBER: PCT/US99/20881

: PRIOR FILING DATE: 1999-09-23

: PRIOR APPLICATION NUMBER: US 60/101,594

: PRIOR FILING DATE: 1998-09-24

: NUMBER OF SEQ ID NOS: 73

: SOFTWARE: PatentIn version 3.1

: SEQ ID NO 5

: LENGTH: 1977

: TYPE: DNA

: ORGANISM: Homo sapiens

: US-09-548-367D-5

Query Match 80.1%; Score 1881; DB 4; Length 1977;

Best Local Similarity 96.3%; Pred. No. 0;

Matches 1966; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

QY 306 ATGGCCCAAGCCCTGCCCTGGCTCTCTGTGGATGGCGGGAGTGTGCTGCTGCCAC 365

Db 1 ATGGCCCAAGCCCTGCCCTGGCTCTCTGTGGATGGCGGGAGTGTGCTGCTGCCAC 60

QY 366 GGCACCCAGCACGGCATCCGGCTGCCCTGGCGAGCGCCCTGGGGGGCCCCCTGGGG 425

Db 61 GGCACCCAGCACGGCATCCGGCTGCCCTGGCGAGCGCCCTGGGGGGCCCCCTGGGG 120

QY 426 CTGGGCTGCCCGGGGAGACCGAGAGCCCGAGGAGCCCGCGGAGCGCCCTGGGGGGCCCCCTGGGG 485

Db 121 CTGGGCTGCCCGGGGAGACCGAGAGCCCGAGGAGCCCGCGGAGCGCCCTGGGGGGCCCCCTGGGG 180

QY 486 GTGAGATGGTGACAACTGAGGGCAAGTGGGGGCAAGTGGGGGCAAGGCTACTACGTGAGATGACC 545

Db 181 GTGAGATGGTGACAACTGAGGGCAAGTGGGGGCAAGTGGGGGCAAGGCTACTACGTGAGATGACC 240

QY 546 GTGGCAGCCCCCGGAGACGGCTCAACATCTGTGTGGATACAGGAGGAGTAACTTTGCA 605

Db 241 GTGGCAGCCCCCGGAGACGGCTCAACATCTGTGTGGATACAGGAGGAGTAACTTTGCA 300

QY 606 GTGGTGTGTCGCCCGCCACCCCTTCTGCTGCTTACTACAGAGGAGGAGTGTCCAGACA 665

Db 301 GTGGTGTGTCGCCCGCCACCCCTTCTGCTGCTTACTACAGAGGAGGAGTGTCCAGACA 360

QY 666 TACCGGAGCTCCCGAAGGCTGTGTATGTCCTTACACCCAGGCAAGTGGGAAGGGAG 725

Db 361 TACCGGAGCTCCCGAAGGCTGTGTATGTCCTTACACCCAGGCAAGTGGGAAGGGAG 420

QY 726 CTGGGACCGGAGCTGGTAAGCATCCGCCATGGCCCCAACAGTCACTGTGCGTGCCCAACATTT 785

Db 421 CTGGGACCGGAGCTGGTAAGCATCCGCCATGGCCCCAACAGTCACTGTGCGTGCCCAACATTT 480

QY 786 GCTGCCATCACTGAATCAGACAAGTCTTTCATCAACGGCTCCAACTGGGAAGGCACTCTG 845

Db 481 GCTGCCATCACTGAATCAGACAAGTCTTTCATCAACGGCTCCAACTGGGAAGGCACTCTG 540

QY 846 GGGCTGGGCTATGCTGTGAGATTGGCAGGCTGACGACTCCCTGGAGCCCTTCTTCTTGTACTCT 905

Db 541 GGGCTGGGCTATGCTGTGAGATTGGCAG-----566

QY 906 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGTGCTGGCTTTC 965

Db 567 -----||||| 585
QY 966 CCCCTCAACAGTCTGAAGTGTGGCTCTGTCTGGAGGAGCATGATCATTTGGAGGTATC 1025
Db 586 CCCCTCAACAGTCTGAAGTGTGGCTCTGTCTGGAGGAGCATGATCATTTGGAGGTATC 645
QY 1026 GACCACTCGCTGTACACAGGAGTCTGTGTATACACCCATCGCGGGGAGTGGTATTAT 1085
Db 646 GACCACTCGCTGTACACAGGAGTCTGTGTATACACCCATCGCGGGGAGTGGTATTAT 705
QY 1086 GAGGTGATCATTTGTGGGTGGAGATCAATGGACAGAGATCTGAATAATGGACTGCAAGGAG 1145
Db 706 GAGGTGATCATTTGTGGGTGGAGATCAATGGACAGAGATCTGAATAATGGACTGCAAGGAG 765
QY 1146 TACAACATATGACAAGAGCATTTGGGAGTGGGACGACCAACCACTTCTGTTTGGCCCAAGAAA 1205
Db 766 TACAACATATGACAAGAGCATTTGGGAGTGGGACGACCAACCACTTCTGTTTGGCCCAAGAAA 825
QY 1206 GTGTTTGAAGTGCAGTCAATCAATCAAGGAGGCTTCCCTCCACGGAGAAAGTTCCTTGAT 1265
Db 826 GTGTTTGAAGTGCAGTCAATCAATCAAGGAGGCTTCCCTCCACGGAGAAAGTTCCTTGAT 885
QY 1266 GTTTCCTGCTAGGAGAGCATTTGGTGTGCTGGCAAGCAGGACCCCTTGGAAACATT 1325
Db 886 GTTTCCTGCTAGGAGAGCATTTGGTGTGCTGGCAAGCAGGACCCCTTGGAAACATT 945
QY 1326 TTCCCACTATCTCACTCTACCTAATGGGTGAGGTACCAACCACTCTTCCGCAATCACC 1385
Db 946 TTCCCACTATCTCACTCTACCTAATGGGTGAGGTACCAACCACTCTTCCGCAATCACC 1005
QY 1386 ATCTTTCCGAGCAATACCTCGCGCCAGTGGAGAGATGTGGCCACGCTCCCAAGACGACTGT 1445
Db 1006 ATCTTTCCGAGCAATACCTCGCGCCAGTGGAGAGATGTGGCCACGCTCCCAAGACGACTGT 1065
QY 1446 TACAAGTTTGGCATCTCACAGTCAATCCACGGGACACTGTTATGGAGCTGTTATCATGGAG 1505
Db 1066 TACAAGTTTGGCATCTCACAGTCAATCCACGGGACACTGTTATGGAGCTGTTATCATGGAG 1125
QY 1506 GCGTCTTACGTTCTCTTGTATCGGGCCGCAAGCAATTTGCTGTGCTGACGCTTGC 1565
Db 1126 GCGTCTTACGTTCTCTTGTATCGGGCCGCAAGCAATTTGCTGTGCTGACGCTTGC 1185
QY 1566 CATGTGCAGATGAGTTTCAGGAGCGGAGCGGTGGAAGGCGCTTTTGTACCTTTGGACATG 1625
Db 1186 CATGTGCAGATGAGTTTCAGGAGCGGAGCGGTGGAAGGCGCTTTTGTACCTTTGGACATG 1245
QY 1626 GAAGACTGTGGCTTACACATTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT 1685
Db 1246 GAAGACTGTGGCTTACACATTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT 1305
QY 1686 GTCATGGCTGCCATCTGCGCCCTTCTCATGCTGCCACTCTGCCCTCATGTTGTGTGTCAGTGG 1745
Db 1306 GTCATGGCTGCCATCTGCGCCCTTCTCATGCTGCCACTCTGCCCTCATGTTGTGTCAGTGG 1365
QY 1746 CGCTGCTCGCTGCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1805
Db 1366 CGCTGCTCGCTGCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1425
QY 1806 AAGTGAGGAGGCCATTTGGGAGAGATAGAGATTTCCCTGGACACACCTCCGTTGGTTCA 1865
Db 1426 AAGTGAGGAGGCCATTTGGGAGAGATAGAGATTTCCCTGGACACACCTCCGTTGGTTCA 1485
QY 1866 CTTTGTGTACAAGTAGGAGACAGATGGCACCTGTGGCCAGAGCAGCTTCAGGACCTCC 1925
Db 1486 CTTTGTGTACAAGTAGGAGACAGATGGCACCTGTGGCCAGAGCAGCTTCAGGACCTCC 1545
QY 1926 CCACCCACCAATATGCTTCTGCTTGTATGGAGAGAGAAAGGCTGGCAAGTGGTTCCAG 1985
Db 1546 CCACCCACCAATATGCTTCTGCTTGTATGGAGAGAGAAAGGCTGGCAAGTGGTTCCAG 1605
QY 1986 GGAAGTGTAGGAAACAGAAAAGAGAAAGAGCACTCTGCTGCGGGAATACT 2045
|||||

Db 1606 GGACTGTACCTGTAGGAAACAGAAAAGAGAAAGCACTCTGCTGCGGAATACT 1665
QY 2046 CTTGGTCACCTCAAAATTTAAGTCGGGAAATTTCTGCTCTTCAAACTTCAGCCCTGAACCT 2105
Db 1666 CTTGGTCACCTCAAAATTTAAGTCGGGAAATTTCTGCTCTTCAAACTTCAGCCCTGAACCT 1725
QY 2106 TTTGCCACCATTCCTTTAAATTTCTCCAAACCAAGATATTTCTTTCTTTAGTTTCAGAA 2165
Db 1726 TTTGCCACCATTCCTTTAAATTTCTCCAAACCAAGATATTTCTTTCTTTAGTTTCAGAA 1785
QY 2166 GTACTGTCATCACAGCAGGTACCTTTGGGCTGTGTCCTGTGTGACCTGGGAGAGAA 2225
Db 1786 GTACTGTCATCACAGCAGGTACCTTTGGGCTGTGTCCTGTGTGACCTGGGAGAGAA 1845
QY 2226 AGACCAAGCTTGTTCCTCTGCTGCCAAAGTTCAGTAGAGAGGATGCACAGTTTGTCTATT 2285
Db 1846 AGACCAAGCTTGTTCCTCTGCTGCCAAAGTTCAGTAGAGAGGATGCACAGTTTGTCTATT 1905
QY 2286 TGCTTTAGACAGAGGAGTGTATATAACCAAGCTTAACATTTGGTGCAAGATTTGCCCTTTGA 2345
Db 1906 TGCTTTAGACAGAGGAGTGTATATAACCAAGCTTAACATTTGGTGCAAGATTTGCCCTTTGA 1965
QY 2346 A 2346
Db 1966 A 1966
RESULT 6
US-09-009-191-3
; Sequence 3, Application US/09009191
; Patent No. 6319689
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID
; APPLICANT: CHAPMAN, CONRAD
; APPLICANT: MURPHY, KAY
; APPLICANT: SMITH, TRUDI
; TITLE OF INVENTION: ASP2
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,191
; FILING DATE: 20-JAN-1998
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: UK 9701684.4
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2370 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-009-191-3

Query Match				78.2%;	Score 1835.4;	DB 4;	Length 2370;
Best Local Similarity				99.1%;	Pred. No. 0;		
Matches 1856;				Conservative	0;	Mismatches 16;	Indels 1;
						Gaps	1;
QY	477	GGCAGCTTTTGGAGATGGTGACAACTGAGGGCAAGTCGGGGCAGGGCTACTAGCTG	536				
DB	1	GGCAGCTTTTGGAGATGGTGACAACTGAGGGCAAGTCGGGGCAGGGCTACTAGCTG	60				
QY	537	GAGATGACCGTGGGACGCCCCCGCAGACGCTCAACATCCTGTGGATACAGGCAGCAGT	596				
DB	61	GAGATGACCGTGGGACGCCCCCGCAGACGCTCAACATCCTGTGGATACAGGCAGCAGT	120				
QY	597	AACCTTTCAGTGGGTGCTGCCCCACCCCTTCTGATCGCTACTACAGAGGACGCTG	656				
DB	121	AACCTTTCAGTGGGTGCTGCCCCACCCCTTCTGATCGCTACTACAGAGGACGCTG	180				
QY	657	TCCAGCACATACCGGGACCTCCGAGAGGGTGTATGTGCCCTACACCCAGGCGAAGTGG	716				
DB	181	TCCAGCACATACCGGGACCTCCGAGAGGGTGTATGTGCCCTACACCCAGGCGAAGTGG	240				
QY	717	GAAGGGAGCTGGGACCGGACCTGGTAAGCATCCCCCATGGCCCAACGTCACCTGTGCGT	776				
DB	241	GAAGGGAGCTGGGACCGGACCTGGTAAGCATCCCCCATGGCCCAACGTCACCTGTGCGT	300				
QY	777	GCCAACTGCTGCCATCAGTGAATCAGACAAAGTTCTTCATCAACGGCTCCAACTGGGAA	836				
DB	301	GCCAACTGCTGCCATCAGTGAATCAGACAAAGTTCTTCATCAACGGCTCCAACTGGGAA	360				
QY	837	GGCATCCTGGGGTGGCTATGCTGAGATGGCAGGCTGACGACCTCCCTGGAGCCTTTC	896				
DB	361	GGCATCCTGGGGTGGCTATGCTGAGATGGCAGGCTGACGACCTCCCTGGAGCCTTTC	420				
QY	897	TTTGACTCTCTGTFHAAAGCAGACCCACGCTTCCAACTCTTCTCCCTGACGCTTTTGGT	956				
DB	421	TTTGACTCTCTGTFHAAAGCAGACCCACGCTTCCAACTCTTCTCCCTGACGCTTTTGGT	480				
QY	957	GCTGGCTTCCCTCAACAGCTGTAAGTGTGGCTCTGTGGAGGGAGCATGATCATTT	1016				
DB	481	GCTGGCTTCCCTCAACAGCTGTAAGTGTGGCTCTGTGGAGGGAGCATGATCATTT	540				
QY	1017	GGAGGTATCGACCACTCGCTTACACAGGAGCTCTGTGTATACCCCATCCCGCGGGAG	1076				
DB	541	GGAGGTATCGACCACTCGCTTACACAGGAGCTCTGTGTATACCCCATCCCGCGGGAG	600				
QY	1077	TGCTATTATGAGTGTATCTGTGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC	1136				
DB	601	TGCTATTATGAGTGTATCTGTGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC	660				
QY	1137	TGCAAGGAGTACAACTATGACAAGAGCATTTGGACAGTGGCACCAACCACTTCGTTTG	1196				
DB	661	TGCAAGGAGTACAACTATGACAAGAGCATTTGGACAGTGGCACCAACCACTTCGTTTG	720				
QY	1197	CCCAAGAAAGTGTGTAAGCTGCACTAAATCCATCAAGGCGAGCCTCCTCCACGGAGAAG	1256				
DB	721	CCCAAGAAAGTGTGTAAGCTGCACTAAATCCATCAAGGCGAGCCTCCTCCACGGAGAAG	780				
QY	1257	TTCCCTGATGGTTTCTGGCTAGGAGAGCAGTGTGTGCTGGCAAGCAGGACCAACCCCT	1316				
DB	781	TTCCCTGATGGTTTCTGGCTAGGAGAGCAGTGTGTGCTGGCAAGCAGGACCAACCCCT	840				
QY	1317	TGGAACATTTTCCAGTCACTCTACTTACCTAATGGGTGAGGTTACCAACCACTCTTC	1376				
DB	841	TGGAACATTTTCCAGTCACTCTACTTACCTAATGGGTGAGGTTACCAACCACTCTTC	900				
QY	1377	CGCATCACCATCTCTCCGACGCAATACCTCGGGCCAGTGGAAAGATGTGGCCAGCTCCCAA	1436				
DB	901	CGCATCACCATCTCTCCGACGCAATACCTCGGGCCAGTGGAAAGATGTGGCCAGCTCCCAA	960				
QY	1437	GACGACTGTTACAGTTTGGCATCTCAGATCATCCAGGGGCACTGTTATGGGAGCTGTT	1496				
DB	961	GACGACTGTTACAGTTTGGCATCTCAGATCATCCAGGGGCACTGTTATGGGAGCTGTT	1020				

RESULT 7

US-09-548-372D-7
; Sequence 7, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548.372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493

QY	1497	ATCATGGAGGCTTCTACGTTTGTCTTGTATGATGGGCCCCGAAACGAAATTTGGCTTTGCTCTC	1556
DB	1021	ATCATGGAGGCTTCTACGTTTGTCTTGTATGATGGGCCCCGAAACGAAATTTGGCTTTGCTCTC	1080
QY	1557	AGCGCTTGGCATGTGCACGATGAGTTTCAGAGCGGACGGTGGAAAGCCCTTTTGTCTAC	1616
DB	1081	AGCGCTTGGCATGTGCACGATGAGTTTCAGAGCGGACGGTGGAAAGCCCTTTTGTCTAC	1140
QY	1617	TTGACATGGAAGACTGTGGCTTACAACTTCCACACACAGATGATGATCAACCTTCATGACC	1676
DB	1141	TTGACATGGAAGACTGTGGCTTACAACTTCCACACACAGATGATGATCAACCTTCATGACC	1200
QY	1677	ATAGCCTATGTCATGGCTGCCATCTGGCCCTTTCATGCTGGCACCTTCCTGCTCATGTG	1736
DB	1201	ATAGCCTATGTCATGGCTGCCATCTGGCCCTTTCATGCTGGCACCTTCCTGCTCATGTG	1260
QY	1737	TGTCAGTGGCGCTGCCCTCCGCTGCCCTGCCACAGCATGATGATGATGATGATGATGATG	1796
DB	1261	TGTCAGTGGCGCTGCCCTCCGCTGCCCTGCCACAGCATGATGATGATGATGATGATGATG	1320
QY	1797	TCCTGCTGAAGTCAGGAGGCCCATGGGCGAGAGATAGATGATGATGATGATGATGATGATG	1855
DB	1321	TCCTGCTGAAGTCAGGAGGCCCATGGGCGAGAGATAGATGATGATGATGATGATGATGATG	1380
QY	1856	CCGTGCTTCACTTTGGTCAACAGTAGGAGACACAGATGATGATGATGATGATGATGATGATG	1915
DB	1381	CCGTGCTTCACTTTGGTCAACAGTAGGAGACACAGATGATGATGATGATGATGATGATGATG	1440
QY	1916	AGGACCTTCCCAACCCACCAATGCTCTGCTGCTGATGAGAGAGGAAAGGCTGGCAAG	1975
DB	1441	AGGACCTTCCCAACCCACCAATGCTCTGCTGCTGATGAGAGAGGAAAGGCTGGCAAG	1500
QY	1976	TGGGTTCCAGGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGGCTGTGCTGG	2035
DB	1501	TGGGTTCCAGGACTGTACCTGTAGGAAACAGAAAGAGAGAAAGGCTGTGCTGG	1560
QY	2036	CGGGAATACCTTCTGGTCACTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTCAG	2095
DB	1561	CGGGAATACCTTCTGGTCACTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTCAG	1620
QY	2096	CCCTGAACCTTTGCCACCACTTCCCTTTAAATTTCCCAACCCCAAGTATCTCTTTCTTT	2155
DB	1621	CCCTGAACCTTTGCCACCACTTCCCTTTAAATTTCCCAACCCCAAGTATCTCTTTCTTT	1680
QY	2156	AGTTTTCAGAACTACTGGCATCACAGCAGGTTACCTTGGCGTGTGCTGCTGCTGCTGCTGCT	2215
DB	1681	AGTTTTCAGAACTACTGGCATCACAGCAGGTTACCTTGGCGTGTGCTGCTGCTGCTGCTGCT	1740
QY	2216	GGCAGAGAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAAGTGGAGAGGATGCACA	2275
DB	1741	GGCAGAGAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAAGTGGAGAGGATGCACA	1800
QY	2276	GTTTGTCTATTGCTTTAGAGACAGGACTGTATAAACAAGCTTAACATTTGTCGCAAGAT	2335
DB	1801	GTTTGTCTATTGCTTTAGAGACAGGACTGTATAAACAAGCTTAACATTTGTCGCAAGAT	1860
QY	2336	TGCTCTTGAATT 2348	
DB	1861	TGCTCTTGAATT 1873	

1501 AAGTAAGGAGGCTCGTGGGACAGATGATGGAGACGCCCTGGACACATCTGGGTGGTTCC 1560
1866 CTTTGGTGCACA--AGTAGGACACAGATGCACCTGTGGCCAGAGCAGCCTCAGAACCT 1923
1561 CTTTGGTGCACATGATGTTGGAGCTATGAGTGATCTGTGGCCAGAGCAGCCTCAGAACCT 1620
1924 CCCACCCACCAAAATTCCTCTGCCTTGATGGAGAAGGAAAGGCTGGCAAGGTGGGTTC 1983
1621 CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAATCAGGCAAGCTGGATTAC 1679
1984 AGGAGCTGTACCTGTAGGAACAGAAAGAGAAAGAGACACTCTGCTGGCGGAATA 2043
1680 AGGGCTTGCACCTCTAGGACACAGAGAGGGAAGGAAAGCAGCGTTCTGGTGGCAGGAATA 1739
2044 CTCCTTGGTCACCTCAAAATTAAGTCGGGAATTCCTGCTGCTTGAACCTTCAGCCCTGAAC 2103
1740 TCCTTAGGCACCAAACTTCAGT-TGGAAATTTGCTGCTTGAAGCTTCAGCCCTTGACC 1798
2104 CTTTGTCCACCATTCCTTTAAATTCCTCAACCCCAAAGTATTCTTTCTTAGTTTCAG 2163
1799 CTCCTGCCAGCA-TCCTTTAGAGTCTCCAACTTAAAGTATTCTTTATGTC---CTTCCAG 1854
2164 AAGTACTGGCATCACACGCAAGTTACCTTGGCGGTGTGCTGCTGGTACCCCTGGCAGAGA 2223
1855 AAGTACTGGCGCTCATCTACGAGTACC-CGGCATGTGCTCCCTGGTGGTACCCCTGGCAGAGA 1913
2224 AGAGACCAGCTGTGTTCCCTGCTGGCCAAAGTACGTAGGAGAGAGTGCACAGTTTGCTA 2283
1914 AAGGGCCAAATC-TCATTTCCCTGCTGGCCAAAGTACGCAAGAGGTTG--AAGTTTGCCA 1970
2284 TTTGCTTTAGACAGAGGAGCTGTATAAACAAAGCCTTAACATTGGTGCAAGATTTGCTCTT 2343
1971 GTTCTTTAGTAGAGGAGCTGCAGACTCAAGCCT-ACACTGGTACAAAGAGTGGTCTT 2029
2344 GA 2345
2030 GA 2031

RESULT 9

US-09-548-372D-29
; Sequence 29, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-29

Query Match 57.7%; Score 1355.8; DB 4; Length 1362;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1357; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 306 ATGGCCCCAAGCCCTGCCCTGCTGCTGATGGCGGGAGTGGCTGCCCCAC 365
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Db 1 ATGCCCCAAGCCCTGCCCTGCTGCTGATGGCGGGAGTGTGCTGCCCCAC 60
Qy GGCACCCAGCAGCAGCATCCGCTGCCCTGCGCAGCGCCCTGGGGGGGCCCCCTGGG 425
|||||
Db 61 GGCACCCAGCAGCAGCATCCGCTGCCCTGCGCAGCGCCCTGGGGGGGCCCCCTGGG 120
Qy CTGGGGCTGCCCGGGAGACGAGAGAGCCGAGAGAGCCCGGCGGAGGGGCGAGCTTT 485
Db 121 CTGGGGCTGCCCGGGAGACGAGAGAGCCGAGAGAGCCCGGCGGAGGGGCGAGCTTT 180
Qy 486 GTGAGATGTGGACAACCTGAGGGGCAAGTCGGGGGAGGGCTACTAGTGGAGATGACC 545
Db 181 GTGAGATGTGGACAACCTGAGGGGCAAGTCGGGGGAGGGCTACTAGTGGAGATGACC 240
Qy 546 GTGGCAGCCCCCGCAGACGCTCAACATCTGCTGGTGGATACAGGCAGCAGTAACCTTCCA 605
Db 241 GTGGCAGCCCCCGCAGACGCTCAACATCTGCTGGTGGATACAGGCAGCAGTAACCTTCCA 300
Qy 606 GTGGTGTGCTGCCCGCCACCCCTTCTGTCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 665
Db 301 GTGGTGTGCTGCCCGCCACCCCTTCTGTCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
Qy 666 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 725
Db 361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
Qy 726 CTGGCAGCCGACCTGGTAAGCATCCCCATGGCCCAACGTCACCTGCGTGCCCAACATT 785
Db 421 CTGGCAGCCGACCTGGTAAGCATCCCCATGGCCCAACGTCACCTGCGTGCCCAACATT 480
Qy 786 GCTGCCATCACTGAATCAGACAAGTCTTCAACAGCGCTCAACCTGGGAAGGCATCTCTG 845
Db 481 GCTGCCATCACTGAATCAGACAAGTCTTCAACAGCGCTCAACCTGGGAAGGCATCTCTG 540
Qy 846 GGGTGGCGCTATGTGTAGATGCGCAGGCTGACGACTCCCTGGAGCGCTTTCTTTGACTCT 905
Db 541 GGGTGGCGCTATGTGTAGATGCGCAGGCTGACGACTCCCTGGAGCGCTTTCTTTGACTCT 600
Qy 906 CTGTTAAAGCAGACCCACGTTCCCAACCTCTCTCCCTGCAGCTTTGTTGGTCTGCGCTTC 965
Db 601 CTGTTAAAGCAGACCCACGTTCCCAACCTCTCTCTCCCTGCAGCTTTGTTGGTCTGCGCTTC 660
Qy 966 CCCCTCAACACGCTCTGAAGTGTGCGCTCTGTGCGGAGGAGCATGATCATTTGGAGGTATC 1025
Db 661 CCCCTCAACACGCTCTGAAGTGTGCGCTCTGTGCGGAGGAGCATGATCATTTGGAGGTATC 720
Qy 1026 GACCACTGCTGTACAGGAGCTCTGTGTATACACCCATCCCGGGAGTGGTATTAT 1085
Db 721 GACCACCTGCTGTACAGGAGCTCTGTGTATACACCCATCCCGGGAGTGGTATTAT 780
Qy 1086 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 1145
Db 781 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 840
Qy 1146 TACAACTATGACAAGAGCATTTGTGGACAGTGGCAGCAGTGGCAGCAGTGGTGGTGGCCCAAGAAA 1205
Db 841 TACAACTATGACAAGAGCATTTGTGGACAGTGGCAGCAGTGGCAGCAGTGGTGGTGGCCCAAGAAA 900
Qy 1206 GTGTTTGAAGTGCAGTCAAAATCCATCAAGGAGCGCTCTCCACGAGAGTTCCTCTGAT 1265
Db 901 GTGTTTGAAGTGCAGTCAAAATCCATCAAGGAGCGCTCTCCACGAGAGTTCCTCTGAT 960
Qy 1266 GGTGTTCTGCTAGGAGAGCAGCTGTGCTGGCAGGAGGAGCAGCAGCCCTTGGACATT 1325
Db 961 GGTGTTCTGCTAGGAGAGCAGCTGTGCTGGCAGGAGGAGCAGCAGCCCTTGGACATT 1020
Qy 1326 TTCCCACTCATCTCACTTACCTTAATGGGTGAGGTTTACCAACAGTTCCTTCGCGCATCAC 1385
Db 1021 TTCCCACTCATCTCACTTACCTTAATGGGTGAGGTTTACCAACAGTTCCTTCGCGCATCAC 1080
Qy 1386 ATCTTCCGCAAGCAATACCTGCGGGCAGTGGGAAGATGTGGCCACGCTGCCAAGACGACTGT 1445
Db 1081 ATCTTCCGCAAGCAATACCTGCGGGCAGTGGGAAGATGTGGCCACGCTGCCAAGACGACTGT 1140

QY 1446 TACAAGTTTGCCATCTCAGATCATCCAGGGGACAGTGTATATGGAGCTGTTATCATGGAG 1505
Db 1141 TACAAGTTTGCCATCTCAGATCATCCAGGGGACAGTGTATATGGAGCTGTTATCATGGAG 1200
QY 1506 GGCCTTACGTTGCTTTGATCGGGCCGAAACAGAAATGGCTTTGCTGTCAGGCTTGC 1565
Db 1201 GGCCTTACGTTGCTTTGATCGGGCCGAAACAGAAATGGCTTTGCTGTCAGGCTTGC 1260
QY 1566 CATGTGACGATGAGTTGAGGACGCGAGCGGTGGAAGGCCCTTTTGTACCTTCGACATG 1625
Db 1261 CATGTGACGATGAGTTGAGGACGCGAGCGGTGGAAGGCCCTTTTGTACCTTCGACATG 1320
QY 1626 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCA 1664
Db 1321 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCA 1359

RESULT 10
US-09-548-367D-29
; Sequence 29, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-367D-29

Query Match 57.7%; Score 1355.8; DB 4; Length 1362;
Best Local Similarity 99.9%; Pred No. 0;
Matches 1357; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 306 ATGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGCGCGGAGTGTGCTGCCCTGCCAC 365
Db 1 ATGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGCGCGGAGTGTGCTGCCCTGCCAC 60
QY 366 GGCACCCAGCAGCGCATCGGCTGCCCTGCCAGCGGCTGGGGGCGGCCCTGGGG 425
Db 61 GGCACCCAGCAGCGCATCGGCTGCCCTGCCAGCGGCTGGGGGCGGCCCTGGGG 120
QY 426 CTGGGGTGGCCCGGAGACCGACGAGCGGAGCGGCGGCGGAGCGGCGGAGCGCTT 485
Db 121 CTGGGGTGGCCCGGAGACCGACGAGCGGAGCGGCGGAGCGGCGGAGCGCTT 180
QY 486 GTGAGATGTGGACAACTGAGGGGCAAGTGGGGGCGAGGCTTACTACGTGGAGATGACC 545
Db 181 GTGAGATGTGGACAACTGAGGGGCAAGTGGGGGCGAGGCTTACTACGTGGAGATGACC 240
QY 546 GTGGGACGCCCGCCAGACCGCTCAACATCTCGTGGATACAGCAGCAGTAACCTTTCGA 605
Db 241 GTGGGACGCCCGCCAGACCGCTCAACATCTCGTGGATACAGCAGCAGTAACCTTTCGA 300
QY 606 GTGGGTGCTGCCCGCCAGACCGCTTCTGTCATCGCTACTACAGAGGCGAGCTGTCCAGCACA 665
Db 301 GTGGGTGCTGCCCGCCAGACCGCTTCTGTCATCGCTACTACAGAGGCGAGCTGTCCAGCACA 360

RESULT 11
US-09-548-372D-31
; Sequence 31, Application US/09548372D
; Patent No. 6420534

QY 666 TACCGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG 725
Db 361 TACCGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG 420
QY 726 CTGGGCAAGGACCTGGTAAAGCATCCGCCATGGCCCCAACGTCTACTGTGCGTGGCCAACT 785
Db 421 CTGGGCAAGGACCTGGTAAAGCATCCGCCATGGCCCCAACGTCTACTGTGCGTGGCCAACT 480
QY 786 GCTGCCATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAACTGGGAAGGATCCCTG 845
Db 481 GCTGCCATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAACTGGGAAGGATCCCTG 540
QY 846 GGGCTGGCTATGCTGAGATTTGCCAGGCTTGAGACTCCCTGGAGCCCTTTCTTTGACTCT 905
Db 541 GGGCTGGCTATGCTGAGATTTGCCAGGCTTGAGACTCCCTGGAGCCCTTTCTTTGACTCT 600
QY 906 CTGTTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGACGCTTTGTGTGGTGGCTTTC 965
Db 601 CTGTTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGACGCTTTGTGTGGTGGCTTTC 660
QY 966 CCCCTCAACCACTGTGAAGTGTGGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC 1025
Db 661 CCCCTCAACCACTGTGAAGTGTGGCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC 720
QY 1026 GACCCTCGCTGTACACAGGCACTCTCTGTATATACCCCATCCCGCGGGAGTGGTATAT 1085
Db 721 GACCCTCGCTGTACACAGGCACTCTCTGTATATACCCCATCCCGCGGGAGTGGTATAT 780
QY 1086 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAGGAG 1145
Db 781 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAGGAG 840
QY 1146 TACAACATGATCAACAGCAGTCTGGACAGTGGCACCAACCACTCTCTTCCGCCAAGAAA 1205
Db 841 TACAACATGATCAACAGCAGTCTGGACAGTGGCACCAACCACTCTCTTCCGCCAAGAAA 900
QY 1206 GTGTTTGAAGCTGCACTCAAAATCCATCAAGGAGCCCTCTCCAGGAGAAAGTTCCTCAT 1265
Db 901 GTGTTTGAAGCTGCACTCAAAATCCATCAAGGAGCCCTCTCCAGGAGAAAGTTCCTCAT 960
QY 1266 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGACCCCTTTGGACATTT 1325
Db 961 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGACCCCTTTGGACATTT 1020
QY 1326 TTCCCAAGTCACTCTACTCTACCTAATGGGTGAGGTTTACCAACCACTCTCTCCGATCACC 1385
Db 1021 TTCCCAAGTCACTCTACTCTACCTAATGGGTGAGGTTTACCAACCACTCTCTCCGATCACC 1080
QY 1386 ATCCTTCCGCAAGCAATACCTGCGGCAAGTGTGGAAGATGTGGCCACGTCCTCCAGAGACTGT 1445
Db 1081 ATCCTTCCGCAAGCAATACCTGCGGCAAGTGTGGAAGATGTGGCCACGTCCTCCAGAGACTGT 1140
QY 1446 TACAAGTTTGGCATCTCAGTCTACCTACCCAGGCGGCTGTTATGGAGCTGTTATCATGGAG 1505
Db 1141 TACAAGTTTGGCATCTCAGTCTACCTACCCAGGCGGCTGTTATGGAGCTGTTATCATGGAG 1200
QY 1506 GGCCTTACGTTGCTTTGATCGGGCCGAAACAGAAATGGCTTTGCTGTGTCAGGCTTTC 1565
Db 1201 GGCCTTACGTTGCTTTGATCGGGCCGAAACAGAAATGGCTTTGCTGTGTCAGGCTTTC 1260
QY 1566 CATGTGACGATGAGTTGAGGACGCGAGCGGTGGAAGGCCCTTTTGTACCTTCGACATG 1625
Db 1261 CATGTGACGATGAGTTGAGGACGCGAGCGGTGGAAGGCCCTTTTGTACCTTCGACATG 1320
QY 1626 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCA 1664
Db 1321 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCA 1359

Query Match	55.3%	Score 1298;	DB 4;	Length 1506;
Best Local Similarity	91.4%	Pred. No. 0;		
Matches 1376;	Conservative	0;	Mismatches 130;	Indels 0; Gaps 0;
QY 306	ATGGCCCAAGCCCTGGCCTCTGCTGTGTGGATGGGCGGGAGTGCCTGCCCTGCCAC	365		
DB 1	ATGGCCCAAGCCCTGGCCTCTGCTATGGGTGGGCTCGGGAATGCTGCCCTGCCAC	60		
QY 366	GGCACCACGACGAGCATCCGGCTGCCCTTGCACAGCGGCTTGGGCGCGCCCTCGGG	425		
DB 61	GGAAACCATCTCGGCATCCGGCTGCCCTTCCAGCGGCTTGCAGGGCCACCCCTGGGC	120		
QY 426	CTCGGCTGCCCGGGAGACGACGAAGAGCCCGAGAGCCCGCGCGAGGGGAGCTTT	485		
DB 121	CTGAGGCTGCCCGGGAGACGACGAGGAATCGAGAGCCTTGCCCGGAGAGGAGCTTT	180		
QY 486	GTGGAGATGTGGACACCTGAGGGGCAAGTCGGGGCAGGGCTTACTGTGGAGATGACC	545		
DB 181	GTGGAGATGTGGACACCTGAGGGGAAAGTCGGGGCAGGGCTTACTGTGGAGATGACC	240		
QY 546	GTGGGAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTCCA	605		
DB 241	GTAGGAGCCCCCGCACAGAGCTCAACATCCTGGTGGACAGGGCAGTAGTAACCTTCCA	300		
QY 606	GTGGGTGCTGCCCGCCCAACCCCTTCTCGATCCGCTACTACAGAGGCAAGCTGTCCAGCACA	665		

Db 301 GTGGGGCTGCCACACACCCCTTTCCTGCATCGCTACTACCAGAGGAGCTGTCCAGCACA 360
Qy TACCGGGACCTCCGGAAGGCTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG 725
Db 361 TATCGAGACCTCGGAAGGCTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAA 420
Qy CTGGCACCAGCCTGGTAAGCATCCCCCATGGGCCCAACCTCACTGTGCGTGCCAACATT 785
Db 421 CTGGCACCAGCCTGGTAAGCATCCCCCATGGGCCCAACCTCACTGTGCGTGCCAACATT 480
Qy 786 GTGGCCATCACTGAATCAGACAAGTTCTTCATCAAGGCTCCAACTGGGAAGGCATCCTG 845
Db 481 GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGTTTCCAACCTGGGAGGCATCCTA 540
Qy 846 GGCTGGCTTCTGATGATGGCAGGCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 905
Db 541 GGCTGGCTTCTGATGATGGCAGGCTGACGACTCTTTGGAGCCTTTCTTTGACTCC 600
Qy 906 CTGCTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGCAGCTTTGTGCTGGCTTC 965
Db 601 CTGCTGAAGCAGACCCATCTCCCAACATCTTTCCCTGCAGCTCTGTGGCGTGGCTTC 660
Qy 966 CCCTCAACAGCTCTGAAGTCTGGGCTCTGTGCGAGGGAGCATGATCATTTGGAGGTATC 1025
Db 661 CCCTCAACAGCAGCCAGGCACTGGGCTCGGTGGGAGGAGCATGATCATTTGGTGTATC 720
Qy 1026 GACCACTCGCTTACACAGCAGCTCTCTGTATACACCCATCCGGCGGGAGTGGTATTAT 1085
Db 721 GACCACTCGCTTACACAGGCACTCTGTGTACACCCATCCGGCGGGAGTGGTATTAT 780
Qy 1086 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGCATCTGAATATGGACTGCAAGGAG 1145
Db 781 GAAGTGATCATTTGACGTGTGGAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG 840
Qy 1146 TACAATATGACAAGACATTTGGAGACATGGGCACACCAACCTTCGTTTGGCCCAAGAAA 1205
Db 841 TACAATATGACAAGACATTTGGAGACATGGGCACACCAACCTTCGTTTGGCCCAAGAAA 900
Qy 1206 GTGTTTGAAGCTGCAGTCAATCATCAAGCAGCAGCTTCCTCCAGGAGAGTTCCCTGAT 1265
Db 901 GTATTTGAAGCTGCCGTCAAGTCCATCAAGCAGCAGCTTCCTCCAGGAGAGTTCCCGGAT 960
Qy 1266 GTTCTTCTGCTAGGAGACAGCTGGTGTGCTGGCAAGCAGCAGCAGCTTGGAAACATT 1325
Db 961 GGCTTTGGCTAGGAGACAGCTGGTGTGCTGGCAAGCAGCAGCAGCTTGGAAACATT 1020
Qy 1326 TTCCAGTCACTCACTCTACCTAATGGGTGAGTTTACCACCAAGTCTTCCCGCATCACC 1385
Db 1021 TTCCAGTCACTCTACCTAATGGGTGAGTTTACCACCAAGTCTTCCCGCATCACC 1080
Qy 1386 ATCTTTCCGAGCAATACCTCGGCCAGTGAAGATGTGCCAGCTGCCAAGACGACTGT 1445
Db 1081 ATCTTTCCCTCAGCAATACCTACGCGCGGTGGAGGAGCTGGCCAGCTGCCAAGACGACTGT 1140
Qy 1446 TACAAGTTTGGCATCTCACAGTATCCACAGGCACTGTATGGAGCTGTATATCATCGAG 1505
Db 1141 TACAAGTTTGGCATCTCACAGTATCCACAGGCACTGTATGGAGCGCTCATCATCGAA 1200
Qy 1506 GGCTTCTACGTTGTCTTTGATCGGGCCCGGAAAGAAATGGCTTTGCTGTACGCGTTGC 1565
Db 1201 GGTTCCTATGTGCTTTCGATCGAGCCCGGAAAGCAATTTGGCTTTGCTGTACGCGCTTC 1260
Qy 1566 CATGTGCACATGATTTACAGAGCGGAGCGGTGGAAGGCCCTTTTGTACCTTTGGAGATG 1625
Db 1261 CATGTGCACATGATTTACAGAGCGGCGGAGTGGGAAGGTCCGTTTGTACGCGACATG 1320
Qy 1626 GAAGACTGTGGCTACAACATTCCACACACAGATGAGTCAACCTTCATGACCATAGCCTAT 1685
Db 1321 GAAGACTGTGGCTACAACATTCCACACACAGATGAGTCAACATTTATGACCATAGCCTAT 1380
Qy 1686 GTCATGGCTGCCATCTCGGCCCTCTTTCATGCTGCCACTCTGCCTCATGTTGTCACTGG 1745

Db 1381 GTCATGGCGCCATCTGCGCCCTTTCATCTTGCCTCTGCTATGTTGCTAGTGG 1440
Qy 1746 CGCTGCTCCGCTGCGCTGCGCCAGCAGCATGATGACTTTTCTGATGACATCTCCCTGCTG 1805
Db 1441 CGCTGCTCCGCTGCGCTGCGCCAGCAGCATGATGACTTTTCTGATGACATCTCCCTGCTG 1500
Qy 1806 AAGTGA 1811
Db 1501 AAGTGA 1506

RESULT 14
US-09-548-372D-21
; Sequence 21, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-21

Query Match 55.1%; Score 1293.8; DB 4; Length 1341;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 368 CACCCAGCAGCGCATCCGGCTGCCCCCTGCGCAGCGGCTGGGGGGCCCCCCCCCTGGGGCT 427
Db 42 CACCCAGCAGCGCATCCGGCTGCCCCCTGCGCAGCGGCTGGGGGGCCCCCCCCCTGGGGCT 101
Qy 428 CGGGCTGCCCGGGAGAGCCAGCAGAGAGCCGAGGAGCCCGGGCGGAGGGGCGACTTTGT 487
Db 102 CGGGCTGCCCGGGAGAGCCAGCAGAGAGCCGAGGAGCCCGGGCGGAGGGGCGACTTTGT 161
Qy 488 GGAGATGGTGACAACTGAGGGGCAAGTCGGGCGAGGCTACTACGTGGAGATGACCGT 547
Db 162 GGAGATGGTGACAACTGAGGGGCAAGTCGGGCGAGGCTACTACGTGGAGATGACCGT 221
Qy 548 GGGCAGCCCCCGGAGAGCGCTCAACATCTCTGGTGATACAGGAGCAGTAACTTTGCACT 607
Db 222 GGGCAGCCCCCGGAGAGCGCTCAACATCTCTGGTGATACAGGAGCAGTAACTTTGCACT 281
Qy 608 GGGTGTGCCCCCGGAGAGCGCTTCTGCTGCTACTACAGAGGAGCTGTCCAGACATA 667
Db 282 GGGTGTGCCCCCGGAGAGCGCTTCTGCTGCTACTACAGAGGAGCTGTCCAGACATA 341
Qy 668 CCGGAGCTCCGGAAGGCTGTATGTGCCCCCTACACCCAGGCAAGTGGGAAGGGGAGCT 727
Db 342 CCGGAGCTCCGGAAGGCTGTATGTGCCCCCTACACCCAGGCAAGTGGGAAGGGGAGCT 401
Qy 728 GGGCAGCGACTGTGTAAGCATCCCGCATGCCCCCAAGCTACTGTGGTGCCAACTTTC 787
Db 402 GGGCAGCGACTGTGTAAGCATCCCGCATGCCCCCAAGCTACTGTGGTGCCAACTTTC 461
Qy 788 TGCCATCACTGAATCAGACAAGTTTCTTCATCAACGGCTTCCAACTGGGAAGGAGCATCTCCG 847
Db 462 TGCCATCACTGAATCAGACAAGTTTCTTCATCAACGGCTTCCAACTGGGAAGGAGCATCTCCG 521

QY	848	CCTGGCCATATGCTGAGATTGCCAGGCCTGCACGACTCCCTTGGAGCCCTTTCTTGACCTCTCT	907
Db	522	GCTGGCCTATGCTGAGATTGCCAGGCCTGCACGACTCCCTTGGAGCCCTTTCTTGACCTCTCT	581
QY	908	GGTAAGAGCAGACCCACGTTCCCAACCTCTCTTCCTCGCAGCTTTGTGGTGCTGGCTTCCC	967
Db	582	GGTAAGAGCAGACCCACGTTCCCAACCTCTCTTCCTCGCAGCTTTGTGGTGCTGGCTTCCC	641
QY	968	CCTCAACAGTCTGAAGTGTGGCCTCTGTTCGGAGGAGCATGATCATTTGGAGGTATPCGA	1027
Db	642	CCTCAACAGTCTGAAGTGTGGCCTCTGTTCGGAGGAGCATGATCATTTGGAGGTATPCGA	701
QY	1028	CCACTCGCTGTACACAGCAGTCTCTGGTATACACCATCCGGCGGAGTGGTATTATGA	1087
Db	702	CCACTCGCTGTACACAGCAGTCTCTGGTATACACCATCCGGCGGAGTGGTATTATGA	761
QY	1088	GGTGATCATTTGTGGGGTGGAGATCAATGGACAGGATCTGAAAATGGAGTGCAGAGGTA	1147
Db	762	GGTGATCATTTGTGGGGTGGAGATCAATGGACAGGATCTGAAAATGGAGTGCAGAGGTA	821
QY	1148	CAACTATCACAAAGACATTTGGACAGTGGCACCAACCAACCTTCGTTTCCCCAAGAAGT	1207
Db	822	CAACTATCACAAAGACATTTGGACAGTGGCACCAACCAACCTTCGTTTCCCCAAGAAGT	881
QY	1208	GTTTTGAAGCTGCAGTCAAATCCATCAAGCAGCCCTCTCCAGGGAGAAGTTCOCCTGATGG	1267
Db	882	GTTTTGAAGCTGCAGTCAAATCCATCAAGCAGCCCTCTCCAGGGAGAAGTTCOCCTGATGG	941
QY	1268	TTTTCTGGCTAGGAGACGCTGGTGTGCTGGCAGCAGCAGCACCCCTTTGGAACAATTTT	1327
Db	942	TTTTCTGGCTAGGAGACGCTGGTGTGCTGGCAGCAGCAGCACCCCTTTGGAACAATTTT	1001
QY	1328	CCCAGTCAATCTCACCTTACCTAANTGGGTGAGGTATACCAACAGTCCCTCCGCAATCACCAT	1387
Db	1002	CCCAGTCAATCTCACCTAANTGGGTGAGGTATACCAACAGTCCCTCCGCAATCACCAT	1061
QY	1388	CCTTCCGAGCAATACTTCGGGCCAGTGGAGAATGTGGCCACGTCCCAAGACACTGTGTTA	1447
Db	1062	CCTTCCGAGCAATACTTCGGGCCAGTGGAGAATGTGGCCACGTCCCAAGACACTGTGTTA	1121
QY	1448	CAAGTTTGCCATCTCACAGTCATCCACGGGCACCTGTATGGAGCTGTATATGAGGG	1507
Db	1122	CAAGTTTGCCATCTCACAGTCATCCACGGGCACCTGTATGGAGCTGTATATGAGGG	1181
QY	1508	CTTCTACGTTGTCTTTGATTCGGGCCCGGAACGAATTTGGCTTTGTGTGTCAGCGCTTGCCA	1567
Db	1182	CTTCTACGTTGTCTTTGATTCGGGCCCGGAACGAATTTGGCTTTGTGTGTCAGCGCTTGCCA	1241
QY	1568	TGTGCACGATGAGTTTCAGAGCGGACGGGTGGAAGGCCCTTTTGTCACTCTTGACATGGA	1627
Db	1242	TGTGCACGATGAGTTTCAGAGCGGACGGGTGGAAGGCCCTTTTGTCACTCTTGACATGGA	1301
QY	1628	AGACTGTGGCTACAACTATTCACACAGACAGATGAGTCA	1664
Db	1302	AGACTGTGGCTACAACTATTCACACAGACAGATGAGTCA	1338

RESULT 15
US-09-548-367D-21
; Sequence 21, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23

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; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-367D-21

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	Query Match	55.1%;	Score 1293.8;	DB 4;	Length 1341;
	Best Local Similarity	99.8%;	Pred. No. 0;		
	Matches 1295;	Conservative	0;	Mismatches	2; Indels 0; Gaps 0;
Qy	368	CACCCAGACGCGATCCGGCTGCGCTGCGACAGCGGCTGGGGCGCCCCCTCGGGGCT	427		
Db	42	CACCCAGACGCGATCCGGCTGCGCTGCGACAGCGGCTGGGGCGCCCCCTCGGGGCT	101		
Qy	428	CGGCTGCCCGGGGACCGACGAAGAGCCGAGAGCCCGCGCGAGGGGAGCTTTGCT	487		
Db	102	CGGCTGCCCGGGGACCGACGAAGAGCCGAGAGCCCGCGCGAGGGGAGCTTTGCT	161		
Qy	488	GGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGT	547		
Db	162	GGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGT	221		
Qy	548	GGGACGCCCCCGCAGACGCTCAACATCTCTGGTGGATACGGCAGCAGTAACCTTTCAGT	607		
Db	222	GGGACGCCCCCGCAGACGCTCAACATCTCTGGTGGATACGGCAGCAGTAACCTTTCAGT	281		
Qy	608	GGGTGCTGCCCGCCCCACCCCTTTCGTGCTGCTACTACAGAGGAGCTGTCCAGCACATA	667		
Db	282	GGGTGCTGCCCGCCCCACCCCTTTCGTGCTGCTACTACAGAGGAGCTGTCCAGCACATA	341		
Qy	668	CCGGACCTCCGGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGAGCT	727		
Db	342	CCGGACCTCCGGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGAGCT	401		
Qy	728	GGGACCGACCTGGTAAGGATCCCCCATGCCCAAGGTCACTGTGCGTGGCAACATTCG	787		
Db	402	GGGACCGACCTGGTAAGGATCCCCCATGCCCAAGGTCACTGTGCGTGGCAACATTCG	461		
Qy	788	TGCCATCACTGAATCAGACAAAGTTCTTTCATCAACGGCTCCAACTGGGAAGGCACTCCTGGG	847		
Db	462	TGCCATCACTGAATCAGACAAAGTTCTTTCATCAACGGCTCCAACTGGGAAGGCACTCCTGGG	521		
Qy	848	GCTGGCCTATGCTGAGATTGCCAGGCGTGAGGACTCCCTGGAGGCTTTCTTTGACTCTCT	907		
Db	522	GCTGGCCTATGCTGAGATTGCCAGGCGTGAGGACTCCCTGGAGGCTTTCTTTGACTCTCT	581		
Qy	908	GGTAAGGAGACCCAGTTGCCAACCTCTTCTCCCTGCGAGCTTTCTGTGCTGGCTTCCC	967		
Db	582	GGTAAGGAGACCCAGTTGCCAACCTCTTCTCCCTGCGAGCTTTCTGTGCTGGCTTCCC	641		
Qy	968	CCTCAACAGCTGTAAGTGTGGCCTCTGTGGAGGGAGCATGATCATTTGGAGGTATCGA	1027		
Db	642	CCTCAACAGCTGTAAGTGTGGCCTCTGTGGAGGGAGCATGATCATTTGGAGGTATCGA	701		
Qy	1028	CCACTCGCTGTATACAGGCGAGTCTGGTATACACCCATCCGGGGGAGTGGTATATCA	1087		
Db	702	CCACTCGCTGTATACAGGCGAGTCTGGTATACACCCATCCGGGGGAGTGGTATATCA	761		
Qy	1088	GGTGATCATTTGTGGGGTGGAGATCAATGGACAGGATCTGAAATGGAGCTGCAAGGATTA	1147		
Db	762	GGTGATCATTTGTGGGGTGGAGATCAATGGACAGGATCTGAAATGGAGCTGCAAGGATTA	821		
Qy	1148	CAACTATCAGACAGCATTTGGACAGTGGCACCACCAACCTTCGTTTGCCTCAAGAACT	1207		
Db	822	CAACTATCAGACAGCATTTGGACAGTGGCACCACCAACCTTCGTTTGCCTCAAGAACT	881		
Qy	1208	GTTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCGCTCTCTCCACGGGAAGATTTCCCTGATGG	1267		


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|||||
Db 882 GTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCGCTCTCCACGGAGAAGTTCCCTGATGG 941
QY 1268 TTTCTGGCTAGGAGAGCAGCTGGTGTGCTGCAAGCAGGACACCCCTTTGGACATTTT 1327
Db 942 TTTCTGGCTAGGAGAGCAGCTGGTGTGCTGCAAGCAGGACACCCCTTTGGACATTTT 1001
QY 1328 CCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACAGTCCCTTCGCGCATCACCAT 1387
Db 1002 CCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACAGTCCCTTCGCGCATCACCAT 1061
QY 1388 CCTTCCGACAGCAATACCTGCGGCGAGTGGGAAGATGTGGCCACGTCGCCAAGACGACTGTTA 1447
Db 1062 CCTTCCGACAGCAATACCTGCGGCGAGTGGGAAGATGTGGCCACGTCGCCAAGACGACTGTTA 1121
QY 1448 CAAGTTTGGCCATCTCACAGTCATCCACGGGCACCTGTTATGGAGCTGTTATCATGGAGGG 1507
Db 1122 CAAGTTTGGCCATCTCACAGTCATCCACGGGCACCTGTTATGGAGCTGTTATCATGGAGGG 1181
QY 1508 CTTCTACGTTGTCTTTGATCGGGCCCGAAACGAATTTGGCTTTGCTGTACGCGCTTGCCA 1567
Db 1182 CTTCTACGTTGTCTTTGATCGGGCCCGAAACGAATTTGGCTTTGCTGTACGCGCTTGCCA 1241
QY 1568 TGTCCACGATGAGTTCAGGACGGCAGCGGTGGGAAGGCCCTTTTGTACCTTTGGACATGGA 1627
Db 1242 TGTGCACGATGAGTTCAGGACGGCAGCGGTGGGAAGGCCCTTTTGTACCTTTGGACATGGA 1301
QY 1628 AGACTGTGGCTACAACATTCACAGACAGATGAGTCA 1664
Db 1302 AGACTGTGGCTACAACATTCACAGACAGATGAGTCA 1338
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Search completed: March 2, 2003, 06:16:13
Job time : 76 secs

QY 366 GGCACCCAGCAGCATCCGGCTGCCCTGCGAGCGGCTGGGGGCGCCGCCCTGGG 425
Db 61 GGCACCCAGCAGCATCCGGCTGCCCTGCGAGCGGCTGGGGGCGCCGCCCTGGG 120
QY 426 CTGGGCTGCCCGGAGACGACGAGCCGAGGAGCCCGCGCGGAGGGGCGAGCTTT 485
Db 121 CTGGGCTGCCCGGAGACGACGAGCCGAGGAGCCCGCGCGGAGGGGCGAGCTTT 180
QY 486 GTGGAGATGTGTGACAACTCTGAGGGGCAAGTCGGGCGAGGGCTTACTACGTGGAGATGACC 545
Db 181 GTGGAGATGTGTGACAACTCTGAGGGGCAAGTCGGGCGAGGGCTTACTACGTGGAGATGACC 240
QY 546 GTGGGACGCCCCCGCAGACGCTCAACATCTGTGGTGATACAGGACGAGCTTAATTTGCA 605
Db 241 GTGGGACGCCCCCGCAGACGCTCAACATCTGTGGTGATACAGGACGAGCTTAATTTGCA 300
QY 606 GTGGGTCTGCCCGCCCGCAGCCCTTCTGCTGATCCCTACTACCAGAGGAGCTGTCCAGCACA 665
Db 301 GTGGGTCTGCCCGCCCGCAGCCCTTCTGCTGATCCCTACTACCAGAGGAGCTGTCCAGCACA 360
QY 666 TACCGGGACCTCCCGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 725
Db 361 TACCGGGACCTCCCGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
QY 726 CTGGGACCGACCTGGTAAGCATCCCCCATGGCCCGCAACGTCACTGTGCGTGGCCAACTT 785
Db 421 CTGGGACCGACCTGGTAAGCATCCCCCATGGCCCGCAACGTCACTGTGCGTGGCCAACTT 480
QY 786 GCTGCCATCACTGAATCAGACAACTTCTCATCAAGGCTCCAACCTGGGAAGGCATCCTG 845
Db 481 GCTGCCATCACTGAATCAGACAACTTCTCATCAAGGCTCCAACCTGGGAAGGCATCCTG 540
QY 846 GGGCTGGCCCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCCTTTCTTTTGACTCT 905
Db 541 GGGCTGGCCCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCCTTTCTTTTGACTCT 600
QY 906 CTGGTAAGCAGACCCAGCTTCCCAACCTCTCTCCCTGCAAGTTGTGGTGTGGCTTC 965
Db 601 CTGGTAAGCAGACCCAGCTTCCCAACCTCTCTCCCTGCAAGTTGTGGTGTGGCTTC 660
QY 966 CCCTCAACAGCTCTGAAGTCTGGCCCTGTGCGGAGGAGCATGATCACTTGGAGGTATC 1025
Db 661 CCCTCAACAGCTCTGAAGTCTGGCCCTGTGCGGAGGAGCATGATCACTTGGAGGTATC 720
QY 1026 GACCACTCGCTGTACACAGGAGCTCTCTGGTATACACCCATCCGGCGGAGTGGTATTAT 1085
Db 721 GACCACTCGCTGTACACAGGAGCTCTCTGGTATACACCCATCCGGCGGAGTGGTATTAT 780
QY 1086 GAGGTGATCATTTGTGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 1145
Db 781 GAGGTGATCATTTGTGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 840
QY 1146 TACAACCTATCACAAGACATTTGTGACAGTGGCACACCAACCTTCGTTTGGCCCAAGAAA 1205
Db 841 TACAACCTATCACAAGACATTTGTGACAGTGGCACACCAACCTTCGTTTGGCCCAAGAAA 900
QY 1206 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCCTCTCCACGGAGAGTTCCCTGTAT 1265
Db 901 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGCCTCTCCACGGAGAGTTCCCTGTAT 960
QY 1266 GGTTCCTGGCTAGAGAGCAGCTGGTGTGGGCAAGCAGGACACCCCTTGGAAACATT 1325
Db 961 GGTTCCTGGCTAGAGAGCAGCTGGTGTGGGCAAGCAGGACACCCCTTGGAAACATT 1020
QY 1326 TTCCCACTATCTCACTCTACCTAATGGGTGAGGTTACCAACAGTCTTCCGCATCACC 1385
Db 1021 TTCCCACTATCTCACTCTACCTAATGGGTGAGGTTACCAACAGTCTTCCGCATCACC 1080
QY 1386 ATCCTTCCGAGCAATACCTCGGCGCAGTGGGAAGATGTGGCCACGCTCCCAAGACGACTGT 1445
Db 1081 ATCCTTCCGAGCAATACCTCGGCGCAGTGGGAAGATGTGGCCACGCTCCCAAGACGACTGT 1140
QY 1446 TACAAGTTTCCCATCTCACAGTCACTCCACGGGCATGTTATGGGAGCTGTTATCATGGAG 1505

Db 1141 TACAAGTTTCCCATCTCACAGTCACTCCACGGGCATGTTATGGAGCTGTTATCATCGAG 1200
QY 1506 GGCTTCTACCTTGTCTTTGATCGGGCCGAAAACGAATTTGGCTTCTGTCAGGCTTGC 1565
Db 1201 GGCTTCTACCTTGTCTTTGATCGGGCCGAAAACGAATTTGGCTTCTGTCAGGCTTGC 1260
QY 1566 CATGTGCACGATGAGTTTCAGGACGCGAGCGGTGGAAGGCCCTTTTGTCTACCTTTGGACATG 1625
Db 1261 CATGTGCACGATGAGTTTCAGGACGCGAGCGGTGGAAGGCCCTTTTGTCTACCTTTGGACATG 1320
QY 1626 GAAGACTGTGGCTACAACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCATT 1685
Db 1321 GAAGACTGTGGCTACAACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCATT 1380
QY 1686 GTCATGCTGCCATCTGGGCCCTCTTTCATGCTGCCACTCTGCTTCATGCTGTGTCTACATGG 1745
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QY 1746 CGCTGCCCTCGCTGCCCTGCGCCAGCAGCATGATGACTTTTGTCTGATGACATCTCCCTGCTG 1805
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Db 1501 AAGTGAAGGCGCCCATGGGCAGAGATAGAGATTTCCCTTGGACACACCTTCCGTGGTTCA 1560
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Db 1621 CCACCCACCAATTCCTTTCATGAGAGAAAGGCTGGCAAGGTGGGTTCAG 1680
QY 1986 GGAATGTACCTGTAGGAAACAGAAAGAGAGAAAGAGCAGCTCTGCTGGCGGGAATACT 2045
Db 1681 GGAATGTACCTGTAGGAAACAGAAAGAGAGAAAGAGCAGCTCTGCTGGCGGGAATACT 1740
QY 2046 CTTTGTGTCACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 2105
Db 1741 CTTTGTGTCACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 1800
QY 2106 TTGTCCACCATTCCTTTAAATTTCTCCAAACCCAAAGTATTTCTTTTCTTAGTTTCAGAA 2165
Db 1801 TTGTCCACCATTCCTTTAAATTTCTCCAAACCCAAAGTATTTCTTTTCTTAGTTTCAGAA 1860
QY 2166 GTACTGGCATCACAGCAGGTTACCTTGGCGTGTGTCCTGTGGTACCCCTGGCAGAGAAG 2225
Db 1861 GTACTGGCATCACAGCAGGTTACCTTGGCGTGTGTCCTGTGGTACCCCTGGCAGAGAAG 1920
QY 2226 AGACCAAGCTTGTTCCTTCCCTGGCCAAAGTCAAGTCAAGAGAGATGCACAGTTTGTCTATT 2285
Db 1921 AGACCAAGCTTGTTCCTTCCCTGGCCAAAGTCAAGTCAAGAGAGATGCACAGTTTGTCTATT 1980
QY 2286 TGTCTTAGAGACAGGAGCTGTATAAACAGCCTAACATTTGGTGCCAAAGATGGCTCTTGA 2345
Db 1981 TGTCTTAGAGACAGGAGCTGTATAAACAGCCTAACATTTGGTGCCAAAGATGGCTCTTGA 2040
QY 2346 ATT 2348
Db 2041 ATT 2043

RESULT 2
US-09-795-847-3
; Sequence 3, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.

APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 28341/6280DE
CURRENT APPLICATION NUMBER: US/09/795.847
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2070
TYPE: DNA
ORGANISM: Homo sapiens
US-09-795-847-3

Query Match 86.9%; Score 2039.8; DB 10; Length 2070;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	306	ATGGCCCCAAGCCCTGCGCTCTCTGTGTGGATGGCGGGGAGTGTGCTGCTGCCAC	365
Db	1	ATGGCCCCAAGCCCTGCGCTCTCTGTGTGGATGGCGGGGAGTGTGCTGCTGCCAC	60
Qy	366	GGCACCCAGCAGCATCCGCTGCCCTGGCGAGCGCTGGGGGGCCCCCTGGGG	425
Db	61	GGCACCCAGCAGCATCCGCTGGCGAGCGCTGGGGGGCCCCCTGGGG	120
Qy	426	CTGGGCTGCCCGGGAGACCGACGAAGAGCCGAGGAGCCCGCGGAGGGGCACTTT	485
Db	121	CTGGGCTGCCCGGGAGACCGACGAAGAGCCGAGGAGCCCGCGGAGGGGCACTTT	180
Qy	486	GTGAGATGTGGACAACCTGAGGGGCAAGTCGGGGAGGGCTACTAGTGGAGATGACC	545
Db	181	GTGAGATGTGGACAACCTGAGGGGCAAGTCGGGGAGGGCTACTAGTGGAGATGACC	240
Qy	546	GTGGCAGCCCCCGCAGACGCTCAACATCTGTGTGGATACAGGAGCAGTAACCTTGA	605
Db	241	GTGGCAGCCCCCGCAGACGCTCAACATCTGTGTGGATACAGGAGCAGTAACCTTGA	300
Qy	606	GTGGGTGTGCCCCCCCCACCCCTTCCTGTCATCGCTACTACAGAGCAGCTGTCCAGCA	665
Db	301	GTGGGTGTGCCCCCCCCACCCCTTCCTGTCATCGCTACTACAGAGCAGCTGTCCAGCA	360
Qy	666	TACCGGACCTCCGGAAGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGAG	725
Db	361	TACCGGACCTCCGGAAGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGAG	420
Qy	726	CTGGCAGCCGACCTGGTAAGCATCCCATGSCCCCAACGTCACGTGCGTSCCAACATT	785
Db	421	CTGGCAGCCGACCTGGTAAGCATCCCATGSCCCCAACGTCACGTGCGTSCCAACATT	480
Qy	786	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAAGGCTCCAACTGGGAAGGCATCCGT	845
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAAGGCTCCAACTGGGAAGGCATCCGT	540
Qy	846	GGGCTGGCCTATGTGTAGATGGCCAGGCTGACGACTCCCTGGAGCCCTTCCTTTGACTCT	905
Db	541	GGGCTGGCCTATGTGTAGATGGCCAGGCTGACGACTCCCTGGAGCCCTTCCTTTGACTCT	600
Qy	906	CTGGTAAAGCAGACCCAGCTTCCCAACCTCTCTCCCTGCAGCTTTGTGGTCTGGCTTC	965
Db	601	CTGGTAAAGCAGACCCAGCTTCCCAACCTCTCTCCCTGCAGCTTTGTGGTCTGGCTTC	660
Qy	966	CCCTCAACCAAGTCTGAAGTGTGCTGCTGTGGAGGAGCATGATCATTTGGAGTATC	1025
Db	661	CCCTCAACCAAGTCTGAAGTGTGCTGCTGTGGAGGAGCATGATCATTTGGAGTATC	720
Qy	1026	GACCACTCGCTGTACACAGGAGTCTCTGGTATACACCATCCCGGGGAGTGTATTAT	1085
Db	721	GACCACTCGCTGTACACAGGAGTCTCTGGTATACACCATCCCGGGGAGTGTATTAT	780
Qy	1086	GAGGTGATCATTTGTCGGGTGGAGATCAATGGACAGGATCTGAAAATGAGCTGCAAGGAG	1145
Db	781	GAGGTGATCATTTGTCGGGTGGAGATCAATGGACAGGATCTGAAAATGAGCTGCAAGGAG	840
Qy	1146	TACAACTATGACAAGAGCATTTGTGACAGTGGCACCAACCAACCTTCGTTTGGCCCAAGAA	1205
Db	841	TACAACTATGACAAGAGCATTTGTGACAGTGGCACCAACCAACCTTCGTTTGGCCCAAGAA	900
Qy	1206	GTGTTTGAAGCTGCAAGTCAAAATCCATCAAGGAGGAGCTCTCCACGAGAGTTCCTGTAT	1265
Db	901	GTGTTTGAAGCTGCAAGTCAAAATCCATCAAGGAGGAGCTCTCCACGAGAGTTCCTGTAT	960
Qy	1266	GGTTTCTGGCTAGGAGAGCAGCTGTGTGCTGGCAAGCAGGACCAACCCCTTTGGAACTT	1325
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGTGTGCTGGCAAGCAGGACCAACCCCTTTGGAACTT	1020
Qy	1326	TTCCCACTCATCTCACTACTACCTAATGGGTGAGTTTACCAACAGTTCCTTCGCGCATCAC	1385
Db	1021	TTCCCACTCATCTCACTACTACCTAATGGGTGAGTTTACCAACAGTTCCTTCGCGCATCAC	1080
Qy	1386	ATCCTTCCGCGAGCAATACCTGGCGCCAGTGGGAAGATGTGGCCACGTCCTCCAAAGACACTGT	1445
Db	1081	ATCCTTCCGCGAGCAATACCTGGCGCCAGTGGGAAGATGTGGCCACGTCCTCCAAAGACACTGT	1140
Qy	1446	TACAACTTGGCATCTCACAGTCATCCAGGCGACTGTATGGAGCTGTTATCATGGAG	1505
Db	1141	TACAACTTGGCATCTCACAGTCATCCAGGCGACTGTTATGGAGCTGTTATCATGGAG	1200
Qy	1506	GGCTTCTACGTTGTCTTTGATCGGGCCGAAACAACTTGGCTTTGCTGTACGCGCTTCG	1565
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCGAAACAACTTGGCTTTGCTGTACGCGCTTCG	1260
Qy	1566	CATGTGACGATGAGTTTACGAGCGCAGCGGTGGGAAGGCCCTTTTGTACCTTGGACATG	1625
Db	1261	CATGTGACGATGAGTTTACGAGCGCAGCGGTGGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1626	GAAGACTGTGGCTCAACATTCACAGACAGATGATGATCAACCTCATGACCATAGCCTAT	1685
Db	1321	GAAGACTGTGGCTCAACATTCACAGACAGATGATGATCAACCTCATGACCATAGCCTAT	1380
Qy	1686	GTATGGGTGGCATCTGGGCCCTCTTTCATGTGCCACTCTGCTCATGTGTGTGAGTGG	1745
Db	1381	GTATGGGTGGCATCTGGGCCCTCTTTCATGTGCCACTCTGCTCATGTGTGTGAGTGG	1440
Qy	1746	CGCTGCCCTCCGCTGGCCAGCAGCATGATGACTTTGCTGTATGACATCTCCCTGCTG	1805
Db	1441	CGCTGCCCTCCGCTGGCCAGCAGCATGATGACTTTGCTGTATGACATCTCCCTGCTG	1500
Qy	1806	AACTGAGGAGGCCATGGCAGAAATAGAGATTCCCTGGACCAACCTCCCTGGTTTCA	1865
Db	1501	AACTGAGGAGGCCATGGCAGAAATAGAGATTCCCTGGACCAACCTCCCTGGTTTCA	1560
Qy	1866	CTTTGGTCAACAGTAGGACACAGATGSCACTGTGGCCAGAGCAGCTCAGGACCCCTCC	1925
Db	1561	CTTTGGTCAACAGTAGGACACAGATGSCACTGTGGCCAGAGCAGCTCAGGACCCCTCC	1620
Qy	1926	CCACCCCAAAATGCTCTGCTTTCATGGAGAAGAAAGGCTGGCAAGTGGTGTCCAG	1985
Db	1621	CCACCCCAAAATGCTCTGCTTTCATGGAGAAGAAAGGCTGGCAAGTGGTGTCCAG	1680
Qy	1986	GGACTGTACCTGTAGAAACAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	2045
Db	1681	GGACTGTACCTGTAGAAACAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	1740
Qy	2046	CTTTGGTCAACCTCAAAATTTAAGTCGGGAAATTTCTGCTGTGAAACTTCAGCCCTGAACCT	2105

Db 1741 CTGGTACCTCAAAATTTAAGTCGGAAATTCGCTCTTGAAACTTCAGCCCTGAACCT 1800
QY 2106 TTGTCCACCATCTTAAATTTCTCAACCCAAAGTATCTCTTTCTTCTAGTTTTCAGAA 2165
Db 1801 TTGTCCACCATCTTAAATTTCTCAACCCAAAGTATCTCTTTCTTCTAGTTTTCAGAA 1860
QY 2166 GTACTGGCATCACAGCAGGTTACCTTTGGGCTGTGTCCCTGTGTGTACCTTGGCAGAGAAG 2225
Db 1861 GTACTGGCATCACAGCAGGTTACCTTTGGGCTGTGTCCCTGTGTGTACCTTGGCAGAGAAG 1920
QY 2226 AGACCAAGCTTGTTCCTTCGTCGGCCAAAGTCAGTAGAGAGGATGACAGTTTCTCTATT 2285
Db 1921 AGACCAAGCTTGTTCCTTCGTCGGCCAAAGTCAGTAGAGAGGATGACAGTTTCTCTATT 1980
QY 2286 TGCTTTAGACAGAGGACTGTATAAACAAGCCCTAACATTTGTCGCAAGATTGCTCTTTGA 2345
Db 1981 TGCTTTAGACAGAGGACTGTATAAACAAGCCCTAACATTTGTCGCAAGATTGCTCTTTGA 2040
QY 2346 ATT 2348
Db 2041 ATT 2043

RESULT 3

US-09-794-743-3
; Sequence 3, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-743-3

Query Match 86.9%; Score 2039.8; DB 10; Length 2070;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 306 ATGCCCAAGCCCTGCCCTGGCTCTCTGCTGTGGATGGCGGGGAGTGCTGCTGCCCCAC 365
Db 1 ATGCCCAAGCCCTGCCCTGGCTCTCTGCTGTGGATGGCGGGGAGTGCTGCTGCCCCAC 60
QY 366 GGCACCCAGCAGCGGATCGCGGCTGCCCTGCGCAGCGGCTGGGGGGGGCCCCCTGGGG 425
Db 61 GGCACCCAGCAGCGGATCGCGGCTGCCCTGCGCAGCGGCTGGGGGGGGCCCCCTGGGG 120
QY 426 CTGGGGTGGCCCCGGGAGACCCAGCAAGAGCCGAGGAGCCGCCGGCGGCGGAGCTTT 485
Db 121 CTGGGGTGGCCCCGGGAGACCCAGCAAGAGCCGAGGAGCCGCCGGCGGCGGAGCTTT 180

QY 486 GTGGAGATGGTGACAACCTGAGGGCAAGTCGGGGCAGGCTACTAGCTGTGGAGATGACC 545
Db 181 GTGGAGATGGTGACAACCTGAGGGCAAGTCGGGGCAGGCTACTAGCTGTGGAGATGACC 240
QY 546 GTGGCAGCCCCCGCAGAGCGCTCAACATCTTGTGTGATACAGGAGCAGTAACTTTGCA 605
Db 241 GTGGCAGCCCCCGCAGAGCGCTCAACATCTTGTGTGATACAGGAGCAGTAACTTTGCA 300
QY 606 GTGGGTGTGCCCCCCCACCCTTCTTCCATCGCTACTACCAGAGCAGCTGTCCAGCACA 665
Db 301 GTGGGTGTGCCCCCCCACCCTTCTTCCATCGCTACTACCAGAGCAGCTGTCCAGCACA 360
QY 666 TACCGGAGCTCTCGGAAGGCTGTGTATGTGCCCTTACACCCAGGCAAGCTGGGAAGGGAG 725
Db 361 TACCGGAGCTCTCGGAAGGCTGTGTATGTGCCCTTACACCCAGGCAAGCTGGGAAGGGAG 420
QY 726 CTGGGACCGCAGCTGGTAAGCATCCGCCATGGCCCCAACGTCATCTGCTGCGGCCAATTT 785
Db 421 CTGGGACCGCAGCTGGTAAGCATCCGCCATGGCCCCAACGTCATCTGCTGCGGCCAATTT 480
QY 786 GCTGCCATCACTGAATCAGACAAGTTCTTTCATCAACGGCTCCAACCTGGGAAGGCATCTG 845
Db 481 GCTGCCATCACTGAATCAGACAAGTTCTTTCATCAACGGCTCCAACCTGGGAAGGCATCTG 540
QY 846 GGGCTGGCTATGCTGAGATTGCCAGGCTTGACGACTCCCTTGGAGCCCTTTCTTTGACTCT 905
Db 541 GGGCTGGCTATGCTGAGATTGCCAGGCTTGACGACTCCCTTGGAGCCCTTTCTTTGACTCT 600
QY 906 CTGTAAAGCAGACCCACCGTTCCCAACCTCTTCTCCCTGCGAGCTTTGTGGTGTGCTTGC 965
Db 601 CTGTAAAGCAGACCCACCGTTCCCAACCTCTTCTCCCTGCGACCTTTGTGGTGTGCTTGC 660
QY 966 CCCCTCAACCGCTGTAAGTGTGGCTCTGTCGGAGGAGCATGATCATCTGAGGTATC 1025
Db 661 CCCCTCAACCGCTGTAAGTGTGGCTCTGTCGGAGGAGCATGATCATCTGAGGTATC 720
QY 1026 GACCACTCGCTTACACAGCAGCTCTCTGCTATACACCCATCCGCGGGAGTGGTATTAT 1085
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Db 781 GAGGTGATCATTTGTCGGGGTGGAGATCAATGGACAGATCTGAAANTGGAGTGAAGGAG 840
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Db 961 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGCACCACCTTGGAAATTT 1020
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Db 1201 GGTTCCTAGTGTCTTTGATCGGGCCGAAAGCAATTTGGCTTTGCTGTCAAGCGCTTGC 1260

Qy 1566 CATCTGCACGATGAGTTTCAGCAGCGCAGCGGTGGAAGGCCCTTTTGTCAACCTTGGACATG 1625
Db 1261 CATCTGCACGATGAGTTTCAGCAGCGCAGCGGTGGAAGGCCCTTTTGTCAACCTTGGACATG 1320
Qy 1626 GAAGACTGTGGCTACACATTCACACACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1685
Db 1321 GAAGACTGTGGCTACACATTCACACACAGATGAGTCAACCCCTCATGACCATAGCCCTAT 1380
Qy 1686 GTCAATGGCTGACATCTGGCCCTCTTATGCTGCGCACCTCTGCCCTCATGCTGTGTGAGTGG 1745
Db 1381 GTCAATGGCTGACATCTGGCCCTCTTATGCTGCGCACCTCTGCCCTCATGCTGTGTGAGTGG 1440
Qy 1746 CGCTGCTCGCTCGCTGCGCCAGCAGCATGATGACTTTGTGTGATGATCATCCCTGCTG 1805
Db 1441 CGCTGCTCGCTCGCTGCGCCAGCAGCATGATGACTTTGTGTGATGATCATCCCTGCTG 1500
Qy 1806 AAGTGAGGAGCCCATGGCCAGAGATAGATATTCCTCTGACACACACCTCCGTGGTTCA 1865
Db 1501 AAGTGAGGAGCCCATGGCCAGAGATAGATATTCCTCTGACACACACCTCCGTGGTTCA 1560
Qy 1866 CTTTGGTTCACAAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCCTCAGGACCCCTCC 1925
Db 1561 CTTTGGTTCACAAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCCTCAGGACCCCTCC 1620
Qy 1926 CCACCCACAAATGCTCTGCTTGTATGAGAGAGAAAGGCTGGCAAGTGGGTTCAG 1985
Db 1621 CCACCCACAAATGCTCTGCTTGTATGAGAGAGAAAGGCTGGCAAGTGGGTTCAG 1680
Qy 1986 GGACTGTACCTGTAGGAACAGAAAGAGAGAAAGAGCAGTCTGCTGGCGGGAATFACT 2045
Db 1681 GGACTGTACCTGTAGGAACAGAAAGAGAGAAAGAGCAGTCTGCTGGCGGGAATFACT 1740
Qy 2046 CTTGGTTCACCTCAAAATTAAGTCGGGAAATTCCTGCTGTGAAACTTCAGCCCTGAACT 2105
Db 1741 CTTGGTTCACCTCAAAATTAAGTCGGGAAATTCCTGCTGTGAAACTTCAGCCCTGAACT 1800
Qy 2106 TTGTCCACCATTCCTTTAAATTCCTCAACCCAAAGTATTCCTTCTTTTCTTAAAGTTCAGAA 2165
Db 1801 TTGTCCACCATTCCTTTAAATTCCTCAACCCAAAGTATTCCTTCTTTTCTTAAAGTTCAGAA 1860
Qy 2166 GTACTGGCATCACGCGAGTTACCTTGGCGTGTGTCCTGTGGTACCCCTGGCAGAGAG 2225
Db 1861 GTACTGGCATCACGCGAGTTACCTTGGCGTGTGTCCTGTGGTACCCCTGGCAGAGAG 1920
Qy 2226 AGACCAAGCTTGTTCCTGCTGCGCAAAAGTCAGTAGGAGGATGCACAGTTTCTGCTATT 2285
Db 1921 AGACCAAGCTTGTTCCTGCTGCGCAAAAGTCAGTAGGAGGATGCACAGTTTCTGCTATT 1980
Qy 2286 TGCTTTAGAGACAGGACTGTATAACCAAGCCTAACATTTGGTGGCAAGATTGCCCTCTTGA 2345
Db 1981 TGCTTTAGAGACAGGACTGTATAACCAAGCCTAACATTTGGTGGCAAGATTGCCCTCTTGA 2040
Qy 2346 ATT 2348
Db 2041 ATT 2043

RESULT 4
US-09-794-748-3
; Sequence 3, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-748-3

Query Match 86.9%; Score 2039.8; DB 10; Length 2070;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 306 ATGGCCCAAGCCCTGCCCTGGCTCCTGTGTGGATGGCGGGGAGTGTGCTGCTGCCAC 365
Db 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGTGTGGATGGCGGGGAGTGTGCTGCTGCCAC 60
Qy 366 GGCACCCAGCAGCGCATCCGCTGCCCTGGCAGCGCCTGGGGGGGCGCCCTGGGG 425
Db 61 GGCACCCAGCAGCGCATCCGCTGCCCTGGCAGCGCCTGGGGGGGCGCCCTGGGG 120
Qy 426 CTGGGCTGCCCGGGAGACCGAGAGCCGAGAGCCGCGGAGCGCGCGGAGGGGCGAGCTTT 485
Db 121 CTGGGCTGCCCGGGAGACCGAGAGCCGAGAGCCGCGGAGCGCGCGGAGGGGCGAGCTTT 180
Qy 486 GTGGAGATGTGGACAACTGTAGGGGCAAGTCTGGGGGAGGCTACTACGTGGAGATGACC 545
Db 181 GTGGAGATGTGGACAACTGTAGGGGCAAGTCTGGGGGAGGCTACTACGTGGAGATGACC 240
Qy 546 GTGGCAGCCCCCGCAGACGCTCAACATCTCTGTGGATACAGCAGCAGTAACCTTTGCA 605
Db 241 GTGGCAGCCCCCGCAGACGCTCAACATCTCTGTGGATACAGCAGCAGTAACCTTTGCA 300
Qy 606 GTGGGTGTGCCCCCGCCCTTCTGTGATCGCTACTACAGAGGAGCTGTCCAGCACA 665
Db 301 GTGGGTGTGCCCCCGCCCTTCTGTGATCGCTACTACAGAGGAGCTGTCCAGCACA 360
Qy 666 TACCGGGACCTCCGGAAGGCTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGAG 725
Db 361 TACCGGGACCTCCGGAAGGCTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGAG 420
Qy 726 CTGGCAGCGACCTGTGAAGCATCCCGCATGCCCGCAAGCTCACCTGTGGTGGCAACATT 785
Db 421 CTGGCAGCGACCTGTGAAGCATCCCGCATGCCCGCAAGCTCACCTGTGGTGGCAACATT 480
Qy 786 GCTGCCATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGATCTCTG 845
Db 481 GCTGCCATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGATCTCTG 540
Qy 846 GGGCTGGCTATGTGTAGATTCGCCAGGCTGAGACTCCCTGGAGCTTTCTTTGACTCT 905
Db 541 GGGCTGGCTATGTGTAGATTCGCCAGGCTGAGACTCCCTGGAGCTTTCTTTGACTCT 600
Qy 906 CTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGACGCTTTGTGGTCTGGCTTC 965
Db 601 CTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGACGCTTTGTGGTCTGGCTTC 660
Qy 966 CCCCTCAACAGCTCTGAAGTGTGGCTCTGTGCGGAGGAGCATGATCATTTGGAGGTATC 1025
Db 661 CCCCTCAACAGCTCTGAAGTGTGGCTCTGTGCGGAGGAGCATGATCATTTGGAGGTATC 720
Qy 1026 GACCACTCGCTACACAGGAGTCTCTGGTATACACCCATCCCGGGGAGTGGTATTAT 1085
Db 721 GACCACTCGCTACACAGGAGTCTCTGGTATACACCCATCCCGGGGAGTGGTATTAT 780

Qy	606	GTGGGTCTGCCCCCCACCCCTTCTTGCAATCCCTACTACAGAGGCACCTGTCCAGACA	665
Db	301	GTGGGTGCTGCCCCCCACCCCTTCTTGCAATCCCTACTACAGAGGCACCTGTCCAGACA	360
Qy	666	TACGGGACCTCCGGAAGGGTGTGATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	725
Db	361	TACGGGACCTCCGGAAGGGTGTGATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	726	CTGGGACCGACCTGGTAAGCATCCCCCATGCCCCAACAGTCACCTGTGCGTGCCTCAACATT	785
Db	421	CTGGGACCGACCTGGTAAGCATCCCCCATGCCCCAACAGTCACCTGTGCGTGCCTCAACATT	480
Qy	786	GCTGCCATCACTGAATACAGCAAGTTCTTTCATCAGGGCTCCAACCTGGGAAGGATCCTG	845
Db	481	GCTGCCATCACTGAATACAGCAAGTTCTTTCATCAGGGCTCCAACCTGGGAAGGATCCTG	540
Qy	846	GGCTGGCCCTATGCTCAGATTCGCAAGGCTGACGACTCCCTGGAGCCCTTCTTTGACTCT	905
Db	541	GGCTGGCCCTATGCTCAGATTCGCAAGGCTGACGACTCCCTGGAGCCCTTCTTTGACTCT	600
Qy	906	CTGCTAAAGCAGACCCACGCTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTCTGGGTTTC	965
Db	601	CTGCTAAAGCAGACCCACGCTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTCTGGGTTTC	660
Qy	966	CCCTTCACCCAGTCTGAAGTGTGGCCTCTGTCGGAGGGAGCATGATCATTTGGAGGTATC	1025
Db	661	CCCTTCACCCAGTCTGAAGTGTGGCCTCTGTCGGAGGGAGCATGATCATTTGGAGGTATC	720
Qy	1026	GACCACTGCTGTACACAGGCAGTCTCTGGTATACACCCATCCCGCGGGAGTGGTATTAT	1085
Db	721	GACCACTGCTGTACACAGGCAGTCTCTGGTATACACCCATCCCGCGGGAGTGGTATTAT	780
Qy	1086	GAGTGATCATTTGCGGGTGGAGATCAATGACACAGGATCTGAAATCGACTGCAAGGAG	1145
Db	781	GAGTGATCATTTGCGGGTGGAGATCAATGACACAGGATCTGAAATCGACTGCAAGGAG	840
Qy	1146	TACAACCTATGACAAGAGCATTTGTGGACAGTGGCACCCACCAACCTTCGTTTCCCAAGAAA	1205
Db	841	TACAACCTATGACAAGAGCATTTGTGGACAGTGGCACCCACCAACCTTCGTTTCCCAAGAAA	900
Qy	1206	GTGTTTGAAGCTGCATCAAAATCCATCAAGGCAGGCTCCTCCACGGAGAAAGTTCCTGAT	1265
Db	901	GTGTTTGAAGCTGCATCAAAATCCATCAAGGCAGGCTCCTCCACGGAGAAAGTTCCTGAT	960
Qy	1266	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACACCCCTTGGAACTT	1325
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACACCCCTTGGAACTT	1020
Qy	1326	TTCCCACTCATCTCACTCTACCTAATGGGTGAGGTAAACCAACAGTCCCTCCCGATCACC	1385
Db	1021	TTCCCACTCATCTCACTCTACCTAATGGGTGAGGTAAACCAACAGTCCCTCCCGATCACC	1080
Qy	1386	ATCCTTCCGAGCAATACCTGGGGCCAGTGGGAAGATGTGGCCACGTCCCAAGAGACTGT	1445
Db	1081	ATCCTTCCGAGCAATACCTGGGGCCAGTGGGAAGATGTGGCCACGTCCCAAGAGACTGT	1140
Qy	1446	TACAAGTTTCCCATCTCACAGTCATCCACGGCAGCTGTTATGGGAGCTGTTATCATGAG	1505
Db	1141	TACAAGTTTCCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGAG	1200
Qy	1506	GGCTTCTACCTTCTTTGATCGGGCCCGAAACAAATTTGGCTTTGCTGTCAAGGCTTGC	1565
Db	1201	GGCTTCTACCTTCTTTGATCGGGCCCGAAACAAATTTGGCTTTGCTGTCAAGGCTTGC	1260
Qy	1566	CATGTGCAGATGAGTTCAGGACGGCAGCGGTGGGAAGGCCCTTTTGTCAACCTTGGACATG	1625
Db	1261	CATGTGCAGATGAGTTCAGGACGGCAGCGGTGGGAAGGCCCTTTTGTCAACCTTGGACATG	1320
Qy	1626	GAACTGTGGCTTACAACATTCACACAGACAGATGATCAACCCCTCATGACCATAGCCTAT	1685
Db	1321	GAACTGTGGCTTACAACATTCACACAGACAGATGATCAACCCCTCATGACCATAGCCTAT	1380

Qy	1686	GTATGGCTGGCATCTGGCGCCCTCTCTTCATGCTGCCACTCTTCGCTCATGGTGTGTCACTGG	1745
Db	1381	GTCATGGCTGCCATCTGGCGCCCTCTTCATGCTGCCACTCTGCCCTCATGGTGTGTCACTGG	1440
Qy	1746	CGCTGCCCTCCGCTCGCTGGCGCCAGCAGCATGATGACTTTGCTGATGACATCCCTCGCTG	1805
Db	1441	CGCTGCCCTCCGCTCGCTGGCGCCAGCAGCATGATGACTTTGCTGATGACATCCCTCGCTG	1500
Qy	1806	AAGTAGGAGGCCATGGGCGAGAGATAGAGATTCCTCTGGACACACACTCCGTGGTTCA	1865
Db	1501	AAGTAGGAGGCCATGGGCGAGAGATAGAGATTCCTCTGGACACACACTCCGTGGTTCA	1560
Qy	1866	CTTTGGTCAAGTAGGAGACACAGATGGCACTGTGGCCAGAGCACCTCAGGACCCCTCC	1925
Db	1561	CTTTGGTCAAGTAGGAGACACAGATGGCACTGTGGCCAGAGCACCTCAGGACCCCTCC	1620
Qy	1926	CCACCCACCAATTCGCTCTGGCTTGTATGGAGAAAGAAAGGCTGGCAAGTGGGTTCAG	1985
Db	1621	CCACCCACCAATTCGCTCTGGCTTGTATGGAGAAAGAAAGGCTGGCAAGTGGGTTCAG	1680
Qy	1986	GGACTGTACCTGTAGGAAACAGAAAGACAGAAAGACCACTCTGCTGGCGGAATACT	2045
Db	1681	GGACTGTACCTGTAGGAAACAGAAAGACAGAAAGACCACTCTGCTGGCGGAATACT	1740
Qy	2046	CTTGGTCACCTCAAAATTAAGTCGGGAAATTCGTGCTTGAACCTTCAGCCCTGAACCT	2105
Db	1741	CTTGGTCACCTCAAAATTAAGTCGGGAAATTCGTGCTTGAACCTTCAGCCCTGAACCT	1800
Qy	2106	TTGTGCCACCAATTCCTTTAAATTCACCCCAAGATATTCCTCTTTCTTATGTTTCAGAA	2165
Db	1801	TTGTGCCACCAATTCCTTTAAATTCACCCCAAGATATTCCTCTTTCTTATGTTTCAGAA	1860
Qy	2166	GTACTGGCATCACACGAGTTACCTTGGCGTGTGTCCTGTGGTACCCTCGCAGAGAAG	2225
Db	1861	GTACTGGCATCACACGAGTTACCTTGGCGTGTGTCCTGTGGTACCCTCGCAGAGAAG	1920
Qy	2226	AGACCAAGCTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCCTATT	2285
Db	1921	AGACCAAGCTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCCTATT	1980
Qy	2286	TGCTTTAGACACAGGACCTGTATTAACAGCCCTAACATTGGTGCAAGATTGCCTCTTGA	2345
Db	1981	TGCTTTAGACACAGGACCTGTATTAACAGCCCTAACATTGGTGCAAGATTGCCTCTTGA	2040
Qy	2346	ATT 2348	
Db	2041	ATT 2043	

RESULT 6

US-09-681-442-3
Sequence 3, Application US/09681442
Patent No. US20020081634A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE S
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 28341/6280FG
CURRENT APPLICATION NUMBER: US/09/681,442
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594

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; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-681-442-3

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Query Match	86.9%;	Score 2039.8;	DB 10;	Length 2070;
Best Local Similarity	99.9%;	Pred. NO. 0;		
Matches 2041;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps 0;				

Qy	306	ATGCGCCCAAGCCCTCCCTGGCTCTGCTGTGTGATGGCGCGGGAGTGTGCTGCTGCCAC	365
Db	1	ATGCGCCCAAGCCCTCCCTGGCTCTGCTGTGTGATGGCGCGGGAGTGTGCTGCTGCCAC	60
Qy	366	GGCACCCAGCACGGCATCGGGTGCCTTCGCCAGCGGGCTGGGGGGCGCCCCCTGGGG	425
Db	61	GGCACCCAGCACGGCATCGGGTGCCTTCGCCAGCGGGCTGGGGGGCGCCCCCTGGGG	120
Qy	426	CTGCGGGTGCCTCCGGGAGACCGACGAAGACCCGAGGAGCCCGGCCCGGAGGGGACGCTTT	485
Db	121	CTGCGGGTGCCTCCGGGAGACCGACGAAGACCCGAGGAGCCCGGCCCGGAGGGGACGCTTT	180
Qy	486	CTGGAGATGGTGACAACCTGAGGGCAAGTCGGGCGAGGCTTACTACGTGGAGATGACC	545
Db	181	CTGGAGATGGTGACAACCTGAGGGCAAGTCGGGCGAGGCTTACTACGTGGAGATGACC	240
Qy	546	GTGGCGACGCCGCCCGAGACGCTCAACAATCTGGTGGATACAGGCAGCAGTAACCTTGCA	605
Db	241	GTGGCGACGCCGCCCGAGACGCTCAACAATCTGGTGGATACAGGCAGCAGTAACCTTGCA	300
Qy	606	TGGGTGCTGCCCCACCCCTTCCTGCATCCCTACTACCAGAGCAGCTGTCCAGCACA	665
Db	301	TGGGTGCTGCCCCACCCCTTCCTGCATCCCTACTACCAGAGCAGCTGTCCAGCACA	360
Qy	666	TACCGGACCTCCGGGAAGGTTGTATGTGCGCTACACCCAGGGCAAGTGGGAAGGGGAG	725
Db	361	TACCGGACCTCCGGGAAGGTTGTATGTGCGCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	726	CTGGCAGCGACCTGGTAAGCATCCCCATGGCGCCCAACGTCTGCTGGTGCCACATTT	785
Db	421	CTGGCAGCGACCTGGTAAGCATCCCCATGGCGCCCAACGTCTGCTGGTGCCACATTT	480
Qy	786	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	845
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Qy	846	GGGTGGCCATGTCTGATGATTTGCCAGGCGCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	905
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Qy	966	CCCTCTCAACCACTCTGAAGTGTGCGCTCTGTCTGGAGGAGCATGATCATTTGGAGTATC	1025
Db	661	CCCTCTCAACCACTCTGAAGTGTGCGCTCTGTCTGGAGGAGCATGATCATTTGGAGTATC	720
Qy	1026	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCTACCGCGGGAGTGGTATTAT	1085
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCTACCGCGGGAGTGGTATTAT	780
Qy	1086	GAGGTGATCATTTGCGGGTGAGATCAATGGACAGGATCTGAAATGGACCTGCAAGGAG	1145
Db	781	GAGGTGATCATTTGCGGGTGAGATCAATGGACAGGATCTGAAATGGACCTGCAAGGAG	840
Qy	1146	TACAACTATGACAGAGCATTTGTGGACAGTGGCACACCAACCTTCGTTTGGCCCAAGAA	1205
Db	841	TACAACTATGACAGAGCATTTGTGGACAGTGGCACACCAACCTTCGTTTGGCCCAAGAA	900

QY	1206	GTGTTTGAAGTCGAGTCAGATCAAAATCCATCAAGGCAGCCTCTCCACGGAGAAAGTTTCCCTTGAT	1266
Db	901	GTGTTTGAAGTCGAGTCAGTCAAAATCCATCAAGGCAGCCTCTCCACGGAGAAAGTTTCCCTGAT	960
QY	1266	GGTTTCTGGCTTAGGAGACGAGTCGTGCTGCGCAAGCAGGCACACCCCTTGGAAACATT	1325
Db	961	GGTTTCTGGCTTAGGAGACGAGTCGTGCTGCGCAAGCAGGCACACCCCTTGGAAACATT	1020
QY	1326	TTCCCACTCATCTCACTCTACCTAATATGGGTGAGGTTTACCAACACAGTCCTTCGCGATCACCC	1385
Db	1021	TTCCCACTCATCTCACTCTACCTAATATGGGTGAGGTTTACCAACACAGTCCTTCGCGATCACCC	1080
QY	1386	ATCCTTCCGCAAGCAATACCTTCGCGCCAGTGGAAAGATGTGGCCACGTCCCAAGACGACTGT	1445
Db	1081	ATCCTTCCGCAAGCAATACCTTCGCGCCAGTGGAAAGATGTGGCCACGTCCCAAGACGACTGT	1140
QY	1446	TACAAGTTTGGCCATCTCACAGTCATCCAGGGCAGCTGTTATGGAGCTGTTATCATATGGAG	1505
Db	1141	TACAAGTTTGGCCATCTCACAGTCATCCAGGGCAGCTGTTATGGAGCTGTTATCATATGGAG	1200
QY	1506	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAACGAATTTGGCTTTGCTGTCTCAGCGCTTCC	1565
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAACGAATTTGGCTTTGCTGTCTCAGCGCTTCC	1260
QY	1566	CATGTGCACGATGAGTTCAGGACGGGAGCGGTGGAAAGCCCTTTTGTACCTTTGGACATG	1625
Db	1261	CATGTGCACGATGAGTTCAGGACGGGAGCGGTGGAAAGCCCTTTTGTACCTTTGGACATG	1320
QY	1626	GAAGACTGTGGCTCAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCAT	1685
Db	1321	GAAGACTGTGGCTCAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCAT	1380
QY	1686	GTGATGGCTGGCATCTGGCCCTCTTTTCATGCTGCCACTTGCCTCATGGTGTGTCTCAGTCGG	1745
Db	1381	GTGATGGCTGGCATCTGGCCCTCTTTTCATGCTGCCACTTGCCTCATGGTGTGTCTCAGTCGG	1440
QY	1746	CGTGGCTTCGCTGCTCGCCAGCAGCATGATGACTTTGCTGTATGACATCTCCCTGTGCTG	1805
Db	1441	CGTGGCTTCGCTGCTCGCCAGCAGCATGATGACTTTGCTGTATGACATCTCCCTGTGCTG	1500
QY	1806	AAGTGAGGAGGCCATGGCGAGAAGATAGAGATTTCCCTTGACACACACCTCCGTGGTTTCA	1865
Db	1501	AAGTGAGGAGGCCATGGCGAGAAGATAGAGATTTCCCTTGACACACACCTCCGTGGTTTCA	1560
QY	1866	CTTTGGTTCACAAGTAGGAGACACAGATGGCACTGTGGCCAGAGCACCTCAGGACCCCTCC	1925
Db	1561	CTTTGGTTCACAAGTAGGAGACACAGATGGCACTGTGGCCAGAGCACCTCAGGACCCCTCC	1620
QY	1926	CCACCCACCAATGCCTCTGCCCTTGATGGAGAGAAAGGCTGGCAAGTGGGTGCTCCAG	1985
Db	1621	CCACCCACCAATGCCTCTGCCCTTGATGGAGAGAAAGGCTGGCAAGTGGGTGCTCCAG	1680
QY	1986	GGACTGTACCTGTAGGAACAGAAAGAGAAAGAGACATCTGCTGGCGGGAAATACT	2045
Db	1681	GGACTGTACCTGTAGGAACAGAAAGAGAAAGAGACATCTGCTGGCGGGAAATACT	1740
QY	2046	CTTTGGTTCACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTTGAAACTTCAGGCCCTGAACCT	2105
Db	1741	CTTTGGTTCACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTTGAAACTTCAGGCCCTGAACCT	1800
QY	2106	TTGTCCACCAATTCCTTTTAAATTTCCCAACCCCAAAGTATCTCTCTTTCTTAGTTTTCAGAA	2165
Db	1801	TTGTCCACCAATTCCTTTTAAATTTCCCAACCCCAAAGTATCTCTCTTTCTTAGTTTTCAGAA	1860
QY	2166	GTACTTGGCATCACAGCGAGTTTACCTTGGCGTGTGTCCTTGTGGTACCCCTGGCAGAGAG	2225
Db	1861	GTACTTGGCATCACAGCGAGTTTACCTTGGCGTGTGTCCTTGTGGTACCCCTGGCAGAGAG	1920
QY	2226	AGACCAAGCTTGTTCCTCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTCTCTATT	2285
Db	1921	AGACCAAGCTTGTTCCTCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTCTCTATT	1980
QY	2286	TGCTTTTAGAGACACGGGACTGTATAAACAGCCCTTAACATTTGGTGCACCAAGATTTGCCTCTTGA	2345

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Db 1981 TGCTTTAGAGACGGGACTGTATAACAAGCCTAACATGGTGCAAGATTGCTCTTGA 2040
Qy 2346 ATT 2348
Db 2041 ATT 2043

RESULT 7
US-09-969-671A-1
; Sequence 1, Application US/09969671A
; Publication No. US20030036112A1
; GENERAL INFORMATION:
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: MURPHY, KAY
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SMITH, TRUDI S.
; TITLE OF INVENTION: ASP2
; FILE REFERENCE: GH-70368-D1
; CURRENT APPLICATION NUMBER: US/09/969,671A
; CURRENT FILING DATE: 2001-10-03
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 09/009,191
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 09/694,200
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unknown
; LOCATION: (2455)(2456)(2463)(2478)(2480)(2497)(2507)(2509)(2512)(2516)
; LOCATION: (2520)(2522)(2525)(2529)(2539)(2540)
; OTHER INFORMATION: Wherein n can be represented by a, c, t, or g
US-09-969-671A-1

Query Match 86.28; Score 2024; DB 9; Length 2541;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2038; Conservative 0; Mismatches 5; Indels 1; Gaps 1:

Qy 306 ATGGCCCAAGCCCTGCCCTGCTCTGCTGTGGATGGCGCGGAGTGCTGCTGCCAC 365
Db 1 ATGGCCCAAGCCCTGCCCTGCTCTGCTGTGGATGGCGCGGAGTGCTGCTGCCAC 60

Qy 366 GGCACCCAGCAGCGCATCCGCTGCCCTGCCGACGCGCCCTGGGGGCGCCCTGGGG 425
Db 61 GGCACCCAGCAGCGCATCCGCTGCCCTGCCGACGCGCCCTGGGGGCGCCCTGGGG 120

Qy 426 CTGGGCTGCCCGGGAGACCGAGACGAGCCGAGGAGCCGCGCGGAGGAGCTTT 485
Db 121 CTGGGCTGCCCGGGAGACCGAGACGAGCCGAGGAGCCGCGCGGAGGAGCTTT 180

Qy 486 GTGGAGATGTGGCAACCTCAGGGGCAAGTCGGGGCAGGCTACTACGTGGAGATGACC 545
Db 181 GTGGAGATGTGGCAACCTCAGGGGCAAGTCGGGGCAGGCTACTACGTGGAGATGACC 240

Qy 546 GTGGGACGCCCCCGGACAGCCTCAACATCCTGTGGATACAGGACGAGTAACTTTGCA 605
Db 241 GTGGGACGCCCCCGGACAGCCTCAACATCCTGTGGATACAGGACGAGTAACTTTGCA 300

Qy 606 GTGGGTGTCGCCCCACCCCTTCTGTCATCGCTACTACAGAGGACGCTGTCCAGCACA 665
Db 301 GTGGGTGTCGCCCCACCCCTTCTGTCATCGCTACTACAGAGGACGCTGTCCAGCACA 360

Qy 666 TACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGGAG 725
Db 361 TACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGGAG 420

Qy 726 CTGGGACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACGTGCGGTGCCAACATT 785
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Db 421 CTGGGACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACGTGCGTGCCAACATT 480
Qy 786 GCTGCCATCACTGAATCAGACAAAGTTCTTTCATCAAGGCTCCAACTGGGAAGCATCTG 845
Db 481 GCTGCCATCACTGAATCAGACAAAGTTCTTTCATCAAGGCTCCAACTGGGAAGCATCTG 540
Qy 846 GGGCTGGCCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCCTTCTTTCACATCT 905
Db 541 GGGCTGGCCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCCTTCTTTCACATCT 600
Qy 906 CTGGTAAAGCAGACCCACGTTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTCTGGCTTC 965
Db 601 CTGGTAAAGCAGACCCACGTTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTCTGGCTTC 660
Qy 966 CCCCTCAACAGCTGTAAGTGTGGCCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC 1025
Db 661 CCCCTCAACAGCTGTAAGTGTGGCCTCTGTGCGAGGAGCATGATCATTTGGAGGTATC 720
Qy 1026 GACCACCTGCTGTACACAGGAGTCTCTGTTATACACCATCCCGCGGAGTGGTATTAT 1085
Db 721 GACCACCTGCTGTACACAGGAGTCTCTGTTATACACCATCCCGCGGAGTGGTATTAT 780
Qy 1086 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGACCTGCAAGGAG 1145
Db 781 GAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGACCTGCAAGGAG 840
Qy 1146 TACAACCTATGACAGAGCATTTGGACAGTGGCAGCACCACACCTTCTGTTGGCCCAAGAA 1205
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Qy 1266 GGTTCCTGGTGGTAGAGACAGCTGGTGTGCTGGCAAGCAGGACACCCCTTGGCAACATT 1325
Db 961 GGTTCCTGGTGGTAGAGACAGCTGGTGTGCTGGCAAGCAGGACACCCCTTGGCAACATT 1020
Qy 1326 TTCCCACTCATCTCACTCACTTAATGGTGGAGTTACCAACCACTCTCTCCGACATCACC 1385
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Qy 1386 ATCTTCCGACAGCAATACCTGCGGCGAGTGAAGATGTGGCCACCTCCCAAGACACTGT 1445
Db 1081 ATCTTCCGACAGCAATACCTGCGGCGAGTGAAGATGTGGCCACCTCCCAAGACACTGT 1140
Qy 1446 TACAAGTTTGGCATCTCACAGTCAATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1505
Db 1141 TACAAGTTTGGCATCTCACAGTCAATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
Qy 1506 GGTTCCTACGTTGCTTTGATCGGGCCGAAACAAATTTGCTGCTCAGGCTTTCG 1565
Db 1201 GGTTCCTACGTTGCTTTGATCGGGCCGAAACAAATTTGCTGCTCAGGCTTTCG 1260
Qy 1566 CATGTGCACGATGAGTCTCAGGACGCGAGCGGTGGAGGCCCTTTTGTACCTTGGACATG 1625
Db 1261 CATGTGCACGATGAGTCTCAGGACGCGAGCGGTGGAGGCCCTTTTGTACCTTGGACATG 1320
Qy 1626 GAAGACTGTGGCTACAACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT 1685
Db 1321 GAAGACTGTGGCTACAACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT 1380
Qy 1686 GTCATGGCTGCCATCTGGCCCTCTTTCATGTGCGCACCTCTGCTCATGTGTGTCAGTGG 1745
Db 1381 GTCATGGCTGCCATCTGGCCCTCTTTCATGTGCGCACCTCTGCTCATGTGTGTCAGTGG 1440
Qy 1746 CGCTGCCCTCGCTGCTGCGCAGCAGCATGATGATGTTGCTGATGACATCTCCCTGCTG 1805
Db 1441 CGCTGCCCTCGCTGCTGCGCAGCAGCATGATGATGTTGCTGATGACATCTCCCTGCTG 1500
Qy 1806 AAGTGAGGAGGCCCATGGCGAGAGATAGAGATTCCCTCT - GGACCCACACCTCCGCTGGTTC 1864
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Qy 1425 GCCACGTCCTCCAGAGGAGCTGTTTACAAAGTTTGCCTCTCACAGTCTATCCACGGGCACTGTT 1484
Db 1081 GCCAGTCCCAAGAGGAGCTGTTTACAAAGTTTGCCTCTCACAGTCTATCCACGGGCACTGTT 1140
Qy 1485 ATGGAGCTGTTTATCATGAGGAGCTTCTACCTGTTGTTTATGCGGCCCCGAAACGAATTT 1544
Db 1141 ATGGAGCTGTTTATCATGAGGAGCTTCTACCTGTTGTTTATGCGGCCCCGAAACGAATTT 1200
Qy 1345 GGCCTTTGCTGTCAGGCTTGCATGTCAGCATGATGATGTCAGAGGAGGCGGCTGGAAGGC 1604
Db 1201 GGCCTTTGCTGTCAGGCTTGCATGTCAGCATGATGATGTCAGAGGAGGCGGCTGGAAGGC 1260
Qy 1605 CTTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACTTCCACAGACAGATGAGTCA 1664
Db 1261 CTTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACTTCCACAGACAGATGAGTCA 1320
Qy 1665 ACCCTCATGACCATAGGCTATGTCATGGCTGCCATCTGGCGCCCTTTCATGCTGCCACTC 1724
Db 1321 ACCCTCATGACCATAGGCTATGTCATGGCTGCCATCTGGCGCCCTTTCATGCTGCCACTC 1380
Qy 1725 TGCCTCATGGTGTCTCAGTGGCGCTGCCCTCGCTGCCCTGCCAGCAGCATGACTTTT 1784
Db 1381 TGCCTCATGGTGTCTCAGTGGCGCTGCCCTCGCTGCCAGCAGCATGACTTTT 1440
Qy 1785 GCTGATGACATCTCCCTGCTGAACTGAGGAGGCGCCATGGGAGAGATAGAGATTCCCT 1844
Db 1441 GCTGATGACATCTCCCTGCTGAACTGAGGAGGCGCCATGGGAGAGATAGAGATTCCCT 1500
Qy 1845 GGACACACCTCGTGGTTCATTTGTTTCAAGTAGAGACACAGATGGCACCTGTGGC 1904
Db 1501 GGACACACCTCGTGGTTCATTTGTTTCAAGTAGAGACACAGATGGCACCTGTGGC 1560
Qy 1905 CAGAGCACTTCAGAGACCTCCACCCACCAACCAATGCCTCTGCCTGATGGAGAGGAAAA 1964
Db 1561 CAGAGCACTTCAGAGACCTCCACCCACCAACCAATGCCTCTGCCTGATGGAGAGGAAAA 1620
Qy 1965 GGCTGGCAAGTGGGTTCCAGGGAGCTGTACCTGTAGGAAACAGAAAAGAGAAAGAAAG 2024
Db 1621 GGCTGGCAAGTGGGTTCCAGGGAGCTGTACCTGTAGGAAACAGAAAAGAGAAAGAAAG 1680
Qy 2025 CACTCTGCTGGCGGGAATACCTTGGTTCACCTCAAAATTAAGTCGGGAAATTCCTGCTCT 2084
Db 1681 CACTCTGCTGGCGGGAATACCTTGGTTCACCTCAAAATTAAGTCGGGAAATTCCTGCTCT 1740
Qy 2085 TGAACCTTCAGCCCTGAACTTTGTCCACCAATTCCTTTTAAATTCCTCAACCCAAAGTATT 2144
Db 1741 TGAACCTTCAGCCCTGAACTTTGTCCACCAATTCCTTTTAAATTCCTCAACCCAAAGTATT 1800
Qy 2145 CTTCTTTTCTTTAGTTTTCAGAACTACTGGCATCACACGAGGTTACCTTTGGCGTGTGCTCC 2204
Db 1801 CTTCTTTTCTTTAGTTTTCAGAACTACTGGCATCACACGAGGTTACCTTTGGCGTGTGCTCC 1860
Qy 2205 TGTGTTACCTTGGCAGAGAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA 2264
Db 1861 TGTGTTACCTTGGCAGAGAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA 1920
Qy 2265 GAGGATGACAGATTGCTTATTTGCTTTTATAGACAGAGGAGTGTATTAACCAAGCCTAACATT 2324
Db 1921 GAGGATGACAGATTGCTTATTTGCTTTTATAGACAGAGGAGTGTATTAACCAAGCCTAACATT 1980
Qy 2325 GGTGCAAGATTGGCTCTTTGAATT 2348
Db 1981 GGTGCAAGATTGGCTCTTTGAATT 2004

RESULT 9

US-09-796-264-1
: Sequence 1, Application US/09796264
: Patent No. US2002004930A1
: GENERAL INFORMATION:
: APPLICANT: Tang, Jordan J.N.
: APPLICANT: Lin, Xinli
: APPLICANT: Koelsch, Gerald

: TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
: TITLE OF INVENTION: of Use Thereof
: FILE REFERENCE: OMRF 179
: CURRENT APPLICATION NUMBER: US/09/796,264
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 09/604,608
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: 60/168,060
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: 60/177,836
: PRIOR FILING DATE: 2000-01-25
: PRIOR APPLICATION NUMBER: 60/178,368
: PRIOR FILING DATE: 2000-01-27
: PRIOR APPLICATION NUMBER: 60/210,292
: PRIOR FILING DATE: 2000-06-08
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 3252
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-796-264-1

Query Match 85.3%; Score 2004; DB 10; Length 3252;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 345 CGGGAGTGTGCTGCCACGCGGACCCAGCAGCGATCCGGCTGCCCTGGCGAGCGGC 404
Db 1 CGGGAGTGTGCTGCCACGCGGACCCAGCAGCGATCCGGCTGCCCTGGCGAGCGGC 60
Qy 405 CTGGGGCGCGCCCTCGGGCTGGCGTGGCGAGACCGAGAGAGAGAGAGAGAGAGAG 464
Db 61 CTGGGGCGCGCCCTCGGGCTGGCGTGGCGAGACCGAGAGAGAGAGAGAGAGAGAG 120
Qy 465 CCCGCCGAGGAGGCGAGCTTTTGGAGATGGTGGACAACTCGAGGGGAAAGTCGGGGGAG 524
Db 121 CCCGCCGAGGAGGCGAGCTTTTGGAGATGGTGGACAACTCGAGGGGAAAGTCGGGGGAG 180
Qy 525 GGCTACTACGTGGAGATGACCGTGGGAGAGCGCCCGGAGAGCGCTCAACATCCTGTGGAT 584
Db 181 GGCTACTACGTGGAGATGACCGTGGGAGAGCGCCCGGAGAGCGCTCAACATCCTGTGGAT 240
Qy 585 ACAGCAGCAGTAACTTTGCGAGTGGTGTGCCCGCCCGCCCGCTTCTGCTGCTACTACTAC 644
Db 241 ACAGCAGCAGTAACTTTGCGAGTGGTGTGCCCGCCCGCCCGCTTCTGCTGCTACTACTAC 300
Qy 645 CAGAGGAGCTGTCCAGCACATACCGGAGCTTCCGGAAGGTTGTATGTGCCCTTACACC 704
Db 301 CAGAGGAGCTGTCCAGCACATACCGGAGCTTCCGGAAGGTTGTATGTGCCCTTACACC 360
Qy 705 CAGGCAAGTGGGAGGAGCTGGGACCGGAGCGCTGTAAGCATCCCGCATGGCCCCCAAC 764
Db 361 CAGGCAAGTGGGAGGAGCTGGGACCGGAGCGCTGTAAGCATCCCGCATGGCCCCCAAC 420
Qy 765 GTCATGTGCGTGGCAACATTTGCTGCCATCACTGAATCAGACAAGTTCTTCTATCAACGCG 824
Db 421 GTCATGTGCGTGGCAACATTTGCTGCCATCACTGAATCAGACAAGTTCTTCTATCAACGCG 480
Qy 825 TCCAACTGGGAGGAGCTCCTGGGGCTGGCCTATGCTGAGATGTCAGGCGCTGACGACTCC 884
Db 481 TCCAACTGGGAGGAGCTCCTGGGGCTGGCCTATGCTGAGATGTCAGGCGCTGACGACTCC 540
Qy 885 CTGGAGCGCTTTCTTGAAGTCTCTGTAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 944
Db 541 CTGGAGCGCTTTCTTGAAGTCTCTGTAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 945 CAGCTTTTGTGCTGGCTTCCCGCTCAACAGTCTGAAGTCTGCGCTCTCTCTCGGAGGG 1004
Db 601 CAGCTTTTGTGCTGGCTTCCCGCTCAACAGTCTGAAGTCTGCGCTCTCTCTCGGAGGG 560
Qy 1005 AGCATGATCATTTGGAGGATCGACCACTCGCTGTATACAGAGGAGCTCTCTGGTATACACC 1064
Db 1005 AGCATGATCATTTGGAGGATCGACCACTCGCTGTATACAGAGGAGCTCTCTGGTATACACC 1064

Db 661 AGCATGATCATTTGGAGGTATCGACCACTCGCTGTACACAGGCACTCTCTGGTATACACCC 720
QY 1065 ATCCGGCGGGAGTGTATATGAGTGTGATCATTTGTCGGGTGGAGATCAATGGACAGGAT 1124
Db 721 ATCCGGCGGGAGTGTATATGAGTGTGATCATTTGTCGGGTGGAGATCAATGGACAGGAT 780
QY 1125 CTGAATATGGACTGCAAGAGGTACAACTATGACAAGAGCATTTGGACAGTGGCAACCACC 1184
Db 781 CTGAATATGGACTGCAAGAGGTACAACTATGACAAGAGCATTTGGACAGTGGCAACCACC 840
QY 1185 AACCTTCCTTTGCCCAAGAAAGTGTGTAAGCTGCAAGTCAAAATCCATCAAGSGACGCTCC 1244
Db 841 AACCTTCCTTTGCCCAAGAAAGTGTGTAAGCTGCAAGTCAAAATCCATCAAGSGACGCTCC 900
QY 1245 TCCACGGAGAAAGTTCCTCGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 1304
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QY 1305 GGCACCAACCTTTGGAACATTTTCCAGTCACTCTCACTCACTCACTCACTCACTCACTCACT 1364
Db 961 GGCACCAACCTTTGGAACATTTTCCAGTCACTCTCACTCACTCACTCACTCACTCACTCACT 1020
QY 1365 AACCAGTCTTCCCGATCACCATCCTTCCGACGCAATACCTGCGCCAGTGGCAAGATGTG 1424
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QY 1425 GCCACGTCACAGAGTGTGTACAGTTTGGCATCTCACAGTCACTCCACGGGCACTGT 1484
Db 1081 GCCACGTCACAGAGTGTGTGTACAGTTTGGCATCTCACAGTCACTCCACGGGCACTGT 1140
QY 1485 ATGGAGCTGTATCATGAGGCTTCTAGTGTGTCTTGTATCGGGCCCGAAACGAAT 1544
Db 1141 ATGGAGCTGTATCATGAGGCTTCTAGTGTGTCTTGTATCGGGCCCGAAACGAAT 1200
QY 1545 GGCTTTGCTGTCAGGCTTGGCATGTGCACGATGTGTCAGGAGCGGCGGTGGAGGC 1604
Db 1201 GGCTTTGCTGTCAGGCTTGGCATGTGCACGATGTGTCAGGAGCGGCGGTGGAGGC 1260
QY 1605 CTTTGTGTCACCTTGGACATGGAAGTGTGGCTTACAACATTCACACAGACAGTGTGCA 1664
Db 1261 CTTTGTGTCACCTTGGACATGGAAGTGTGGCTTACAACATTCACACAGACAGTGTGCA 1320
QY 1665 ACCCTCATGACATGACCTATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1724
Db 1321 ACCCTCATGACATGACCTATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1725 TGCTCATGTGTGTGTCAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1784
Db 1381 TGCTCATGTGTGTGTCAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1785 GCTGATGACATCTCCCTGCTGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1844
Db 1441 GCTGATGACATCTCCCTGCTGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
QY 1845 GGACCAACCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1904
Db 1501 GGACCAACCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1905 CAGAGCACTCAGGACCTCCGCCACCCACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1964
Db 1561 CAGAGCACTCAGGACCTCCGCCACCCACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1965 GGCTGGAAGGTGGGTTCAGGAGTGTACCTGTAGGAACAGAGAGAGAGAGAGAGAGAGAGAG 2024
Db 1621 GGCTGGAAGGTGGGTTCAGGAGTGTACCTGTAGGAACAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 2025 CACTCTGCTGGCGGAATACTTCTGGTCACTCAAAATTTAAGTCGGGAAATTTCTGCTGCT 2084
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QY 2085 TGAACCTTCAGCCCTGAAACCTTTGTCCACCATTTCCCTTTTAAATTCCTCAACCCCAAGATTT 2144
Db 1741 TGAACCTTCAGCCCTGAAACCTTTGTCCACCATTTCCCTTTTAAATTCCTCAACCCCAAGATTT 1800

QY 2145 CTTCTTTTCTTTAGTTTTCAGAAGTACTGGCATCACACGAGGTTACCTTTGGCGTGTGTCCC 2204
Db 1801 CTTCTTTTCTTTAGTTTTCAGAAGTACTGGCATCACACGAGGTTACCTTTGGCGTGTGTCCC 1860
QY 2205 TGTGTTACCTTGGCAGAGAGAGACCAAGCTTTGTTTCCCTGCTGGCCAAAGTCAAGTACGA 2264
Db 1861 TGTGTTACCTTGGCAGAGAGAGACCAAGCTTTGTTTCCCTGCTGGCCAAAGTCAAGTACGA 1920
QY 2265 GAGGATGCACAGTTCCTTATTTAGAGACAGGAGTGTATTAACAAAGCTTAACATTT 2324
Db 1921 GAGGATGCACAGTTCCTTATTTAGAGACAGGAGTGTATTAACAAAGCTTAACATTT 1980
QY 2325 GGTCAAAAGATTGCTCTTTGAATT 2348
Db 1981 GGTCAAAAGATTGCTCTTTGAATT 2004

RESULT 10

US-09-845-226-1
; Sequence 1, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-226-1

Query Match 85.3%; Score 2004; DB 10; Length 3252;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 GCGGAGTGTGCTGCTGCGCCACGCGCACCCAGCAGCGGATCCGGCTGCGCCCTCGCGCAGCGC 404
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QY 405 CTGGGGGCGCGCCCTTGGGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 464
Db 61 CTGGGGGCGCGCCCTTGGGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 120
QY 465 CCGGGCGGAGGGGCGAGCTTTGTGGAGATGGTGGACAACTGAGGGGCAAGTCGGGGGAG 524
Db 121 CCGGGCGGAGGGGCGAGCTTTGTGGAGATGGTGGACAACTGAGGGGCAAGTCGGGGGAG 180
QY 525 GGCTACTACGTGGAGATGACCGTGGCAGCGCCCGCCAGAGCGCTCAACATCCTGCTGCTGAT 584
Db 181 GGCTACTACGTGGAGATGACCGTGGCAGCGCCCGCCAGAGCGCTCAACATCCTGCTGCTGAT 240
QY 585 ACAGGACGACGTAACCTTTGTCAGTGGTGTGCTGCGCCCGCCAGCGCTTCTGCTGCTGCTGCTGCT 644
Db 241 ACAGGACGACGTAACCTTTGTCAGTGGTGTGCTGCGCCCGCCAGCGCTTCTGCTGCTGCTGCTGCT 300
QY 645 CAGAGGAGCTGTCCAGCACATACCGGGACCTCCGGAGGGGTGTGTATGTGCCCTTACACC 704

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-927-5

Query Match 80.1%; Score 1881; DB 10; Length 1977;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1966; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

QY 306 ATGGCCCAAGCCCTGCGCTGGCTGCTGCTGGATGGCGGGAGTCTGCTGCCAC 365
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Db 61 GGCACCCAGCAGCGATCCGGCTGCCCTGCGCAGCGCCCTGGGGGGCCCTTGGGG 120
QY 426 CTGGGGCTGCCCCGGGAGACCGAAGAGCCGAGAGCCGCGCGGAGGGGAGCTTT 485
Db 121 CTGGGGCTGCCCCGGGAGACCGAAGAGCCGAGAGCCGCGCGGAGGGGAGCTTT 180
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Db 181 CTGGAGATGGTGACAACTGAGGGCAAGTCCGGGGCAGGGCTACTACGTGGAGATGACC 240
QY 546 GTGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGACGAGTAACCTTTGCA 605
Db 241 GTGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGACGAGTAACCTTTGCA 300
QY 606 GTGGGTGCTGCCCCCACCCTTCCCTGCATCGCTACTACAGAGGACGCTGTCCAGCACA 665
Db 301 GTGGGTGCTGCCCCCACCCTTCCCTGCATCGCTACTACAGAGGACGCTGTCCAGCACA 360
QY 666 TACGGGAGACCTCGGAAGGGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG 725
Db 361 TACGGGAGACCTCGGAAGGGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG 420
QY 726 CTGGGCACCGACTGGTAGCATCCCTTGGCCCAAGCTGCTGCTGCTGCTGCTGCTGCT 785
Db 421 CTGGGCACCGACTGGTAGCATCCCTTGGCCCAAGCTGCTGCTGCTGCTGCTGCTGCT 480
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QY 966 CCCCTCAACCACTGCTGAAGTGGCTGCTGCTGGAGGAGCATGATCATTTGGAGGTATC 1025
Db 586 CCCCTCAACCACTGCTGAAGTGGCTGCTGCTGGAGGAGCATGATCATTTGGAGGTATC 645
QY 1026 GACCACCTCGCTGTACACAGGCACTCTGCTGTATACACCCCTCCGGCGGAGTGGTATTAT 1085
Db 646 GACCACCTCGCTGTACACAGGCACTCTGCTGTATACACCCCTCCGGCGGAGTGGTATTAT 705
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QY 1146 TACAACATATGCAAGAGCATTTGGAGAGTGGCACCACCAACCTTGTGTTGCCCAAGAAA 1205
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QY 1266 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGCGCAAGCAGCACCACCTTGGACATT 1325

Db 886 GCTTCTTGGCTAGGAGAGCAGCTGCTGCTGGCAAGCAGCACCACCTTGGAAATTT 945
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Db 946 TTCCCAAGTCACTCACTCTACCTAATGGGTGAGGTTACCAACAGTCTTCCGCATCAC 1005
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Db 1006 ATCCCTTCCCGCAGCAATACCTTCCGCCAGTGGGAAGATGGCCACGCTCCCAACAGCACTGT 1065
QY 1446 TACAAGTTTGGCCATCTCACAGTCTCACAGGCGCACTGTATGGAGCTGTATCATCGAG 1505
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QY 1506 GCTTCTTACGTTGCTTTTGTATCGGGCCGCGGAAACAAATTTGGCTGTGCTGACGGCTTGC 1565
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QY 1566 CATGTGCACGATCAGTTTCAGGACGCGAGCGTGGGAAGCCCTTTTGTCACTTGGACATG 1625
Db 1186 CATGTGCACGATCAGTTTCAGGACGCGAGCGTGGGAAGCCCTTTTGTCACTTGGACATG 1245
QY 1626 GAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGGCTAT 1685
Db 1246 GAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGGCTAT 1305
QY 1686 GTCATGGCTGGCCATCTGCGCCCTTTCATGCTGCGCACTCTGCTCATGCTGTGCTGCTGCTG 1745
Db 1306 GTCATGGCTGGCCATCTGCGCCCTTTCATGCTGCGCACTCTGCTCATGCTGTGCTGCTGCTG 1365
QY 1746 CGCTGCCCTCCGCTGCGCTGCGCCAGCAGCATGATGACTTTTGTGATGACATCTCCCTGCTG 1805
Db 1366 CGCTGCCCTCCGCTGCGCTGCGCCAGCAGCATGATGACTTTTGTGATGACATCTCCCTGCTG 1425
QY 1806 AAGTGAAGAGGCGCCATGGGCAGAGATAGAGATTTCCCTTGGACCACACCTTCCCTGGTGTCA 1865
Db 1426 AAGTGAAGAGGCGCCATGGGCAGAGATAGAGATTTCCCTTGGACCACACCTTCCCTGGTGTCA 1485
QY 1866 CTTTGGTCAAGTAGGAGACAGATGGCAGCTTGTGGCAGAGCACTTCAGGACCTTCC 1925
Db 1486 CTTTGGTCAAGTAGGAGACAGATGGCAGCTTGTGGCAGAGCACTTCAGGACCTTCC 1545
QY 1926 CCACCCACCAATGCTCTGCTTGTATGGGAAGAAAGGCTGGCAAGTGGGTGGTCCAG 1985
Db 1546 CCACCCACCAATGCTCTGCTTGTATGGGAAGAAAGGCTGGCAAGTGGGTGGTCCAG 1605
QY 1986 GGACTGTACCTGTAGGAACAGAAAGAGAAAGAGCACTCTGCTGGCGGGAATACT 2045
Db 1606 GGACTGTACCTGTAGGAACAGAAAGAGAAAGAGCACTCTGCTGGCGGGAATACT 1665
QY 2046 CTTTGGTCACTTCAAAATTTAAGTGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 2105
Db 1666 CTTTGGTCACTTCAAAATTTAAGTGGGAAATTTCTGCTGCTTGAACCTTCAGCCCTGAACCT 1725
QY 2106 TTGTCCACCAATTTCTTAAATTTCTCCAAACCAAGATTTCTTTTCTTTAGTTTTCAGAA 2165
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QY 2166 GTACTGGCATCAGCCAGGTTACCTTTGGGGTGTGTCCTGTGGTACCTTGGCAGAGAG 2225
Db 1786 GTACTGGCATCAGCCAGGTTACCTTTGGGGTGTGTCCTGTGGTACCTTGGCAGAGAG 1845
QY 2226 AGACCAAGCTTCTTCCCTGCTGCGCAAGTCACTAGGAGAGGATGCACAGTTTGTGATTT 2285
Db 1846 AGACCAAGCTTCTTCCCTGCTGCGCAAGTCACTAGGAGAGGATGCACAGTTTGTGATTT 1905
QY 2286 TGCCTTAGACAGAGGAGCTGTATAAACAAGCCTAACATTTGGTGAACAAGATTCCTCTTGA 2345
Db 1906 TGCCTTAGACAGAGGAGCTGTATAAACAAGCCTAACATTTGGTGAACAAGATTCCTCTTGA 1965
QY 2346 A 2346

Db 1486 CTTTGGTACAAAGTAGGAGACACAGATGACCTGTGGCAGAGCAGCTCAGAGCCCTCC 1545
QY 1926 CCACCCACCAATGCTCTGCTGCTGATGAGAGGAAAAGGCTGGCAAGTGGGTTCAG 1985
Db 1546 CCACCCACCAATGCTCTGCTGCTGATGAGAGGAAAAGGCTGGCAAGTGGGTTCAG 1605
QY 1986 GGAAGTACCTGTAGGAAACAGAAAGAGAAAGAAAGCACTCTGCTGGCGGGAATACT 2045
Db 1606 GGAAGTACCTGTAGGAAACAGAAAGAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1665
QY 2046 CTTGGTCACTCAATTTAAGTCGGGAAATTTCTGCTGTTGAACTTCAAGCCCTGAACCT 2105
Db 1666 CTTGGTCACTCAATTTAAGTCGGGAAATTTCTGCTGTTGAACTTCAAGCCCTGAACCT 1725
QY 2106 TTGTCACCACTCTTAAATTTCTCAACCCCAAGATTTCTTTCTTAGTTTCAGAA 2165
Db 1726 TTGTCACCACTCTTAAATTTCTCAACCCCAAGATTTCTTTCTTAGTTTCAGAA 1785
QY 2166 GTACTGGCATCACAGCAGGTTTACCTTTGGCGTGTGTGCTGTTGCTGACCCCTGGCAGAGAG 2225
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Db 1846 AGACCAAGCTTTTCCCTGCTGGGCAAGTGTAGTAGGAGGATGACAGTTTGTCTATT 1905
QY 2286 TGCTTTAGACAGAGGACTGTATAACAAGCCCTTAACATTTGTTGCAAGATTTGCTCTTGA 2345
Db 1906 TGCTTTAGACAGAGGACTGTATAACAAGCCCTTAACATTTGTTGCAAGATTTGCTCTTGA 1965
QY 2346 A 2346
Db 1966 A 1966

RESULT 13
US-09-794-743-5
; Sequence 5, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-743-5

Query Match 80.1%; Score 1881; DB 10; Length 1977;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1966; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

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RESULT 14

US-09-794-748-5

; Sequence 5, Application US/09794748

; Patent No. US20020037315A1

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; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
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Query Match 80.1%; Score 1881; DB 10; Length 1977;

Best Local Similarity 96.3%; Pred. No. 0;

Matches 1966; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

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Search completed: March 2, 2003, 13:26:27
Job time : 123 secs

COMMENT

Contact: Ye M
Shanghai Institute of Hematology
Shanghai Second Medical University, Rui-Jin Hospital
197 Rui-Jin Road II, Shanghai, 200025, P. R. China
Email: zchen@sh.cn

FEATURES
source

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Matches 1092; Conservative 0; Mismatches 20; Indels 10; Gaps 8;

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AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
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2
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
3
REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
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Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
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sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
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REFERENCE
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,

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Db	541	TGCGTCCCTGCTGCGCCAGCAGCATGATGACTTGTCTGATGACATCTCCCTGCTGAAG	600
QY	1809	TGAGGAGGCCCTATGGCAGAAAGATAGAGATTCCTCCCTGGACACACCTCCCTGGTTCACAT	1868
Db	601	TGAGGAGGCCCTATGGCAGAAAGATAGAGATTCCTCCCTGGACACACCTCCCTGGTTCACAT	660
QY	1869	TGGTCAAGTAGGAGACACAGATGGCAGCTGTGGCAGAGCAGCCTCAGGACCCCTCCCA	1928
Db	661	TGGTCAAGTAGGAGACACAGATGGCAGCTGTGGCAGAGCAGCCTCAGGACCCCTCCCA	720
QY	1929	CCACCAAAATGCCTCTGCTTGTGATGAGAGGAAAGCTGGCAAGGTGGGTTCATCA-GGG	1987

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Db 721 CCCACCAATGCGCTCGCTTGTGGAGAGAAAGTGGCAAGGTGNGTTCCAGGG 780
Qy 1988 ACTGTACTGTAGGAAACAGAGAAAGAGAAAGACACTCTGTCGGCGGGAATCTC- 2046
      |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 781 ACTGTACCCTGTAGAACNCCNAGAGAGAAAGACACTCTGTCGGCGGGAATCTCN 840
Qy 2047 TTGTGTACCTCAAAATTTAAGTCGGGAATTCCT-CTGCTGTGAAACTTTCAGCC 2098
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 841 TTGTGTACCTCAAAATTTAAGTCGGGAATTCCTGCTGCTGTGAAACTTCAGGCC 893

RESULT 5
BI084083 1059 bp mRNA linear EST 20-JUN-2001
LOCUS 602869445F1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5013994 5',
DEFINITION mRNA sequence.
ACCESSION BI084083
VERSION BI084083.1 GI:14502413
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1059)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: CLONETECH Laboratories, Inc.
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1CMI820 row: j column: 11
          High quality sequence stop: 794.
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              /clone_lib="NIH_MGC_102"
              /tissue_type="epidermoid carcinoma, cell line"
              /lab_host="DH10B (phage-resistant)"
              /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
              Site_2: EcoRI; cDNA made by oligo-dT priming.
              Directionally cloned into EcoRI/XhoI sites using the
              following 5' adaptor: GGCACGAG(G). Library constructed
              by Ling Hong in the laboratory of Gerald M. Rubin
              (University of California, Berkeley) using ZAP-cDNA
              synthesis kit (Stratagene) and Superscript II RT (Life
              Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 243 a 300 c 273 g 243 t
ORIGIN
Query Match 31.5%; Score 740.6; DB 13; Length 1059;
Best Local Similarity 92.5%; Pred. No. 7.5e-171;
Matches 837; Conservative 0; Mismatches 54; Indels 14; Gaps 5;
Qy 1157 CAAGAGCATTTGGACAGTGGCACCACCAACCTTCGTTTGGCCCAAGAAAGTGTGGAAGC 1216
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 2 CAAGAGCATTTGGACAGTGGCACCACCAACCTTCGTTTGGCCCAAGAAAGTGTGGAAGC 61
Qy 1217 TGCAGTCAAATTCATCAAGGAGCGCTCTCCACGAGAGAGTTCCCTGTATGTTCTGGCT 1276
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 62 TGCAGTCAAATTCATCAAGGAGCGCTCTCCACGAGAGAGTTCCCTGTATGTTCTGGCT 121
Qy 1277 AGGAGAGCAGTGTGCTGGCAGCAGGACCAACCCCTTGGACATTTTCCAGTTCAT 1336
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Db 122 AGGAGAGCAGTGTGCTGGCAGCAGGACCAACCCCTTGGACATTTTCCAGTTCAT 181

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Qy 1337 CTACTCTTACCTAATAGGTGAGGTTACCAACAGTCCCTTCGCGCATCACCATCTTCCGCA 1396
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 182 CTCACTCTTACCTAATAGGTGAGGTTACCAACAGTCCCTTCGCGCATCACCATCTTCCGCA 241
Qy 1397 GCATACCTTGGCGGCAGTGGGAAGATGGGCCAGCTCCCAAGACGACTGTTACAAGTTTGC 1456
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 242 GCAATACCTTGGCGGCAGTGGGAAGATGGGCCAGCTCCCAAGACGACTGTTACAAGTTTGC 301
Qy 1457 CATCTCACAGTCATCCACGGGCACCTGTTATGGAGCTCTTATCATGGAGGGCTTCTAGCT 1516
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 302 CATCTCACAGTCATCCACGGGCACCTGTTATGGAGCTCTTATCATGGAGGGCTTCTAGCT 361
Qy 1517 TGTCTTTGATCGGCCCGCGGAAACGAATTTGCTGTCTCAGCGCTTCCCATGTGACAGA 1576
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 362 TGTCTTTGATCGGCCCGCGGAAACGAATTTGCTGTCTCAGCGCTTCCCATGTGACAGA 421
Qy 1577 TGAGTTTCAAGGACGGCAGCGGTGGAAAGGCCCTTTTGTCACTTGGACATGGAAGACTGTGG 1636
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 422 TGAGTTTCAAGGACGGCAGCGGTGGAAAGGCCCTTTTGTCACTTGGACATGGAAGACTGTGG 481
Qy 1637 CTACAACATTCCACAGACAGATGAGTCAACCTCTCATGACCATAGCCTATGTCTATGCTGTC 1696
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Db 482 CTACAACATTCCACAGACAGATGAGTCAACCTCTCATGACCATAGCCTATGTCTATGCTGTC 541
Qy 1697 CATCTGCGCCCTCTTCACTGCTGCCACTCTGCCTCATGTGTGTCTAGTGGCGCTGCTCCG 1756
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 542 CATCTGCGCCCTCTTCACTGCTGCCACTCTGCCTCATGTGTGTCTAGTGGCGCTGCTCCG 601
Qy 1757 CTGCTTGGCCAGCAGCATGATGACTTTGCTGTAGTACATCTCCCTGTCTGAAGTGAAGAGG 1816
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 602 CTGCTTGGCCAGCAGCATGATGACTTTGCTGTAGTACATCTCCCTGTCTGAAGTGAAGAGG 661
Qy 1817 CCCATGGCCACAAGATAGAGATTCCTTGGACACACCTCCGTGGTTCACATTGGTTCACA 1876
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 662 CCCATGGCCACAAGATAGAGATTCCTTGGACACACCTCCGTGGTTCACATTGGTTCACA 721
Qy 1877 AGTAGGACACAGATGGCACCTGTGGCCAGAGCAGCAGCCTCCACCCACCCACCA 1936
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 722 AGTAGGACACAGATGGCACCTGTGGCCAGAGCAGCAGCCTCCACCCACCA 778
Qy 1937 ATGCTCTGCTTGTATGAGAGAAAGAGGCTGGCAAGGTGGTTCAGAGGAGCTTACT 1996
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 779 ATGCTCTGTG-CTTGTATGAGAGCCG-ACAGGCTGGCAGCAGCTGGGTTC- -GGACTGTACT 833
Qy 1997 GTAGAAACAGAAAAGAGAAAGAACACTCTGCTGCGGGAATCTCTTGGTCACT 2056
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 834 GTACGAACACGA- - - - -AGCAAGAAGAAAGTCTCTGTGCGGGAATCTCTTGGTCACTC 887
Qy 2057 CAAAT 2061
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Db 888 AATTT 892

RESULT 6
BI018588/c 747 bp mRNA linear EST 27-MAR-2002
LOCUS UI-H-DH1-awu-c-12-0-UI-s1 NCI_CGAP_DH1 Homo sapiens cDNA clone
DEFINITION IMAGE:5823683 3', mRNA sequence.
ACCESSION BI018588
VERSION BI018588.1 GI:19753865
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 747)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Dr. Jose Mercuende

```

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 1-22, >AT-rich/low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Source

Location/Qualifiers

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/db_xref="taxon:9606"
/clone="IMAGE:5823683"
/clone_lib="NCI_CGAP_DH1"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_DH1 is a normalized cDNA library containing the
following tissue(s): VS-8 Cell line from Metastatic
Chondrosarcoma in Lung. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is AGATCATTCG.
TAG_LIB=UI-H-DH1
TAG_TISSUE=Lung
TAG_SEQ=AGATCATTCG

BASE COUNT 176 a 178 c 192 g 200 t 1 others

Query Match 31.0%; Score 728; DB 14; Length 747;
Best Local Similarity 99.9%; Pred. No. 8.8e-168;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1620 GACATGAAGACTGTGGCTACACATTCACAGACAGATGAGTCAACCCCTCATGACCATTA 1679
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DB 747 GACATGAAGACTGTGGCTACACATTCACAGACAGATGAGTCAACCCCTCATGACCATTA 688
|||||
QY 1680 GCCTATGTGTCATGCGCTGCGCCCTCTTCATGCTGCCACTCTGCCCTCATGCTGTGT 1739
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DB 687 GCNTATGTGTCATGCGCTGCGCCCTCTTCATGCTGCCACTCTGCCCTCATGCTGTGT 628
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QY 1740 CAGTGGCGCTGCCCTGCCCTGCGCCAGCAGATGATGACTTTGCTGATGACATCTCC 1799
|||||
DB 627 CAGTGGCGCTGCCCTGCCCTGCGCCAGCAGATGATGACTTTGCTGATGACATCTCC 568
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QY 1800 CTGCTGAAGTGAAGGCCCATGCGCAGAAGATAGAGATTCCTCCCTGGACACACCTCCGT 1859
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DB 567 CTGCTGAAGTGAAGGCCCATGCGCAGAAGATAGAGATTCCTCCCTGGACACACCTCCGT 508
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QY 1860 GGTTCACCTTTGGTGCACAGTAGGACACACAGATGGCACCTGTGGCCAGACACCTCAGGA 1919
|||||
DB 507 GGTTCACCTTTGGTGCACAGTAGGACACACAGATGGCACCTGTGGCCAGACACCTCAGGA 448
|||||
QY 1920 CCCTCCCAACCCACCAATGCTCTGCTCTGATGGAGAAGAAAGCTGGCAAGGTGGG 1979
|||||
DB 447 CCCTCCCAACCCACCAATGCTCTGCTCTGATGGAGAAGAAAGCTGGCAAGGTGGG 388
|||||
QY 1980 TTCCAGGACTGTACCTCTAGGAACACAGAAAAGAGAAAGGACACTCTGCTGGCGGG 2039
|||||
DB 387 TTCCAGGACTGTACCTCTAGGAACACAGAAAAGAGAAAGGACACTCTGCTGGCGGG 328
|||||
QY 2040 AATACTCTTGCTACCTCAATTTAAGTCGGGAAATTCGCTCTGAAACTTCAGCCCT 2099
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DB 327 AATACTCTTGCTACCTCAATTTAAGTCGGGAAATTCGCTCTGAAACTTCAGCCCT 268
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QY 2100 GAACCTTTGTCCACCATTCTTTAAATCTTCCAAACCAAGATATCTCTTTCTTTAGTT 2159
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DB 267 GAACCTTTGTCCACCATTCTTTAAATCTTCCAAACCAAGATATCTCTTTCTTTAGTT 208
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QY 2160 TCAGAACTACTGGCATCACACGAGGTACCTTTGGCGTGTGCCCTGTGGTACCCCTGGCA 2219
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DB 207 TCAGAACTACTGGCATCACACGAGGTACCTTTGGCGTGTGCCCTGTGGTACCCCTGGCA 148
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QY 2220 GAGAAGAGACCAAGCTTTGTTTCCCTGCTGGCCAAAGTCACTAGGAGAGGATGCACATTT 2279
|||||
DB 147 GAGAAGAGACCAAGCTTTGTTTCCCTGCTGGCCAAAGTCACTAGGAGAGGATGCACATTT 88
|||||
QY 2280 GCTATTGCTTTAGACACAGGACTGTATAAACAAGCCCTAAACATTTGGTGCACAAAGATTTGCC 2339
|||||
DB 87 GCTATTGCTTTAGACACAGGACTGTATAAACAAGCCCTAAACATTTGGTGCACAAAGATTTGCC 28
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QY 2340 TCTTGAATT 2348
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DB 27 TCTTGAATT 19
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RESULT 7
BI084878/c
LOCUS
DEFINITION
602869445T1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5013994 3',
mRNA sequence.
ACCESSION
BI084878
VERSION
BI084878.1 GI:14503208
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 865)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1820 row: j column: 11
High quality sequence start: 18
High quality sequence stop: 821.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(C). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 207 a 224 c 228 g 205 t 1 others
ORIGIN
Query Match 30.8%; Score 723.8; DB 13; Length 865;
Best Local Similarity 95.3%; Pred. No. 9.7e-167;
Matches 810; Conservative 0; Mismatches 33; Indels 7; Gaps 6;

Qy	1413	GTGGAAGATGTCGGCCAGCTGCCAAGACGACTGTTTACAAAGTTTGCCATCTCACATCATCC	1472
Db	865	GTGGAAGATGTCGGCCAGCTGCCAAGACGACTGTTTAC-AGGTTGCCATCTCACATCATCC	807
Qy	1473	ACGGGCACTGTTATGGAG-CTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGC	1531
Db	806	ACGGCAACTGTTATGGAGGCTGTTATCATGGGAGGCTTCTACGTTGTCTTTGATCGGGC	747
Qy	1532	CCGAAAACGAATTGGCTTTGCTGCAGCGTTGGCA-TGTGCAGATGAGTTTCAGGACGG	1590
Db	746	CCGAAAACGAATTGGCTTTGCTGCAGCGTTGGCCATGTGCACAGATGAGTTTCAGGACGG	687
Qy	1591	CAGCGTGGAGGCGCTTTTGTACCTTGACATGGAAGACTGTGGC--TACAACATTC	1648
Db	686	CAGCGTGGAGGCGCTTTTGTCACTTGGGACATGGAAGACTGTGGCATACANACATTC	627
Qy	1649	ACAGACAGATGAGTCAACCCCTCATGACCATAGCCATATGTCATGCTGCCATCTCGGCCCT	1708
Db	626	ACAGACAGATGAGTCAACCCCTCATGACCATAGCCATATGTCATGCTGCCATCTCGGCCCT	567
Qy	1709	CTTCATCTGCCACTCTGCCTCATGCTGTGTCAGTGGCGCTGCCCTCGCTCGGCCA	1768
Db	566	CTTCATCTGCCACTCTGCCTCATGCTGTGTCAGTGGCGCTGCCCTCGCTCGGCCA	507
Qy	1769	GCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAAGAGGCCCATGGCAGA	1828
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Qy	1829	AGATAGAGATTCCTCGTGGACACACCTCCGTTGTTTCACTTTGGTTCACAAGTAGGAGAC	1888
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Qy	1889	AGATGGCACCTGTGGCCAGACACCTCAGGACCCCTCCGCCCGCTGCCCTCGCTCGCT	1948
Db	387	AGATGGCACCTGTGGCCAGACACCTCAGGACCCCTCCGCCCGCTGCCCTCGCTCGCT	328
Qy	1949	TGATGGAGAAGAAAGGCTGGCAAGTGGTTCAGGGAGTGTACCTGTAGGAACAGA	2008
Db	327	TGATGGAGAAGAAAGGCTGGCAAGTGGTTCAGGGAGTGTACCTGTAGGAACAGA	268
Qy	2009	AAAGAGAAGAAAGACACTGTGCTGGGGGAATACTCTTGGTCACTCAAAATTAAGTC	2068
Db	267	AAAGAGAAGAAAGACACTGTGCTGGGGGAATACTCTTGGTCACTCAAAATTAAGTC	208
Qy	2069	GGGAAATTCGCTCTTGAACCTTCAAGCTTGAACCTTGTCCACCATTCCTTTAAATTC	2128
Db	207	GGGAAATTCGCTCTTGAACCTTCAAGCTTGAACCTTGTCCACCATTCCTTTAAATTC	148
Qy	2129	TCCAACCCAAAGATTTCTTTTCTTTAGTTTCAGAAAGTACTGGCATCACACGAGTTA	2188
Db	147	TCCAACCCAAAGATTTCTTTTCTTTAGTTTCAGAAAGTACTGGCATCACACGAGTTA	88
Qy	2189	CTTTGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2248
Db	87	CTTTGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	29
Qy	2249	GCCAAAGTCA 2258	
Db	28	GCCAAAGTCA 19	
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DEFINITION	mRNA sequence.		
ACCESSION	BM016288		
VERSION	BM016288.1	GI:16530642	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		

REFERENCE	1	(bases 1 to 761)
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/ .	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12068 row: h column: 16 High quality sequence stop: 728.	
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	/tissue_type="mammary adenocarcinoma, cell line"	
	/lab_host="DH10B (phage-resistant)"	
	/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."	
BASE COUNT	170 a	221 c 197 g 171 t
ORIGIN	2 others	
Query Match	30.4%	Score 713.8; DB 13; Length 761;
Best Local Similarity	99.3%	Pred. No. 2.7e-164;
Matches	726;	Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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Qy	1281	GAGCAGCTGGTGTCTGGCAAGCAGGACACCCCTTGGAAACATTTCCCGAGTATCTCA 1340
Db	61	GAGCAGCTGGTGTCTGGCAAGCAGGACACCCCTTGGAAACATTTCCCGAGTATCTCA 120
Qy	1341	CTCTACCTTAATGGGTGAGTTTACCAACCACTCTTCCGCATCACCATCTTCCCGAGCAA 1400
Db	121	CTCTACCTTAATGGGTGAGTTTACCAACCACTCTTCCGCATCACCATCTTCCCGAGCAA 180
Qy	1401	TACCTGGCGGCAAGTGTGGCCACGCTGCCAAGACGACTGTTTACAAGTTTGGCCATC 1460
Db	181	TACCTGGCGGCAAGTGTGGCCACGCTGCCAAGACGACTGTTTACAAGTTTGGCCATC 240
Qy	1461	TCACAGTATCCACGGGCACTGTTATGGAGCTGTTATCGAGGCTTCTACGTTGTC 1520
Db	241	TCACAGTATCCACGGGCACTGTTATGGAGCTGTTATCGAGGCTTCTACGTTGTC 300
Qy	1521	TTTGTATCGGGCCGAAACAGAAATGGCTTGTCTGCAGCGCTTGCATGTGCACCATGAG 1580
Db	301	TTTGTATCGGGCCGAAACAGAAATGGCTTGTCTGCAGCGCTTGCATGTGCACCATGAG 360
Qy	1581	TTCAGGACGCGGCTGGAAAGGCCCTTTTGTACCTTTGGACATGGAAGCTGTGGCTAC 1640
Db	361	TTCAGGACGCGGCTGGAAAGGCCCTTTTGTACCTTTGGACATGGAAGCTGTGGCTAC 420
Qy	1641	AACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCTATGTCATGCTGCCATC 1700
Db	421	AACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCTATGTCATGCTGCCATC 480
Qy	1701	TCCGCCCTCTTCATCTGCCACTCTGCCCTCATGCTGTGTGTCACTGGCGCTGCTCCGCTGC 1760
Db	481	TCCGCCCTCTTCATCTGCCACTCTGCCCTCATGCTGTGTGTCACTGGCGCTGCTCCGCTGC 540
Qy	1761	CTGGCCGACAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAAGAGGCCCA 1820


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Db 541 CTCGCCAGCAGCATGATGACTTTGCTGATGATCTCCCTGCTGAAGTGAGGAGGCCCA 600
QY 1821 TGGCAGAAGATAGAGATTCCCTCGACACACACCTCCGCTGGTTTCACTTTGGTTCACAAGTA 1880
Db 501 TGGCAGAAGATAGAGATTCCCTCGACACACACCTCCGCTGGTTTCACTTTGGTTCACAAGTA 660
QY 1881 GGAGACACAGATGGCACCCTGTGGCCAGAGACACCTCTCAGGACCCCTCCCAACCAACATGC 1940
Db 661 GGACACACAGATGGCACCCTGTGGCCAGAGACACCTCTCAGGACCCCTCCCA-CCACAAATGC 719
QY 1941 CTCTGCCTTGA 1951
Db 720 CTCTGCCTTGA 730

RESULT 9
AL570757/c
LOCUS
DEFINITION
AL570757 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1022YF22 3
prime, mRNA sequence.
ACCESSION
AL570757
VERSION
AL570757.1 GI:12927378
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 700)
Li,W.B., Gruber,C., Jessee,J. and Pollayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1..700
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1022YF22"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="vector: pCMVSPORT 6; site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 169 a 173 c 191 g 161 t 6 others
ORIGIN

Query Match 29.3%; Score 688.6; DB 9; Length 700;
Best Local Similarity 99.3%; Pred. No. 4e-158;
Matches 688; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1555 TCAGCGCTTGCATGTGCACGATGAGTTCAGGACGCGGTGGAGGCCCTTTTGTCA 1614
Db 693 TCAGCGCTTGCATGTGCACGATGAGTTCAGGACGCGGTGGAGGCCCTTTTGTCA 634
QY 1615 CTTGGACATGGAAGACTGTGCTACACATTTCCACAGACAGATGAGTCAACCTCATGA 1674
Db 633 CYTTGYACATGGAGACTGTGCTACACATTTCCACAGACAGATGAGTCAACCTCATGA 574
QY 1675 CCATAGCCTATGTCTATGCTGCCCTCTTTCATGCTGCCACTCTGCCTCATGG 1734
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Db 513 TGTGTCAAGTGGCGTGCCTCGCTCGCCAGCAGCATGATGACTTGTGTATGACA 454
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Db 453 TCTCCCTGCTGAAGTGGAGAGGCCCATGGGAGAGATAGACATTCCTCCCTGGACACACC 394
QY 1855 TCCGTGCTTCACTTTGGTCAACAAGTAGGAGACACAGATGGCACCTCTGTGGCCAGAGACCT 1914
Db 393 TCCGTGCTTCACTTTGGTCAACAAGTAGGAGACACAGATGGCACCTCTGTGGCCAGAGACCT 334
QY 1915 CAGGACCCCTCCCAACCCACCAAAATTCCTTGCCTTGTAGGAGAGAAAGGTGCAAG 1974
Db 333 CAGGACCCCTCCCAACCCACCAAAATTCCTTGCCTTGTAGGAGAGAAAGGTGCAAG 274
QY 1975 GTGGGTTCCAGGACTCTACCTGTAGGAAACAGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 2034
Db 273 GTGGGTTCCAGGACTCTACCTGTAGGAAACAGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 214
QY 2035 GCGGGAATACTCTTGGTCAACCTCAAAATTTAAAGTCGGGAAATTCCTGCTTGAACCTTCA 2094
Db 213 GCGGGAATACTCTTGGTCAACCTCAAAATTTAAAGTCGGGAAATTCCTGCTTGAACCTTCA 154
QY 2095 GCGCTGAACCTTTGTCACCATTCCTTTAAATTTCTTCAACCCAAAGATATCTTCTTTCT 2154
Db 153 GCGCTGAACCTTTGTCACCATTCCTTTAAATTTCTTCAACCCAAAGATATCTTCTTTCT 94
QY 2155 TAGTTTTCAGAACTGCTGCTACATCACAGCAGGTTCCTTGGCGTGTCTCCCTGTGGTACCC 2214
Db 93 TAGTTTTCAGAACTGCTGCTACATCACAGCAGGTTCCTTGGCGTGTCTCCCTGTGGTACCC 34
QY 2215 TGGCAGAGAGAGACCAAGCTTGTTCCTCTGCT 2247
Db 33 TGGCAGAGAGAGACCAAGCTTGTTCCTCTGCT 1

RESULT 10
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DEFINITION
601237528F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609631 5',
mRNA sequence.
ACCESSION
BE378929
VERSION
BE378929.1 GI:9324294
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 904)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW264 row: g column: 08
High quality sequence stop: 735.
Location/Qualifiers
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/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOT87; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'

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KEYWORDS	EST.	SOURCE
	human.	

2025

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QY 2031 GCTGGCGGGGAATACTCTTGGTACACCTCAAAATTTAAAGTCGGGAAATTTCTGCTGCTTGAAC 2090
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QY 2091 TTGACGCTTGAACCTTTTGGTCCACCATTCCTTTAAATTTCTCAACCCAAAGTATTTCTTCT 2149
Db 240 TTGACGCTTGAACCTTTTGGTCCACCATTCCTTTAAATTTCTCAACCCAAAGTATTTCTTCT 181
QY 2150 TTCTTCTAGTTTTCAGAAAGTACTGGCATCACAGCAGGTTTACCTTGGGCTGTGCTCCCTGTGG 2209
Db 180 TTCTTCTAGTTTTCAGAAAGTACTGGCATCACAGCAGGTTTACCTTGGGCTGTGCTCCCTGTGG 121
QY 2210 TACCTGGCAGAGAGAGACCAAGCTTGTTCCTGCTGCTGCCCAAGTCAAGTAGGAGAGGA 2269
Db 120 TACCTGGCAGAGAGAGACCAAGCTTGTTCCTGCTGCTGCCCAAGTCAAGTAGGAGAGGA 61
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RESULT 12
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LOCUS AGENCOURT_8354446 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275949
DEFINITION 5', mRNA sequence.
ACCESSION BQ669630
VERSION BQ669630.1 GI:21780464
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL 1 (bases 1 to 945)
COMMENT National Institutes of Health; Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2459 row: 0 column: 22
High quality sequence stop: 506.
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/clone="IMAGE:6275949"
/clone_lib="NIH_MGC_102"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAGAG(o). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH MGC Library."
BASE COUNT 253 a 231 c 245 g 214 t
ORIGIN
Query Match 28.3%; Score 664.4; DB 14; Length 945;
Best Local Similarity 99.4%; Pred. NO. 3.7e-152;
Matches 676; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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Db 61 CATGGTGTGTCAGTGGCGCTGCCCTCGCTCGCCAGCAGCATGATGACTTTGCTGA 120
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Db 121 TGACATCTCCCTCTGCTGAAGTGAGGAGGCCCATGGCAGAGAATAGAGATTTCCCTCGAC 180
QY 1850 ACACCTCCGCTGGTTTCACTTTGGTGCACAGTAGGAGACACAGATGGACCTGTGGCCAGAG 1909
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Db 181 ACACCTCCGCTGGTTTCACTTTGGTGCACAGTAGGAGACACAGATGGACCTGTGGCCAGAG 240
QY 1910 CACCTCAGACACCTCCGCCACCCACCAATGCTCTGCTTGTAGTGAAGAGAAAGGCTG 1969
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Db 241 CACCTCAGGACCTCCGCCACCCACCAATGCTCTGCTTGTAGTGAAGAGAAAGGCTG 300
QY 1970 GCAAGGTGGTTTCCAGGAGCTGTACCTGTAGGAAACAGAAAAGAGAAGAACGACCTC 2029
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Db 301 GCAAGGTGGTTTCCAGGAGCTGTACCTGTAGGAAACAGAAAAGAGAAGAACGACCTC 360
QY 2030 TGTGCGGGGAATACTCTTGGTCACTCAAAATTTAAAGTCGGGAAATTTCTGCTTGAAC 2089
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Db 361 TGTGCGGGGAATACTCTTGGTCACTCAAAATTTAAAGTCGGGAAATTTCTGCTTGAAC 420
QY 2090 CTTTACGCTTGAACCTTTTGTCCACCATTTCTTAAATTTCTCCACCCCAAAGTATTTCTTCT 2149
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QY 2150 TTTCTTAGTTTTCAGAAAGTACTGGCATCACAGCAGGTTTACCTTGGCGTGTGCTCCCTGTGG 2209
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Db 481 TTTCTTAGTTTTCAGAAAGTACTGGCATCACAGCAGGTTTACCTTGGCGTGTGCTCCCTGTGG 540
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Db 541 TACCCTGGCAGAGAGAGACCAAGCTTTTCCCTGCTGGCCAAAGTCAAGTAGGAGAGG 600
QY 2269 ATGCACAGTTTGTCTATTGCTTTAGAGACAGGAGCTGTATAAACAAGCCTTAACATTTGGTG 2328
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Db 601 ATGCACAGTTTGTCTATTGCTTTANAGACAGGAGCTGTATAAACAAGCCTTAACATTTGGTG 660
QY 2329 CAAAGATTGCTCTTGAATT 2348
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Db 661 CAAAGATTGCTCTTGAATT 680

RESULT 13
BQ669630 684 bp mRNA linear EST 22-NOV-2000
LOCUS 602036021F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184140
DEFINITION 5', mRNA sequence.
ACCESSION BQ669630
VERSION BQ669630.1 GI:11285371
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM49501 row: 1 column: 05
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High quality sequence stop: 652.

FEATURES

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/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="organ: brain; Vector: PCMV-SPORT6; Site: 1. NotI;
Site: 2. SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 161 a 189 c 172 g 162 t
ORIGIN

Query Match 28.0%; Score 657.8; DB 12; Length 684;
Best Local Similarity 99.4%; Pred. No. 1.5e-150;
Matches 681; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 1534 GAAACGAATTGGCTTTGCTGTGTCAGCGCTTGCCATGTGCACGATGAGTTTCAGGACGGCAG 1593
DB 1 GAAACGAATTGGCTTTGCTGTGTCAGCGCTTGCCATGTGCACGATGAGTTTCAGGACGGCAG 60
QY 1594 CGGTGGAAGGCCCTTTGTACCTTGGACATGGAAGACTGTGGCTACAACTTCCACAGA 1653
DB 61 CGGTGGAAGGCCCTTTGTACCTTGGACATGGAAGACTGTGGCTACAACTTCCACAGA 120
QY 1654 CAGATGAGTCAACCCCTCATGACCATGACCTATGTCATGGCTGCCATCTGGCCCTCTTCA 1713
DB 121 CAGATGAGTCAACCCCTCATGACCATGACCTATGTCATGGCTGCCATCTGGCCCTCTTCA 180
QY 1714 TGCTGCCACTCTGCCCTCATGCTGTGTCAGTGGCGCTGCCCTGCCCTGCCGACGAGC 1773
DB 181 TGCTGCCACTCTGCCCTCATGCTGTGTCAGTGGCGCTGCCCTGCCCTGCCGACGAGC 240
QY 1774 ATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAAGAGGCCATGGCCAGAGAATA 1833
DB 241 ATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAAGAGGCCATGGCCAGAGAATA 300
QY 1834 GAGATTCCTCTGGACACACCTCCGTGGTTCACCTTTGGTTCACAAGTAGGAGACACAGATG 1893
DB 301 GAGATTCCTCTGGACACACCTCCGTGGTTCACCTTTGGTTCACAAGTAGGAGACACAGATG 360
QY 1894 GCACCTGTGGCCAGACACCTCTAGGACCTCCGCCACCCACCAATGCTCTGCTTGTATG 1953
DB 361 GCACCTGTGGCCAGACACCTCTAGGACCTCCGCCACCCCAATGCTCTGCTTGTATG 420
QY 1954 GAGAAGAAAAGGCTGGCAAGTGGGTTCAGGGACTGTACCTGTAGGAACACAGAAAAGA 2013
DB 421 GAGAAGAAAAGGCTGGCAAGTGGGTTCAGGGACTGTACCTGTAGGAACACAGAAAAGA 479
QY 2014 GAAGAAGAAGCACTCTGCTGGCGGAATACTCTTGGTTCACCTCAATTTAAGTCGGGAA 2073
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QY 2074 ATTCTGCTGCTCAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCCTCAA 2133
DB 540 ATTCTGCTGCTCAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCCTCAA 599
QY 2134 CCC-AAAGTATTCTCTTTTCTTTAGTTTCAGAAGTACTGGCATCACACGAGGTTACCTT 2192
DB 600 CCCAAAGTATTCTCTTTCTTTAGTTTCAGAAGTACTGGCATCACACGAGGTTACCTT 659
QY 2193 GGGCTGTGCTGCTGGTGTACCTGG 2217
DB 660 GGGCTGTGCTGCTGGTGTACCTGG 684

RESULT 14

BM048418 730 bp mRNA linear EST 07-NOV-2001
LOCUS
DEFINITION 603625683F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5452052 5',

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

mRNA sequence.
BM048418
BM048418.1 GI:16777685
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 730)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI943 row: f column: 21
High quality sequence stop: 696.

Location/Qualifiers
1. 730
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5452052"
/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pOTB7; Site: 1. XhoI;
Site: 2. EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 163 a 210 c 206 g 151 t
ORIGIN

Query Match 27.6%; Score 647.4; DB 13; Length 730;
Best Local Similarity 97.0%; Pred. No. 5.2e-148;
Matches 713; Conservative 0; Mismatches 16; Indels 6; Gaps 5;
QY 539 GATGACCGTGGGAGCCGCCCGCAGACGCTCAACATCTGTGTGATACAGCAGCAGTAA 598
DB 2 GATGACCGTGGGAG-CCCCCGCAGACGCTCAACATCTGTGTGATACAGCAGCAGTAA 60
QY 599 CTTTGGCAGTGGGTGCTGCCGCCACCCCTTCTTCATCGCTTACACAGAGGAGCTGTC 658
DB 61 CTTTGGCAGTGGGTGCTGCCGCCACCCCTTCTTCATCGCTTACACAGAGGAGCTGTC 120
QY 659 CAGCACATACCGGGACCTCCGGAGGGTGTATGTGTCCTTACACCCAGGCAAGTGGGA 718
DB 121 CAGCACATACCGGGA-CTCCGGAGGGTGTATGTGTCCTTACACCCA-GGCAAGTGGGA 178
QY 719 AGGGAGCTGGGCACCGACCTGGTAAGCATCCGCCATGGCCCCCAACGTCAGTGTGCGTGC 778
DB 179 AGGGAGCTGGGCACCGACCTGGTAAGCATCCGCCATGG-CCCAACGTCAGTGTGCGTGC 237
QY 779 CAACATTGCTGCCATCACTGAATCAGACAAGTTCTTTCATCAACGGCTCCCACTGGGAAG 838
DB 238 CAACATTGCTGCCATCACTGAATCAGACAAGTTCTTTCATCAACGGCTCCCACTGGGAAG 297
QY 839 CATCCTGGGCTGGCCTATGCTGAGATTGGCAGGCTCCGACACTCCCTGGAGCCTTTCTT 898
DB 298 CATCCTGGGCTGGCCTATGCTGAGATTGGCAGGCTCCGACACTCCCTGGAGCCTTTCTT 357
QY 899 TGACTCTCTGTAAGCAGACACCCACGTTCCCAACCTCTTCTCCCTGAGCAGCTTTGTGTCG 958
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QY 959 TGCTTCCCTCAACACAGTCTGAAGTCTGCCTCTGTGCGAGGAGCATGATCATTTGG 1018
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Db 418 TGGCTTCCCTCAACACAGTCTGAAGTCTGCCTCTGTGCGAGGAGCATGATCATTTGG 477
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QY 1019 AGTATCGACCATCGCTGTACACAGGAGTCTCTGGTATACACCCATCCGGGGGAGTG 1078
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Db 478 AGTATCGACCATCGCTGTACACAGGAGTCTCTGGTATACACCCATCCGGGGGAGTG 537
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QY 1079 GTATTATGAGTGATCATTTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGAGTG 1138
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QY 1139 CAAGGAGTACAACATGACAAAGACATTTGGACAGTGGCACACCAACCTTCCTTTGCC 1198
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Db 598 CAAGGAGTACAAGTATGACAAAGACATTTGGGACAGTGGCACAC--AACCTGCGATGCC 655
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QY 1199 CAAGAAAGTGTTCAGCTGACAGTCAATCCATCAAGGAGGAGCTCTCCACGGAGAGATT 1258
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Db 656 CAAGAAAGTGTTCAGCTGACAGTCAATCCATCAAGGAGGAGCTCTCCACGGAGAGATT 715
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RESULT 15
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DEFINITION 601508937F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910376 5',
mRNA sequence.
ACCESSION BE885725
VERSION BE885725.1 GI:10339345
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9725 row: j column: 09
High quality sequence stop: 628.

FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:3910376"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_i: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
BASE COUNT 167 a 216 c 248 g 209 t
ORIGIN
Query Match 27.0%; Score 634.2; DB 12; Length 840;
Best Local Similarity 94.4%; Pred. NO. 9.3e-145;
Matches 690; Conservative 0; Mismatches 38; Indels 3; Gaps 3;
QY 944 GCAGCTTTGGTCTGCTCCCTCAACACAGTCTGAAGTCTGCCTCTGTGCGAGG 1003
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Db 1 GCAGCTTTGGTCTGCTCCCTCAACACAGTCTGAAGTCTGCCTCTGTGCGAGG 60
QY 1004 GAGCATGATCATTTGGAGGTATCGACACTCGCTGTACACAGGAGTCTCTGGTATACACC 1063
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Db 61 GAGCATGATCATTTGGAGGTATCGACACTCGCTGTACACAGGAGTCTCTGGTATACACC 120
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QY 1064 CATCCGGGGAGTGGTATTATGAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGA 1123
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Db 121 CATCCGGGGAGTGGTATTATGAGGTGATCATTTGCGGGTGGAGATCAATGGACAGGA 180
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Db 181 TCTGAANAATGGACTGCAAGGAGTACAACATATCACAAGACCATTTGTGGACAGTGGCACAC 240
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QY 1184 CAACCTTCGTTTGGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGGCTC 1243
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Db 241 CAACCTTCGTTTGGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAAATCCATCAAGGAGGCTC 300
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QY 1484 TATGGGAGCTGTTATCATGGAGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAAACGAAT 1543
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QY 1544 TGCTTTGTCTGTCAGCGCTTCCCATGTGCACGA-TGAGTTTCAGGAGCGG-CAGCGGTGGAA 1601
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Db 601 TGCTTTGTCTGTCAGCGCTTCCCATGTGCACGA-TGAGTTTCAGGAGCGGCGGCGTGGAA 660
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QY 1602 GGCCTTTTGTCTACCTT-TGGACATGGAAGAGTGTGGCTACAACATTTCCACAGACAGATGA 1660
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Db 661 GTGCTTTTGTCTTCCCTTTGGGCTTTGGGAGACCTGGGGTACCAGTGTCCCCGACGATGTGT 720
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QY 1661 GTCAACCCCTCA 1671
|||||
Db 721 TTAACCTATGA 731
|||||

Search completed: March 2, 2003, 05:48:38
Job time : 2192.5 secs

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OM protein - protein search, using sw model

Run on: March 4, 2003, 10:00:56 ; Search time 85 Seconds
(without alignments)
714.850 Million cell updates/sec

Title: US-09-723-722A-43
Perfect score: 2419
Sequence: 1 ETDPEPEPRGRSGFVEMVD.....CLRLRQHQHDDFADDISLLK 456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002:*

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4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

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14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*

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17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2419	100.0	456	21 AAB07897	Active enzyme port
2	2419	100.0	488	22 AAB66572	Human memapsin 2.
3	2419	100.0	488	23 AAB61334	Memapsin 2 protein
4	2419	100.0	488	23 AAU99488	Human memapsin 2.
5	2419	100.0	501	21 AAY94767	Human beta-secreta
6	2419	100.0	501	21 AAB07896	Amino acid sequenc
7	2419	100.0	503	22 AAB66573	Human pro-memapsin
8	2419	100.0	503	22 AAB61335	T7 promoter and ve
9	2419	100.0	503	23 AAU99489	pro-memapsin 2 enc
10	2419	100.0	509	23 AAM52697	FLAG-tagged human

11	2414	99.8	501	21 AAY88425	Human aspartyl pro
12	2414	99.8	501	22 AAE10629	Human aspartyl pro
13	2414	99.8	501	22 AAE06859	Human aspartyl pro
14	2414	99.8	501	22 AAU06603	Human Aspartyl pro
15	2414	99.8	501	22 AAU07202	Human aspartyl pro
16	2414	99.8	501	22 AAE02581	Human aspartyl pro
17	2414	99.8	501	23 ABB78590	Human Asp-2(a) pro
18	2414	99.8	501	23 ABB06409	Human aspartyl pr
19	2413	99.8	501	19 AAW59807	Amino acid sequenc
20	2392	98.9	501	21 AAY94769	Rat beta-secretase
21	2390	98.8	501	21 AAY94768	Murine beta-secret
22	2390	98.8	501	21 AAY88427	Murine aspartyl pr
23	2390	98.8	501	22 AAE10631	Murine aspartyl pr
24	2390	98.8	501	22 AAE06861	Murine aspartyl pr
25	2390	98.8	501	22 AAU06605	Mouse Aspartyl pro
26	2390	98.8	501	22 AAU07204	Mouse aspartyl pro
27	2390	98.8	501	22 AAB84948	Mouse aspartic sec
28	2390	98.8	501	22 AAE02583	Murine aspartyl pr
29	2390	98.8	501	23 ABB78592	Mouse Asp-2(a) pro
30	2351.5	97.2	969	22 ABG09611	Novel human diagno
31	2320	95.9	790	19 AAW59808	Partial amino acid
32	2264.5	93.6	476	21 AAY88426	Human aspartyl pro
33	2264.5	93.6	476	22 AAE10630	Human aspartyl pro
34	2264.5	93.6	476	22 AAE06860	Human aspartyl pro
35	2264.5	93.6	476	22 AAU06604	Human Aspartyl pro
36	2264.5	93.6	476	22 AAU07203	Human aspartyl pro
37	2264.5	93.6	476	22 AAE02582	Human aspartyl pro
38	2264.5	93.6	476	23 ABB78591	Human Asp-2(b) pro
39	2264.5	93.6	476	23 ABB06410	Human aspartyl pro
40	2264.5	93.6	476	23 ABB06120	Human NS protein s
41	2238.5	92.5	476	22 AAE06909	Murine aspartyl pr
42	2238.5	92.5	476	22 AAE02619	Murine aspartyl pr
43	2212	91.4	427	22 AAY93866	Human polypeptide,
44	2160	89.3	453	21 AAY88438	Modified human asp
45	2160	89.3	453	22 AAE10642	Human-Asp 2(a) pro

ALIGNMENTS

RESULT 1

AAB07897

ID AAB07897 standard; Protein: 456 AA.

AC AAB07897;

XX

XX

XX

DT 14-NOV-2000 (first entry)

XX

DE Active enzyme portion of human beta-secretase enzyme.

XX

KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;

KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;

KW inhibitor; ss.

XX

OS Homo sapiens.

XX

PN WO200047618-A2.

XX

PD 17-AUG-2000.

XX

PF 10-FEB-2000; 2000WO-US03819.

PR

PR 10-FEB-1999; 99US-0119571.

PR 15-JUN-1999; 99US-0139172.

XX

XX (ELAN-) ELAN PHARM INC.

XX

PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

XX

DR WPI; 2000-533011/48.

XX

PT Purified beta-secretase protein used in assays to discover inhibitors

PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease

PS Claim 24; Fig 2B; 121pp; English.

XX The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to
 CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
 CC disease-like pathology to test if they maintain or improve cognitive
 CC ability or reduce the plaque burden. The compounds are used for the
 CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
 CC present sequence represents the active enzyme portion of human
 CC beta-secretase enzyme.

XX Sequence 456 AA;

Query Match 100.0%; Score 2419; DB 21; Length 456;
 Best Local Similarity 100.0%; Pred. No. 4.7e-242;
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETDEPEEPGRGSGFVEMVDNLGRKSGQGYVEMTVGSPQTLNLLVDTGSSNFVGAAP 60
 Db 1 ETDEPEEPGRGSGFVEMVDNLGRKSGQGYVEMTVGSPQTLNLLVDTGSSNFVGAAP 60
 Qy 61 HPFLHRYQRLSSTYRDLRGVYVPTQGWEGELGTLVSIHPGPNVTVRANIAAITE 120
 Db 61 HPFLHRYQRLSSTYRDLRGVYVPTQGWEGELGTLVSIHPGPNVTVRANIAAITE 120
 Qy 121 SDKFFINGSNWEGILGLAYAEIARPDSDLVSKQTHVPLNLSLQLCGAGFPLNQS 180
 Db 121 SDKFFINGSNWEGILGLAYAEIARPDSDLVSKQTHVPLNLSLQLCGAGFPLNQS 180
 Qy 181 EVLASVGGSMITGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNDK 240
 Db 181 EVLASVGGSMITGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNDK 240
 Qy 241 SIVDSGTTNLRPKKVFEEAAVKSIKAASSTKPPDGFWLGQVLCVQAGTTPWNIFFPVIS 300
 Db 241 SIVDSGTTNLRPKKVFEEAAVKSIKAASSTKPPDGFWLGQVLCVQAGTTPWNIFFPVIS 300
 Qy 301 LYLMEVNTNQSFRITILPQOYLRPVEDVATSDDDCYKFAISQSSTGTVMGAVIMEGFYV 360
 Db 301 LYLMEVNTNQSFRITILPQOYLRPVEDVATSDDDCYKFAISQSSTGTVMGAVIMEGFYV 360
 Qy 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPTQDESTLMTIAYVMAAI 420
 Db 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPTQDESTLMTIAYVMAAI 420
 Qy 421 CALFMLPLCLMVCOMRCLRLCRLQHQHDDFADDISLLK 456
 Db 421 CALFMLPLCLMVCOMRCLRLCRLQHQHDDFADDISLLK 456

RESULT 2

AAB66572

ID AAB66572 standard; Protein; 488 AA.

XX AC AAB66572;

XX DT 12-APR-2001 (first entry)

XX DE Human memapsin 2.

XX Human; memapsin 2; neurotropic; neuroprotective; amyloid precursor protein;
 KW App; memapsin 2 inhibitor; Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO200100665-A2.

XX

PD 04-JAN-2001.

XX 27-JUN-2000; 2000WO-US17742.

XX 28-JUN-1999; 99US-0141363.

PR 30-NOV-1999; 99US-0168060.

PR 25-JAN-2000; 2000US-0177836.

PR 27-JAN-2000; 2000US-0178368.

PR 08-JUN-2000; 2000US-0210292.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PA (UNII) UNIV ILLINOIS FOUND.

XX Tang JJN, Hong L, Ghosh AK;

XX WPI; 2001-137933/14.

DR N-PSDB; AAF31848.

XX Novel memapsin 2 inhibitors which bind to active site of memapsin 2

PT having 2 catalytic aspartic residues and substrate binding cleft, used

PT to treat Alzheimer's disease by blocking amyloid precursor protein

PT cleavage

XX Example 1; Page 72-74; 86pp; English.

PS The present sequence is given in a specification relating to an inhibitor

CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2

CC active site, which is defined by the presence of two catalytic aspartic

CC residues and a substrate binding cleft. The inhibitor is useful for

CC the treatment and diagnosis of Alzheimer's disease. It is useful in

CC screens for individuals with a genetic predisposition to Alzheimer's

CC disease. The inhibitor is useful as a reagent for specifically binding to

CC memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2

CC isolation, purification and characterisation.

XX Sequence 488 AA;

SQ Query Match 100.0%; Score 2419; DB 22; Length 488;

Best Local Similarity 100.0%; Pred. No. 5.2e-242;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETDEPEEPGRGSGFVEMVDNLGRKSGQGYVEMTVGSPQTLNLLVDTGSSNFVGAAP 60

Db 33 ETDEPEEPGRGSGFVEMVDNLGRKSGQGYVEMTVGSPQTLNLLVDTGSSNFVGAAP 92

Qy 61 HPFLHRYQRLSSTYRDLRGVYVPTQGWEGELGTLVSIHPGPNVTVRANIAAITE 120

Db 93 HPFLHRYQRLSSTYRDLRGVYVPTQGWEGELGTLVSIHPGPNVTVRANIAAITE 152

Qy 121 SDKFFINGSNWEGILGLAYAEIARPDSDLVSKQTHVPLNLSLQLCGAGFPLNQS 180

Db 153 SDKFFINGSNWEGILGLAYAEIARPDSDLVSKQTHVPLNLSLQLCGAGFPLNQS 212

Qy 181 EVLASVGGSMITGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNDK 240

Db 213 EVLASVGGSMITGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNDK 272

Qy 241 SIVDSGTTNLRPKKVFEEAAVKSIKAASSTKPPDGFWLGQVLCVQAGTTPWNIFFPVIS 300

Db 273 SIVDSGTTNLRPKKVFEEAAVKSIKAASSTKPPDGFWLGQVLCVQAGTTPWNIFFPVIS 332

Qy 301 LYLMEVNTNQSFRITILPQOYLRPVEDVATSDDDCYKFAISQSSTGTVMGAVIMEGFYV 360

Db 333 LYLMEVNTNQSFRITILPQOYLRPVEDVATSDDDCYKFAISQSSTGTVMGAVIMEGFYV 392

Qy 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPTQDESTLMTIAYVMAAI 420

Db 393 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPTQDESTLMTIAYVMAAI 452

Qy 421 CALFMLPLCLMVCOMRCLRLCRLQHQHDDFADDISLLK 456

Db 453 CALFMLPLCLMVCOMRCLRLCRLQHQHDDFADDISLLK 488

```
RESULT 3
AAB61334
ID AAB61334 standard; protein; 488 AA.
XX
AC AAB61334;
XX
DT 02-APR-2001 (first entry)
XX
DE Memapsin 2 protein.
XX
XX Memapsin 2; catalyst; Alzheimer's.
XX
XX Homo sapiens.
OS
PN W0200100663-A2.
XX
PD 04-JAN-2001.
XX
PF 27-JUN-2000; 2000WO-US17661.
XX
PR 28-JUN-1999; 99US-0141363.
PR 30-NOV-1999; 99US-0168060.
PR 23-JAN-2000; 2000US-0177836.
PR 27-JAN-2000; 2000US-0178368.
PR 08-JUN-2000; 2000US-0210292.
XX
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
XX Tang JJN, Lin X, Koelsch G;
PI
XX WPI; 2001-102885/11.
XX
XX Purified recombinant catalytically active memapsin 2, used to screen
PT inhibitors of it, which are used to treat and prevent Alzheimer's
PT disease -
XX
XX Claim 2; Page 73-75; 86pp; English.
XX
XX The present invention relates to a purified recombinant
CC catalytically active memapsin 2. The invention may be used for
CC isolating inhibitors which are used to treat or prevent
CC Alzheimer's disease. The invention may also be used to screen
CC for individuals more genetically prone to develop Alzheimer's
CC disease.
XX
XX Sequence 488 AA;
XX
Query Match 100.0%; Score 2419; DB 22; Length 488;
Best Local Similarity 100.0%; Pred. No. 5.2e-242;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETDEEPEEPPGRGGSFVEMVDNLKSGQGYVEMTVGSPPTLNILVDGTSSNFVGAAP 60
DB 33 ETDEEPEEPPGRGGSFVEMVDNLKSGQGYVEMTVGSPPTLNILVDGTSSNFVGAAP 92
QY 61 HPFLHRYQRLSTYRDLKRGVVPVYTOGWKEGELGTLVSIPIHGNVTVRANIAITE 120
DB 93 HPFLHRYQRLSTYRDLKRGVVPVYTOGWKEGELGTLVSIPIHGNVTVRANIAITE 152
QY 121 SDKFFINGSNWEGILGLAYAEIARPDSDLRPFDSLKQTHVPNLFSLQCGAGFPLNQS 180
DB 153 SDKFFINGSNWEGILGLAYAEIARPDSDLRPFDSLKQTHVPNLFSLQCGAGFPLNQS 212
QY 181 EVLASVCGSMIIGIDHSLTGSLSWYTPIRREWYEVIIIVRVEINGODLKWDCKEYNDK 240
DB 213 EVLASVCGSMIIGIDHSLTGSLSWYTPIRREWYEVIIIVRVEINGODLKWDCKEYNDK 272
QY 241 SIYDSGTNLRNLRPKVFAAASKAASSTKPPDGFNLGCVQAGTTPWNIPFVVS 300
DB 273 SIYDSGTNLRNLRPKVFAAASKAASSTKPPDGFNLGCVQAGTTPWNIPFVVS 332
QY 301 LYLMEVNTQSFRTILPQOYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 333 LYLMEVNTQSFRTILPQOYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYV 392
QY 361 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPTQDESTLMTIAYVMAAI 420
DB 393 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPTQDESTLMTIAYVMAAI 452
QY 421 CALFMLPLCLMVCMQWRCRLRCLRQHQHDDFADDISLLK 456
DB 453 CALFMLPLCLMVCMQWRCRLRCLRQHQHDDFADDISLLK 488
RESULT 4
AAU99488
ID AAU99488 standard; Protein; 488 AA.
XX
AC AAU99488;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human memapsin 2.
XX
XX Human; memapsin 2; beta secretase; aspartic protease; APP;
KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;
KW neuroprotective; nootropic; enzyme.
XX
XX Homo sapiens.
XX
XX US2002049303-A1.
PN
XX 25-APR-2002.
XX
XX 28-FEB-2001; 2001US-0796264.
XX
XX 28-JUN-1999; 99US-141363P.
PR 30-NOV-1999; 99US-168060P.
PR 25-JAN-2000; 2000US-177836P.
PR 27-JAN-2000; 2000US-178368P.
PR 27-JUN-2000; 2000US-0604608.
XX
XX (TANG/) TANG J J N.
PA (LINX/) LIN X.
PA (KOEL/) KOELSCH G.
PA (HONG/) HONG L.
XX
XX Tang JJN, Lin X, Koelsch G, Hong L;
PI
XX WPI; 2002-507280/54.
DR
XX N-PSDB; ABK88641.
XX
XX New recombinant catalytically active memapsin 2, useful to screen for
PT inhibitors of memapsin 2 which can be used to prevent and treat
PT Alzheimer's disease
XX
XX Claim 2; Page 22-23; 44pp; English.
XX
XX The present invention relates to methods for the production of
CC purified, recombinant catalytically active, memapsin 2 (beta
CC secretase). Memapsin 2, a member of the aspartic protease family,
CC cleaves beta-amyloid precursor protein (APP) found in amyloid plaques.
CC The recombinant memapsin 2 is useful for identifying inhibitors of
CC memapsin 2 in the design of drugs for the treatment and/or prevention
CC of Alzheimer's disease. The recombinant memapsin 2 can be used to
CC immunise against Alzheimer's disease. The present sequence represents
CC human memapsin 2.
XX
XX Sequence 488 AA;
Query Match 100.0%; Score 2419; DB 23; Length 488;
Best Local Similarity 100.0%; Pred. No. 5.2e-242;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETDEEPEEPPGRGGSFVEMVDNLKSGQGYVEMTVGSPPTLNILVDGTSSNFVGAAP 60
```

Db 33 ETDEPEEPGRGSEVEMVDNLKSGQGYVEMTVCSPPTLNILVDTGSSNFAVGAAP 92
QY 61 HPFLHRYQROLSTYRDLKGVYVPTQGWEGELGTLVSPHGPNTVVRANIAATE 120
Db 93 HPFLHRYQROLSTYRDLKGVYVPTQGWEGELGTLVSPHGPNTVVRANIAATE 152
QY 121 SDRFFINGSNWEGILGLAYAEIARPDSDSLEPPFDSLVKQTHVFNLFSLQLCGAGFPLNQS 180
Db 153 SDRFFINGSNWEGILGLAYAEIARPDSDSLEPPFDSLVKQTHVFNLFSLQLCGAGFPLNQS 212
QY 181 EVLASVCGSMIIGGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGODLKMCKEYNYDK 240
Db 213 EVLASVCGSMIIGGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGODLKMCKEYNYDK 272
QY 241 SIVDSGTTNLRPKKVFEAAVKSIIKAASSTKFPDGFGLGEQLVCMWAGTTPWNIFFPVIS 300
Db 273 SIVDSGTTNLRPKKVFEAAVKSIIKAASSTKFPDGFGLGEQLVCMWAGTTPWNIFFPVIS 332
QY 301 LYLMEVNTNQSFRITILPQQYLPRVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
Db 333 LYLMEVNTNQSFRITILPQQYLPRVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 392
QY 361 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
Db 393 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 452
QY 421 CALFMPLPCLMVCWRCRLRQHQHDDFADDISLLK 456
Db 453 CALFMPLPCLMVCWRCRLRQHQHDDFADDISLLK 488

RESULT 5
ID AAY94767 standard; Protein; 501 AA.
AC AAY94767;
DT 12-FEB-2001 (first entry)
XX Human beta-secretase amino acid sequence.
DE Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease; human;
KW Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective.
XX Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..45
FT Protein /label= putative signal peptide
FT FT 46..501
FT FT /label= Beta-secretase
XX WO200058479-A1.
XX 05-OCT-2000.
XX 23-MAR-2000; 2000WO-US07755.
XX 26-MAR-1999; 99US-0277229.
XX (AMGE-) AMGEN INC.
XX Citron M, Vassar RJ, Bennett BD;
XX WPI; 2000-594643/56.
XX N-PSDB; AAA28278.
XX Isolated beta-secretase' nucleic acids and encoded polypeptides, useful
PT for diagnosis and gene therapy of Alzheimer's disease
XX
XX Claim 1; Fig 4; 145pp; English.

CC This invention relates to 3 nucleotide sequences encoding beta-secretase
CC proteins. Beta-secretase is an enzyme involved in the production of one
CC of the components of amyloid plaques involved in Alzheimer's disease. The
CC invention includes an expression vector comprising the nucleotide
CC sequence, a host cell comprising the expression vector, and a process for
CC producing the protein through culturing the transformed cells. Also
CC included in the invention are a polypeptide derivative of the
CC beta-secretase protein, a fusion protein comprising beta-secretase fused
CC to a heterologous amino acid sequence, and a method for modulating the
CC levels of beta-secretase polypeptide in a mammal comprising administering
CC the polynucleotide sequence. Beta-secretase exhibits neuroprotective and
CC neurotropic activity. The beta-secretase nucleotide sequence may be used to
CC map locations of the beta-secretase gene and related genes on chromosomes
CC and as hybridization probes in diagnostic assays to test for the presence
CC of beta-secretase DNA or RNA, such as in Alzheimer's disease, Down's
CC syndrome, and amyloid angiopathy. The nucleotide sequence may also be
CC used as anti-sense inhibitors of beta-secretase expression, in gene
CC therapy of Alzheimer's disease, and for the identification of compounds
CC that modulate beta-secretase activity. Antibodies to the beta-secretase
CC protein may be used for in vitro and in vivo diagnostic purposes to
CC detect the presence of beta-secretase polypeptide in a body fluid or cell
CC sample. The present sequence represents the human beta-secretase protein.
XX
SQ Sequence 501 AA:
Query Match 100.0%; Score 2419; DB 21; Length 501;
Best Local Similarity 100.0%; Pred. No. 5,5e-242;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETDEPEEPGRGSEVEMVDNLKSGQGYVEMTVCSPPTLNILVDTGSSNFAVGAAP 60
Db 46 ETDEPEEPGRGSEVEMVDNLKSGQGYVEMTVCSPPTLNILVDTGSSNFAVGAAP 105
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Db 106 HPFLHRYQROLSTYRDLKGVYVPTQGWEGELGTLVSPHGPNTVVRANIAATE 165
QY 121 SDRFFINGSNWEGILGLAYAEIARPDSDSLEPPFDSLVKQTHVFNLFSLQLCGAGFPLNQS 180
Db 166 SDRFFINGSNWEGILGLAYAEIARPDSDSLEPPFDSLVKQTHVFNLFSLQLCGAGFPLNQS 225
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Db 226 EVLASVCGSMIIGGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGODLKMCKEYNYDK 285
QY 241 SIVDSGTTNLRPKKVFEAAVKSIIKAASSTKFPDGFGLGEQLVCMWAGTTPWNIFFPVIS 300
Db 286 SIVDSGTTNLRPKKVFEAAVKSIIKAASSTKFPDGFGLGEQLVCMWAGTTPWNIFFPVIS 345
QY 301 LYLMEVNTNQSFRITILPQQYLPRVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
Db 346 LYLMEVNTNQSFRITILPQQYLPRVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 405
QY 361 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465
QY 421 CALFMPLPCLMVCWRCRLRQHQHDDFADDISLLK 456
Db 466 CALFMPLPCLMVCWRCRLRQHQHDDFADDISLLK 501
RESULT 6
ID AAB07896
XX AAB07896 standard; Protein; 501 AA.
AC AAB07896;
XX 14-NOV-2000 (first entry)
XX Amino acid sequence of a human beta-secretase enzyme.
DE Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW

KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
inhibitor.

XX Homo sapiens.

XX WO200047618-A2.

XX 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US03819.

XX 10-FEB-1999; 99US-0119571.

XX 15-JUN-1999; 99US-0139172.

XX (ELAN-) ELAN PHARM INC.

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
PI Sinh S, Tatsuno G, Tung J, Wang J, McConlogue L;

XX WPI; 2000-533011/48.

XX N-PSDB; AAA59550, AAA59551.

XX Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease -

XX Claim 17; Fig 2A; 121pp; English.

XX The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to
CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
CC disease-like pathology to test if they maintain or improve cognitive
CC ability or reduce the plaque burden. The compounds are used for the
CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
CC present sequence represents a human beta-secretase enzyme.

XX Sequence 501 AA;

Query Match 100.0%; Score 2419; DB 21; Length 501;
Best Local Similarity 100.0%; Pred. No. 5.5e-242;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETDEEPEPCRRGSGFVEMVDNLKSGQYVEMTVGSPPTLNLVDTGSSNFAVGAAP 60

DB 46 ETDEEPEPCRRGSGFVEMVDNLKSGQYVEMTVGSPPTLNLVDTGSSNFAVGAAP 105

QY 61 HPFLHRYQRLSSTYRDLRKGVPVPTQGWEGELGTDLSVIPHGPNTVVRANIAAITE 120

DB 106 HPFLHRYQRLSSTYRDLRKGVPVPTQGWEGELGTDLSVIPHGPNTVVRANIAAITE 165

QY 121 SDRFFINGSNWEGTLGLAYAEIARPDSDSLEPFDSLKVQTHVPLNLSLQLCGAGFPLNQS 180

DB 166 SDRFFINGSNWEGTLGLAYAEIARPDSDSLEPFDSLKVQTHVPLNLSLQLCGAGFPLNQS 225

QY 181 EVLASVCGSMITIGIDHSLTGSLWYTPIRREWYEVYIIVRVEINGODLKMCKEYNVDK 240

DB 226 EVLASVCGSMITIGIDHSLTGSLWYTPIRREWYEVYIIVRVEINGODLKMCKEYNVDK 285

QY 241 SIYDSGTTNLRPKKVFEEAAVKSIKAASSTKPKPDGFWLGEQLVCWQAGTTPWNIFPVIS 300

DB 286 SIYDSGTTNLRPKKVFEEAAVKSIKAASSTKPKPDGFWLGEQLVCWQAGTTPWNIFPVIS 345

QY 301 LYLMEVNTNSFRITILPQOYLRPEVDVATSQDDCYKFAISQSSTGTVMGAVIMEGYV 360

DB 346 LYLMEVNTNSFRITILPQOYLRPEVDVATSQDDCYKFAISQSSTGTVMGAVIMEGYV 405

QY 361 FDRARKRIGFAVSACHVDEFTAAVGPVFTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420

DB 406 FDRARKRIGFAVSACHVDEFTAAVGPVFTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465

QY 421 CALFMLPLCLMVCQWRCRLCRLRQHQHDDFADDISLLK 456
DB 466 CALFMLPLCLMVCQWRCRLCRLRQHQHDDFADDISLLK 501

RESULT 7

AAB66573

ID AAB66573 standard; Protein; 503 AA.

XX AAB66573;

XX 12-APR-2001 (first entry)

XX Human pro-memapsin 2.

XX Human; memapsin 2; nootropic; neuroprotective; amyloid precursor protein;
KW APP; memapsin 2 inhibitor; Alzheimer's disease; ss.

XX Homo sapiens.

XX WO200100665-A2.

XX 04-JAN-2001.

XX 27-JUN-2000; 2000WO-US17742.

XX 28-JUN-1999; 99US-01411363.

XX 30-NOV-1999; 99US-0168060.

XX 25-JAN-2000; 2000US-0177836.

XX 27-JAN-2000; 2000US-0178368.

XX 08-JUN-2000; 2000US-0210292.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX (UNII) UNIV ILLINOIS FOUND.

XX Tang JJN, Hong L, Ghosh AK;

XX WPI; 2001-137933/14.

XX Novel memapsin 2 inhibitors which bind to active site of memapsin 2

PT having 2 catalytic aspartic residues and substrate binding cleft, used

PT to treat Alzheimer's disease by blocking amyloid precursor protein

PT cleavage -

XX Example 4; Fig 1; 86pp; English.

PS The present sequence is given in a specification relating to an inhibitor

CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2

CC active site, which is defined by the presence of two catalytic aspartic

CC residues and a substrate binding cleft. The inhibitor is useful for

CC the treatment and diagnosis of Alzheimer's disease. It is useful in

CC screens for individuals with a genetic predisposition to Alzheimer's

CC disease. The inhibitor is useful as a reagent for specifically binding to

CC memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2

CC isolation, purification and characterisation.

XX Sequence 503 AA;

Query Match 100.0%; Score 2419; DB 22; Length 503;

Best Local Similarity 100.0%; Pred. No. 5.5e-242;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETDEEPEPCRRGSGFVEMVDNLKSGQYVEMTVGSPPTLNLVDTGSSNFAVGAAP 60

DB 48 ETDEEPEPCRRGSGFVEMVDNLKSGQYVEMTVGSPPTLNLVDTGSSNFAVGAAP 107

QY 61 HPFLHRYQRLSSTYRDLRKGVPVPTQGWEGELGTDLSVIPHGPNTVVRANIAAITE 120

DB 108 HPFLHRYQRLSSTYRDLRKGVPVPTQGWEGELGTDLSVIPHGPNTVVRANIAAITE 167

QY 121 SDRFFINGSNWEGTLGLAYAEIARPDSDSLEPFDSLKVQTHVPLNLSLQLCGAGFPLNQS 180

DB 168 SDRFFINGSNWEGTLGLAYAEIARPDSDSLEPFDSLKVQTHVPLNLSLQLCGAGFPLNQS 227

PT Inhibitors of memapsin 2 which can be used to prevent and treat
PT Alzheimer's disease -
PS Example 3; Fig 1; 44pp; English.
XX
XX The present invention relates to methods for the production of
CC purified, recombinant catalytically active, memapsin 2 (beta
CC secretase). Memapsin 2, a member of the aspartic protease family,
CC cleaves beta-amyloid precursor protein (APP) found in amyloid plaques.
CC The recombinant memapsin 2 is useful for identifying inhibitors of
CC memapsin 2 in the design of drugs for the treatment and/or prevention
CC of Alzheimer's disease. The recombinant memapsin 2 can be used to
CC immunize against Alzheimer's disease. The present sequence represents
XX pro-memapsin 2 encoded by plasmid construct pET-11a-memapsin 2.
XX
XX Sequence 503 AA;
SQ
Query Match 100.0%; Score 2419; DB 23; Length 503;
Best Local Similarity 100.0%; Pred. No. 5.5e-242;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETDEEPEEGRGSGFVEMVDNLKSGQGYVEMTVGSPPTNLILVDTGSSNFVGAAP 60
DB 48 ETDEEPEEGRGSGFVEMVDNLKSGQGYVEMTVGSPPTNLILVDTGSSNFVGAAP 107
QY 61 HPFLHRYQQLSSTYRDLRKGVPVPTQGWEGELGTDLSVPHGPNVTVRANIAAITE 120
DB 108 HPFLHRYQQLSSTYRDLRKGVPVPTQGWEGELGTDLSVPHGPNVTVRANIAAITE 167
QY 121 SDRFFINGSNWEGILGLAYAEIARPDSDLVSKQTHVPLNLSLQLCGAGFPLNQS 180
DB 168 SDRFFINGSNWEGILGLAYAEIARPDSDLVSKQTHVPLNLSLQLCGAGFPLNQS 227
QY 181 EVLASVGGSMIIGIDHSLTSGSLWYTPIRREWYEVIIIVRVEINGDLMCKEYNDK 240
DB 228 EVLASVGGSMIIGIDHSLTSGSLWYTPIRREWYEVIIIVRVEINGDLMCKEYNDK 287
QY 241 SIYDSGTTNLRPKKVFEEAAVKSIKAASSTKFPDGLVQWAGTTPWNIPFVVIS 300
DB 288 SIYDSGTTNLRPKKVFEEAAVKSIKAASSTKFPDGLVQWAGTTPWNIPFVVIS 347
QY 301 LYLMEVNTQSFRTITLPPQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 348 LYLMEVNTQSFRTITLPPQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 407
QY 361 FDRARKRIGFAVSACHVDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
DB 408 FDRARKRIGFAVSACHVDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 467
QY 421 CALFMLPLCLMWQWRCRLRQHQHDDFADDISLLK 456
DB 468 CALFMLPLCLMWQWRCRLRQHQHDDFADDISLLK 503
RESULT 10
AAM52697
ID AAM52697 standard; Protein; 509 AA.
AC AAM52697;
XX
XX 26-FEB-2002 (first entry)
XX
XX FLAG-tagged human beta-secretase.
XX
XX Human; beta-secretase; FLAG tag; inhibitor; amine compound;
KW beta amyloid protein production; head injury; spinal injury;
KW amyloid precursor protein alpha secretion; nerve damage;
KW meningitis sequela; cerebral paralysis; memory disorder;
KW mental disease; nootropic; neuroprotective; cerebroprotective.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Region 502..509
FT /label= FLAG_tag
XX
PN WO200187293-A1.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP04144.
XX
PR 19-MAY-2000; 2000JP-0152758.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
XX Miyamoto M, Matsui J, Fukumoto H, Tarui N;
XX
XX WPI; 2002-055640/07.
DR N-PSDB; ABA02406.
XX
XX Beta-secretase inhibitor used for treating e.g. Alzheimer's disease and
PT injury to brain or spine, and neurodegeneration, comprises amine
PT compound -
XX
XX Examples; Page 79-81; 86pp; Japanese.
XX
XX The invention relates to novel amine compounds which are beta-secretase
CC inhibitors. The beta-secretase compounds also have the ability to
CC promote amyloid precursor protein alpha secretion and to inhibit beta
CC amyloid protein production. The beta-secretase inhibitors of the
CC invention can be used for treating head or spinal injuries, nerve damage,
CC sequelae of meningitis, cerebral paralysis, memory disorders and mental
CC diseases. The present sequence represents a FLAG-tagged human
CC beta-secretase used in the exemplifications of the invention.
XX
SQ Sequence 509 AA;
Query Match 100.0%; Score 2419; DB 23; Length 509;
Best Local Similarity 100.0%; Pred. No. 5.6e-242;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETDEEPEEGRGSGFVEMVDNLKSGQGYVEMTVGSPPTNLILVDTGSSNFVGAAP 60
DB 46 ETDEEPEEGRGSGFVEMVDNLKSGQGYVEMTVGSPPTNLILVDTGSSNFVGAAP 105
QY 61 HPFLHRYQQLSSTYRDLRKGVPVPTQGWEGELGTDLSVPHGPNVTVRANIAAITE 120
DB 106 HPFLHRYQQLSSTYRDLRKGVPVPTQGWEGELGTDLSVPHGPNVTVRANIAAITE 165
QY 121 SDRFFINGSNWEGILGLAYAEIARPDSDLVSKQTHVPLNLSLQLCGAGFPLNQS 180
DB 166 SDRFFINGSNWEGILGLAYAEIARPDSDLVSKQTHVPLNLSLQLCGAGFPLNQS 225
QY 181 EVLASVGGSMIIGIDHSLTSGSLWYTPIRREWYEVIIIVRVEINGDLMCKEYNDK 240
DB 226 EVLASVGGSMIIGIDHSLTSGSLWYTPIRREWYEVIIIVRVEINGDLMCKEYNDK 285
QY 241 SIYDSGTTNLRPKKVFEEAAVKSIKAASSTKFPDGLVQWAGTTPWNIPFVVIS 300
DB 286 SIYDSGTTNLRPKKVFEEAAVKSIKAASSTKFPDGLVQWAGTTPWNIPFVVIS 345
QY 301 LYLMEVNTQSFRTITLPPQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 346 LYLMEVNTQSFRTITLPPQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 405
QY 361 FDRARKRIGFAVSACHVDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
DB 406 FDRARKRIGFAVSACHVDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465
QY 421 CALFMLPLCLMWQWRCRLRQHQHDDFADDISLLK 456
DB 466 CALFMLPLCLMWQWRCRLRQHQHDDFADDISLLK 501

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RESULT 11
AAY88425
ID AAY88425 standard; Protein; 501 AA.
XX
AC AAY88425;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human aspartyl protease 2 (a) (Asp2) amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US20881.
XX
PR 24-SEP-1998; 98US-0101594.
XX
PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR N-PSDB; AAL15662.
XX
XX
PT New enzyme designated human aspartase useful in research into
PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at
PT the beta secretase site to produce amyloid beta peptide -
PS Claim 48; Fig 2; 183pp; English.
XX
CC This sequence represents the human aspartyl protease 2 (Asp2) amino acid
CC sequence. The invention relates to a protease (e.g. Asp2) capable of
CC cleaving the beta secretase site of amyloid precursor protein (APP). The
CC protease contains a sequence encoding the amino acid sequence DTG and a
CC sequence encoding DSG or DTG separated by 100-300 amino acids. When
CC mutated the APP gene causes an autosomal dominant form of Alzheimer's
CC disease. APP localises to the cell surface membrane and have a single
CC C-terminal transmembrane domain. Proteolytic processing of APP produces
CC the amyloid beta protein, which is possibly very important in Alzheimer's
CC disease. The invention includes a nucleotide sequence encoding the
CC protease, a vector containing the nucleotide sequence, and a cell line
CC comprising the vector. Methods for screening for inhibitors of beta
CC secretase activity are also given in the invention. The human aspartase
CC protein and nucleotide sequences and the methods for identifying
CC inhibitors of the protease, are useful in the treatment of and research
CC in to Alzheimer's disease.
XX
SQ Sequence 501 AA;
Query Match 99.8%; Score 2414; DB 21; Length 501;
Best Local Similarity 99.8%; Pred. No. 1.8e-241;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ETDEEPEPEGRGSGFVEMVDNLKSGGGYVEMTVGSPPTLNILVDTGSSNFVAGAAP 60
Db 46 ETDEEPEPEGRGSGFVEMVDNLKSGGGYVEMTVGSPPTLNILVDTGSSNFVAGAAP 105
QY 61 HPFLHRYQRLSTYRDLRGVYPYQKGWEGELGTDLVSLPHGPNVTVRANIAAITE 120
Db 106 HPFLHRYQRLSTYRDLRGVYPYQKGWEGELGTDLVSLPHGPNVTVRANIAAITE 165
QY 121 SDRFFINGSNWEGILGLAYAEIARDDSLPEFDSLVKQTHVPNLFSLQCGAGFPLNQS 180
Db 166 SDRFFINGSNWEGILGLAYAEIARDDSLPEFDSLVKQTHVPNLFSLHCGAGFPLNQS 225
QY 181 EVLASVGGSMIGGDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDK 240

```

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Db 226 EVLASVGGSMIIGGDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDK 285
QY 241 SIVDSGTTNLRPKVFEAAVKSIKAASSTSEKFPDGFVLGQVCMQAGTTWNIPFVVIS 300
Db 286 SIVDSGTTNLRPKVFEAAVKSIKAASSTSEKFPDGFVLGQVCMQAGTTWNIPFVVIS 345
QY 301 LYLGMGEVTTNOSFRITILPQOYLRPVEDVATSDDCYKFAISOSSTGTVNGAVIMEGFYVV 360
Db 346 LYLGMGEVTTNOSFRITILPQOYLRPVEDVATSDDCYKFAISOSSTGTVNGAVIMEGFYVV 405
QY 361 FDRARKRIGFAVSACHVHDEFRTAAVSGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFRTAAVSGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465
QY 421 CALFMLPLCLMVCMQWRCRLCRLRQHQHDDFADDISLLK 456
Db 466 CALFMLPLCLMVCMQWRCRLCRLRQHQHDDFADDISLLK 501

RESULT 12
AAE10629
ID AAE10629 standard; Protein; 501 AA.
XX
AC AAE10629;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human aspartyl protease 2(a) [hu-Asp2(a)] protein.
XX
KW Human; aspartyl protease 2(a); Asp2(a); amyloid precursor protein; APP;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; neurotrophic; neuroprotective;
KW chromosome 11q23.3-24.1.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide 1..21 Location/Qualifiers
FT Peptide 22..45 /label= Signal_peptide
FT Peptide 46..57 /label= Asp_2a_prepropeptide
FT Peptide 58..501 /label= Asp_2a_propeptide
FT Protein 58..501 /label= Mature_human_Asp_2a_protein
FT Region 420..454 /label= Alpha-helical_spacer_region
FT Domain 455..477 /label= Transmembrane_domain
FT Domain 478..501 /label= Cytoplasmic_domain
XX
GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-0023315.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
(PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Bienkowski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
DR N-PSDB; AAD17865.
XX
PT Polypeptide comprising fragments of human aspartyl protease with
amyloid precursor protein processing activity and alpha-secretase

```

PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
PS Example 2; Fig 2; 187pp; English.
XX The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC Asp1 proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is long form of
CC human Asp2 protein, designated as Asp2(a). Asp2 gene is localised
CC on chromosome 11q23.3-24.1.
XX
SQ Sequence 501 AA;
Query Match 99.8%; Score 2414; DB 22; Length 501;
Best Local Similarity 99.8%; Pred. No. 1.8e-241;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ETDEEPEEPPGRGSGFVEMVDNLKSGQGYVYVEMTVGSPPTLNILVDTGSSNFAVGAAP 60
DB 46 ETDEEPEEPPGRGSGFVEMVDNLKSGQGYVYVEMTVGSPPTLNILVDTGSSNFAVGAAP 105
QY 61 HPFLHRYRQQLSSTYRDLKRGVYVPTQCKWEGELGTLVSIHPGPNVTVRANIAITE 120
DB 106 HPFLHRYRQQLSSTYRDLKRGVYVPTQCKWEGELGTLVSIHPGPNVTVRANIAITE 165
QY 121 SDRFFINGSNWEGILGLAYAEIARPDLSLPPFDLSLVKQTHVPLNLSLQCGAGFPLNQS 180
DB 166 SDRFFINGSNWEGILGLAYAEIARPDLSLPPFDLSLVKQTHVPLNLSLQCGAGFPLNQS 225
QY 181 EVLASVGGSMIIGIDHSLTGLSWYTPIRREWYEVYIIVRVEINGQDLKMDCKEYNDK 240
DB 226 EVLASVGGSMIIGIDHSLTGLSWYTPIRREWYEVYIIVRVEINGQDLKMDCKEYNDK 285
QY 241 SIYDSGTTNLRPKKVEAAVSKIAASSTKFPDGFMLGEQLVCWAGTTPWNIFPVIS 300
DB 286 SIYDSGTTNLRPKKVEAAVSKIAASSTKFPDGFMLGEQLVCWAGTTPWNIFPVIS 345
QY 301 LYLMEVNTQSFRTILPQOYLRPVEDVATSDDDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 346 LYLMEVNTQSFRTILPQOYLRPVEDVATSDDDCYKFAISQSSTGTVMGAVIMEGFYV 405
QY 361 FDRARRIGFAVSACHVDFEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
DB 406 FDRARRIGFAVSACHVDFEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465
QY 421 CALFMPLPLCLMWQWRCRLCRLQHQHDFADDISLLK 456
DB 466 CALFMPLPLCLMWQWRCRLCRLQHQHDFADDISLLK 501
RESULT 13
AAE06859
ID AAE06859 standard; Protein; 501 AA.
XX
AC AAE06859;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human aspartyl protease 2a (Hu-Asp2a) protein.
XX
KW Human; aspartyl protease 2a; Asp 2a; beta-amyloid precursor protein; APP;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;

KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW neuroprotective; antisense therapy; gene therapy;
KW chromosome 11q23.3-24.1.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Peptide 1..21
FT /label= Signal_peptide
FT Protein 22..501
FT /note= "Mature human aspartyl protease 2a (Hu-Asp2a)"
FT Region 420..454
FT /note= "Alpha helical spacer region"
FT Domain 455..477
FT /label= Transmembrane_domain
FT Domain 478..501
FT /label= Cytoplasmic_domain
XX
XX WO200150829-A2.
PN
XX
XX 19-JUL-2001.
PD
XX
XX 09-MAY-2001; 2001WO-IB00799.
PF
XX
XX 09-MAY-2001; 2001WO-IB00799.
PR
XX
XX (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX WPI; 2001-483072/52.
DR N-PSDB; AAD13021.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity
XX
XX Claim 49; Fig 2; 185pp; English.
PS
XX
XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC blots. The present sequence is human aspartyl protease 2 (Hu-Asp2), a
CC 'long' form designated as (Hu-Asp2a). Hu-Asp 2 gene is localised on
CC chromosome 11q23.3-24.1.
XX
SQ Sequence 501 AA;
Query Match 99.8%; Score 2414; DB 22; Length 501;
Best Local Similarity 99.8%; Pred. No. 1.8e-241;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ETDEEPEEPPGRGSGFVEMVDNLKSGQGYVYVEMTVGSPPTLNILVDTGSSNFAVGAAP 60
DB 46 ETDEEPEEPPGRGSGFVEMVDNLKSGQGYVYVEMTVGSPPTLNILVDTGSSNFAVGAAP 105

QY 61 HPFLHRYQRLSTYRDLRGVYVPYTGQKWEGLGTHDLSVPHGPNVTVRANIAAITE 120
Db 106 HPFLHRYQRLSTYRDLRGVYVPYTGQKWEGLGTHDLSVPHGPNVTVRANIAAITE 165
QY 121 SKKFFINGSNWEGILGLAYAEIARPDSDLEPFEDSLVKQTHVPNLFSLHLCGAGFPLNQS 180
Db 166 SKKFFINGSNWEGILGLAYAEIARPDSDLEPFEDSLVKQTHVPNLFSLHLCGAGFPLNQS 225
QY 181 EVLASVGGSMIIGDHSLSYTGSLWYTPIRREWYVEIIVRVEINGODLKMCKEYNDK 240
Db 226 EVLASVGGSMIIGDHSLSYTGSLWYTPIRREWYVEIIVRVEINGODLKMCKEYNDK 285
QY 241 SIVDSGTTNLRPKKVFEEAAVKSIAASSTKFPDGFMLGEOVCWQAGTTPWNIFFPVIS 300
Db 286 SIVDSGTTNLRPKKVFEEAAVKSIAASSTKFPDGFMLGEOVCWQAGTTPWNIFFPVIS 345
QY 301 LYLMGEVTVNSFRITILPQQYLPRVEDVATSDDCYKFAISOSSTGTVMGAVIMEGFYVV 360
Db 346 LYLMGEVTVNSFRITILPQQYLPRVEDVATSDDCYKFAISOSSTGTVMGAVIMEGFYVV 405
QY 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDDESTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDDESTLMTIAYVMAAI 465
QY 421 CALFMLPLCLMVCMOWRCLRLRQOHHDDFADDISLLK 456
Db 466 CALFMLPLCLMVCMOWRCLRLRQOHHDDFADDISLLK 501

RESULT 14

AAU06603
ID AAU06603 standard; Protein: 501 AA.
AC AAU06603;
XX
XX 24-OCT-2001 (first entry)
XX Human Aspartyl protease 2(a), Asp2(a).
DE
XX Human: Aspartyl protease; Asp2(a); beta-secretase; neurotropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..21
FT Peptide /label= Signal peptide
FT Peptide 22..45
FT Peptide /label= Pre_pro-peptide
FT Peptide 46..57
FT Protein /label= Pro-peptide
FT Protein 57..501
FT Region /label= Mature_Asp2(a)
FT Region 420..454
FT Domain /label= Alpha_helical_spacer_region
FT Domain 455..477
FT Domain /label= Transmembrane_domain
FT Domain 478..501
FT Domain /label= Cytoplasmic_domain
XX
PN WO200149098-A2.
XX
XX 12-JUL-2001.
XX
XX 09-MAY-2001; 2001WO-IB00798.
XX
XX 09-MAY-2001; 2001WO-IB00798.
XX
XX (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.

(YANR/) YAN R.
Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
WPI: 2001-502549/55.
N-PSDB: AAS11517.

Novel purified polypeptide comprising fragment of mammalian aspartyl
protease 2, lacking Asp2 transmembrane domain and retaining beta
secretase activity of Asp2 useful for identifying inhibitors of Asp2
activity

Claim 49; Fig 2; 185pp; English.

The invention relates to a purified polypeptide comprising a fragment of
mammalian aspartyl protease (Asp2) protein which lacks the Asp2
transmembrane domain and the Asp2 protein, and where the polypeptide and
the fragment retain the beta-secretase activity of the mammalian Asp2
protein. The invention also details polynucleotides for the Asp
proteins and vectors expressing them, and a polypeptide (isoform of
amyloid protein precursor (APP)) comprising the amino acid sequence of an
APP or its fragment containing an APP cleavage site recognizable by a
mammalian beta-secretase, and further comprising two lysine residues at
the carboxyl terminus of the amino acid sequence of the mammalian APP or
APP fragment. Also included in the invention are methods of identifying
modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
useful for treating Alzheimer's disease. APP is useful in methods for
identifying inhibitors or modulators of human Asp2 activity and
amyloid-beta (Abeta) peptide production. APP is also useful in designing
therapeutics for the treatment or prevention of Alzheimer's disease.
APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
is associated with increased levels of Abeta processing is useful in
assays relating the Alzheimer's research. The expression vector is useful
for recombinantly expressing APP. Nucleic acids that hybridize to
Asp oligonucleotides are useful as probes or primers. The probes are
useful for detecting Hu-Asp nucleic acids in in vitro assays and in
Northern and Southern blots. The present sequence is human Asp2(a).

Sequence 501 AA:

Query Match 99.8%; Score 2414; DB 22; Length 501;
Best Local Similarity 99.8%; Pred. NO. 1.8e-241;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETDEPEPEGRGRGSFVEMVDNLRGKSGQGYVEMTVGSPPTLNLVDGSSNFAVGAAP 60
Db 46 ETDEPEPEGRGRGSFVEMVDNLRGKSGQGYVEMTVGSPPTLNLVDGSSNFAVGAAP 105
QY 61 HPFLHRYQRLSTYRDLRGVYVPYTGQKWEGLGTHDLSVPHGPNVTVRANIAAITE 120
Db 106 HPFLHRYQRLSTYRDLRGVYVPYTGQKWEGLGTHDLSVPHGPNVTVRANIAAITE 165
QY 121 SKKFFINGSNWEGILGLAYAEIARPDSDLEPFEDSLVKQTHVPNLFSLHLCGAGFPLNQS 180
Db 166 SKKFFINGSNWEGILGLAYAEIARPDSDLEPFEDSLVKQTHVPNLFSLHLCGAGFPLNQS 225
QY 181 EVLASVGGSMIIGDHSLSYTGSLWYTPIRREWYVEIIVRVEINGODLKMCKEYNDK 240
Db 226 EVLASVGGSMIIGDHSLSYTGSLWYTPIRREWYVEIIVRVEINGODLKMCKEYNDK 285
QY 241 SIVDSGTTNLRPKKVFEEAAVKSIAASSTKFPDGFMLGEOVCWQAGTTPWNIFFPVIS 300
Db 286 SIVDSGTTNLRPKKVFEEAAVKSIAASSTKFPDGFMLGEOVCWQAGTTPWNIFFPVIS 345
QY 301 LYLMGEVTVNSFRITILPQQYLPRVEDVATSDDCYKFAISOSSTGTVMGAVIMEGFYVV 360
Db 346 LYLMGEVTVNSFRITILPQQYLPRVEDVATSDDCYKFAISOSSTGTVMGAVIMEGFYVV 405
QY 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDDESTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDDESTLMTIAYVMAAI 465
QY 421 CALFMLPLCLMVCMOWRCLRLRQOHHDDFADDISLLK 456

Db 466 CALFMLPLCLMWQWRCRLRQHQHDDFADDISLLK 501

RESULT 15

AAU07202
ID AAU07202 standard; Protein: 501 AA.

XX AC AAU07202;

XX DT 24-OCT-2001 (first entry)

XX DE Human aspartyl protease 2a (Asp-2a).

XX KW Human: aspartyl protease 1; Asp-1; nootropic; neuroprotective;

XX KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;

XX KW beta-secretase; Alzheimer's disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..21 "Signal peptide"

XX FT Misc_feature 22..45 "Pre-propeptide"

XX FT Misc_feature 46..57 "Propeptide"

XX FT Protein 58..501

XX FT Region 420..454 "Mature Aspartyl protease-2a"

XX FT Domain 455-477 "Alpha helical spacer region"

XX FT Domain 478..501 "Transmembrane domain"

XX FT Domain /note= "Cytoplasmic domain"

XX PN WO200149097-A2.

XX PD 12-JUL-2001.

XX PF 09-MAY-2001; 2001WO-IB00797.

XX PR 09-MAY-2001; 2001WO-IB00797.

XX PA (BIEN/) BIENKOWSKI M J.

XX PA (GURN/) GURNEY M E.

XX PA (HEIN/) HEINRIKSON R L.

XX PA (PARO/) PARODI L A.

XX PA (YANR/) YAN R.

XX PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

XX DR WPI: 2001-502548/55.

XX DR N-PSDB: AAS11702.

XX PT Novel purified polypeptide comprising fragment of mammalian aspartyl

XX PT protease 2, lacking Asp2 transmembrane domain and retaining beta

XX PT secretase activity of Asp2 useful for identifying inhibitors of Asp2

XX PT activity -

XX PS Claim 49; Fig 2; 185pp; English.

XX CC The invention relates to a novel purified polypeptide comprising a

XX CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the

XX CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide

XX CC and the fragment retain the beta-secretase activity of the mammalian Asp2

XX CC protein. Also included is an isoform of amyloid protein precursor (APP)

XX CC comprising the amino acid sequence of a APP or its fragment containing

XX CC an APP cleavage site recognisable by a mammalian beta-secretase, and

XX CC further comprising two lysine residues at the carboxyl terminus of the

XX CC amino acid sequence of the mammalian APP or APP fragment. The

XX CC polypeptides are used for assaying for modulators of beta-secretase

XX CC activity; identifying agents that inhibit the APP processing activity

CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC modulate the activity of Asp2; and for reducing cellular production of
CC amyloid beta (Abeta) from APP. Agents identified by the above methods
CC are useful for treating Alzheimer's disease; and for identifying
CC modulators of amyloid-beta (Abeta) peptide production, for use in
CC designing therapeutics for the treatment or prevention of Alzheimer's
CC disease. Probes and primers derived from Asp nucleic acid sequences
CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence represents the
CC amino acid sequence of human Asp-2a used in the methods of the invention.
XX

SQ Sequence 501 AA;

Query Match 99.8%; Score 2414; DB 22; Length 501;

Best Local Similarity 99.8%; Pred No. 1.8e-241;

Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETDEEPEEPRRGSGFVEMVDNLKRGSGQGYVEMTVGSPPTLNILVDTGSSNFAVGAAP 60

DB 46 ETDEEPEEPRRGSGFVEMVDNLKRGSGQGYVEMTVGSPPTLNILVDTGSSNFAVGAAP 105

QY 61 HPFLHRYRQRLSSYRDLKRGVYVPTQGWEGELGTLVSPHGPNTVTRANIAITE 120

DB 106 HPFLHRYRQRLSSYRDLKRGVYVPTQGWEGELGTLVSPHGPNTVTRANIAITE 165

QY 121 SDKFFINGSNWEGILGLAYAEIARPDSDLPRFDSLKQTHVPLNLSLQICGAGFPLNQS 180

DB 166 SDKFFINGSNWEGILGLAYAEIARPDSDLPRFDSLKQTHVPLNLSLQICGAGFPLNQS 225

QY 181 EVLASVGGSMIIGGIDHSYTGSLWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYDK 240

DB 226 EVLASVGGSMIIGGIDHSYTGSLWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYDK 285

QY 241 SIVDSGTTNLRPLPKVFEAAVKSIIKAASTKEPPDGFNLGEQLVCWQAGTTPWNIFFVIS 300

DB 286 SIVDSGTTNLRPLPKVFEAAVKSIIKAASTKEPPDGFNLGEQLVCWQAGTTPWNIFFVIS 345

QY 301 LYLMGEVTNOSFRITILPOQYLRPVEDVATSDDCYKFAISQSSTGTVMGAVIMEGFYV 360

DB 346 LYLMGEVTNOSFRITILPOQYLRPVEDVATSDDCYKFAISQSSTGTVMGAVIMEGFYV 405

QY 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPTQDESLMTIAYVMAAI 420

DB 406 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPTQDESLMTIAYVMAAI 465

QY 421 CALFMLPLCLMWQWRCRLRQHQHDDFADDISLLK 456

DB 466 CALFMLPLCLMWQWRCRLRQHQHDDFADDISLLK 501

Search completed: March 4, 2003, 10:03:45

Job time : 88 secs

OTHER INFORMATION: 273-275, 282-285, 316-318, 331-336, 342-348,
OTHER INFORMATION: 354-357, 366-370, 372-375, 380-383, 390-395,
OTHER INFORMATION: 400-405, and 418-420 are C-lobe Beta Strands
OTHER INFORMATION: Amino Acids 286-299, 307-310, 350-353, 384-387,
OTHER INFORMATION: and 427-431 are C-lobe Helices
US-09-795-903A-2

Query Match 100.0%; Score 2419; DB 9; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.3e-224;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETDEPEPEGRGSGFVEMVDNLGRKSGQGYVEMTVGSPPTNLILVDTGSSNFVGAAP 60
DQ 33 ETDEPEPEGRGSGFVEMVDNLGRKSGQGYVEMTVGSPPTNLILVDTGSSNFVGAAP 92
QY 61 HPFLHRYQRLSSYRDLRGKGVVPTQCKWEGELGTDLSVPHGPNVTVRANIAAITE 120
DQ 93 HPFLHRYQRLSSYRDLRGKGVVPTQCKWEGELGTDLSVPHGPNVTVRANIAAITE 152
QY 121 SDKFFINGSNWEGILGLAYAEIARPDSDLPPFDLSLVKQTHVNPFLSLQLCGAGPPLNQS 180
DQ 153 SDKFFINGSNWEGILGLAYAEIARPDSDLPPFDLSLVKQTHVNPFLSLQLCGAGPPLNQS 212
QY 181 EVLASVGSMTIGGDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNDK 240
DQ 213 EVLASVGSMTIGGDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNDK 272
QY 241 SIVDSGTTNLRPKKVFEEAAVKSIRKAASSTKPEPDGFWLGEOLVCWQAGTTPWNIIPVLS 300
DQ 273 SIVDSGTTNLRPKKVFEEAAVKSIRKAASSTKPEPDGFWLGEOLVCWQAGTTPWNIIPVLS 332
QY 301 LYLMGEVNTQSFRTILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVV 360
DQ 333 LYLMGEVNTQSFRTILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVV 392
QY 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
DQ 393 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 452
QY 421 CALFMLPLCLMVCQWRCRLRQOHHDDFADDDISLLK 456
DQ 453 CALFMLPLCLMVCQWRCRLRQOHHDDFADDDISLLK 488

RESULT 2
US-09-796-264-2
Sequence 2, Application US/09796264
Patent No. US20020049303A1
GENERAL INFORMATION:
APPLICANT: Tang, Jordan J.N.
APPLICANT: Lin, Xinli
APPLICANT: Koelsch, Gerald
TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
TITLE OF INVENTION: of Use Thereof
FILE REFERENCE: OMRF 179
CURRENT APPLICATION NUMBER: US/09/796,264
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 09/604,608
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/178,368
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/210,292
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 488
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: Purified Memapsin 2
OTHER INFORMATION: Amino Acids 28-48 are remnant putative propeptide
OTHER INFORMATION: residues
OTHER INFORMATION: Amino Acids 58-61, 78, 80, 82-83, 116, 118-121,
OTHER INFORMATION: 156, 166, 174, 246, 274, 276, 278-281, 283, and
OTHER INFORMATION: 376-377 are residues in contact with the OM99-2
OTHER INFORMATION: inhibitor
OTHER INFORMATION: Amino acids 54-57, 61-68, 73-80, 86-89, 109-111,
OTHER INFORMATION: 113-118, 123-134, 143-154, 165-168, 198-202, and
OTHER INFORMATION: 220-224 are N-lobe Beta Strands
OTHER INFORMATION: Amino Acids 184-191 and 210-217 are N-lobe Helices
OTHER INFORMATION: Amino acids 237-240, 247-249, 251-256, 259-260,
OTHER INFORMATION: 273-275, 282-285, 316-318, 331-336, 342-348,
OTHER INFORMATION: 354-357, 366-370, 372-375, 380-383, 390-395,
OTHER INFORMATION: 400-405, and 418-420 are C-lobe Beta Strands
OTHER INFORMATION: Amino Acids 286-299, 307-310, 350-353, 384-387,
OTHER INFORMATION: and 427-431 are C-lobe Helices
US-09-796-264-2

Query Match 100.0%; Score 2419; DB 10; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.3e-224;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETDEPEPEGRGSGFVEMVDNLGRKSGQGYVEMTVGSPPTNLILVDTGSSNFVGAAP 60
DQ 33 ETDEPEPEGRGSGFVEMVDNLGRKSGQGYVEMTVGSPPTNLILVDTGSSNFVGAAP 92
QY 61 HPFLHRYQRLSSYRDLRGKGVVPTQCKWEGELGTDLSVPHGPNVTVRANIAAITE 120
DQ 93 HPFLHRYQRLSSYRDLRGKGVVPTQCKWEGELGTDLSVPHGPNVTVRANIAAITE 152
QY 121 SDKFFINGSNWEGILGLAYAEIARPDSDLPPFDLSLVKQTHVNPFLSLQLCGAGPPLNQS 180
DQ 153 SDKFFINGSNWEGILGLAYAEIARPDSDLPPFDLSLVKQTHVNPFLSLQLCGAGPPLNQS 212
QY 181 EVLASVGSMTIGGDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNDK 240
DQ 213 EVLASVGSMTIGGDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNDK 272
QY 241 SIVDSGTTNLRPKKVFEEAAVKSIRKAASSTKPEPDGFWLGEOLVCWQAGTTPWNIIPVLS 300
DQ 273 SIVDSGTTNLRPKKVFEEAAVKSIRKAASSTKPEPDGFWLGEOLVCWQAGTTPWNIIPVLS 332
QY 301 LYLMGEVNTQSFRTILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVV 360
DQ 333 LYLMGEVNTQSFRTILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVV 392
QY 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
DQ 393 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 452
QY 421 CALFMLPLCLMVCQWRCRLRQOHHDDFADDDISLLK 456
DQ 453 CALFMLPLCLMVCQWRCRLRQOHHDDFADDDISLLK 488

RESULT 3
US-09-845-226-2
Sequence 2, Application US/09845226
Patent No. US20020115600A1
GENERAL INFORMATION:
APPLICANT: Tang, Jordan J.N.
APPLICANT: Hong, Lin
APPLICANT: Ghosh, Arun K.
TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REFERENCE: OMRF 182
CURRENT APPLICATION NUMBER: US/09/845,226
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 09/603,713
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/178,368
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/210,292
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 488
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Purified Memapsin 2
OTHER INFORMATION: Amino Acids 28-48 are remnant putative propeptide
OTHER INFORMATION: residues
OTHER INFORMATION: Amino Acids 58-61, 78, 80, 82-83, 116, 118-121,
OTHER INFORMATION: 156, 166, 174, 246, 276, 278-281, 283, and
OTHER INFORMATION: 376-377 are residues in contact with the OM99-2
OTHER INFORMATION: inhibitor
OTHER INFORMATION: Amino acids 54-57, 61-68, 73-80, 86-89, 109-111,
OTHER INFORMATION: 113-118, 123-134, 143-154, 165-168, 198-202, and
OTHER INFORMATION: 220-224 are N-lobe Beta Strands
OTHER INFORMATION: Amino Acids 184-191 and 210-217 are N-lobe Helices
OTHER INFORMATION: Amino acids 237-240, 247-249, 251-256, 259-260,
OTHER INFORMATION: 273-275, 282-285, 316-318, 331-336, 342-348,
OTHER INFORMATION: 354-357, 366-370, 372-375, 380-383, 390-395,
OTHER INFORMATION: 400-405, and 418-420 are C-lobe Beta Strands
OTHER INFORMATION: Amino Acids 286-299, 307-310, 350-353, 384-387,
OTHER INFORMATION: and 427-431 are C-lobe Helices
US-09-843-226-2

Query Match 100.0%; Score 2419; DB 10; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.3e-224;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETDEEPEEPCRRGSGFVEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFVAGAAP 60
DB 33 ETDEEPEEPCRRGSGFVEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFVAGAAP 92
QY 61 HPFLHRYRQSLSTYRDLRKGVYVPYTOGKWEGLGTDLVSPHGPNTVTRANIAAITE 120
DB 93 HPFLHRYRQSLSTYRDLRKGVYVPYTOGKWEGLGTDLVSPHGPNTVTRANIAAITE 152
QY 121 SDKFFINGSNWEGILGLAYAEIARPDSDLPEFFDSLVKQTHVNPFLSLQLCGAGFPLNOS 180
DB 153 SDKFFINGSNWEGILGLAYAEIARPDSDLPEFFDSLVKQTHVNPFLSLQLCGAGFPLNOS 212
QY 181 EVLASVGGSMIIIGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDK 240
DB 213 EVLASVGGSMIIIGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDK 272
QY 241 SIVDSGTTNLRPKPKVFEAAVKSIAASSTKFPDGFMLGEQLVCWQAGTTPNIPFVLS 300
DB 273 SIVDSGTTNLRPKPKVFEAAVKSIAASSTKFPDGFMLGEQLVCWQAGTTPNIPFVLS 332
QY 301 LYLMGEVNTQSFRTITLPOQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 333 LYLMGEVNTQSFRTITLPOQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 392
QY 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPEVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
DB 393 FDRARKRIGFAVSACHVHDEFRTAAVEGPEVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 452
QY 421 CALFMLPLCLMWQWRCRLCRLRQHQHDDFADDISLLK 456
DB 453 CALFMLPLCLMWQWRCRLCRLRQHQHDDFADDISLLK 488

RESULT 4
US-09-795-903A-3
; Sequence 3, Application US/09795903A
; Patent No. US20020164760A1

GENERAL INFORMATION:
APPLICANT: Tang, Jordan J.N.
APPLICANT: Lin, Xinli
APPLICANT: Koelsch, Gerald
TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
TITLE OF INVENTION: of Use Thereof
FILE REFERENCE: OMRF 179
CURRENT APPLICATION NUMBER: US/09/795,903A
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 09/604,608
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/178,368
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/210,292
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 503
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: pro-memapsin 2
OTHER INFORMATION: Amino Acids 1-15 are vector-derived residues
OTHER INFORMATION: Amino Acids 16-64 are a putative pro peptide
OTHER INFORMATION: Amino Acids 1-13 are the T7 promoter
OTHER INFORMATION: Amino Acids 16-456 are pro-memapsin 2-T1
OTHER INFORMATION: Amino Acids 16-421 are Promemapsin 2-T2
US-09-795-903A-3

Query Match 100.0%; Score 2419; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.4e-224;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETDEEPEEPCRRGSGFVEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFVAGAAP 60
DB 48 ETDEEPEEPCRRGSGFVEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFVAGAAP 107
QY 61 HPFLHRYRQSLSTYRDLRKGVYVPYTOGKWEGLGTDLVSPHGPNTVTRANIAAITE 120
DB 108 HPFLHRYRQSLSTYRDLRKGVYVPYTOGKWEGLGTDLVSPHGPNTVTRANIAAITE 167
QY 121 SDKFFINGSNWEGILGLAYAEIARPDSDLPEFFDSLVKQTHVNPFLSLQLCGAGFPLNOS 180
DB 168 SDKFFINGSNWEGILGLAYAEIARPDSDLPEFFDSLVKQTHVNPFLSLQLCGAGFPLNOS 227
QY 181 EVLASVGGSMIIIGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDK 240
DB 228 EVLASVGGSMIIIGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDK 287
QY 241 SIVDSGTTNLRPKPKVFEAAVKSIAASSTKFPDGFMLGEQLVCWQAGTTPNIPFVLS 300
DB 288 SIVDSGTTNLRPKPKVFEAAVKSIAASSTKFPDGFMLGEQLVCWQAGTTPNIPFVLS 347
QY 301 LYLMGEVNTQSFRTITLPOQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 348 LYLMGEVNTQSFRTITLPOQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 407
QY 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPEVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
DB 408 FDRARKRIGFAVSACHVHDEFRTAAVEGPEVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 467
QY 421 CALFMLPLCLMWQWRCRLCRLRQHQHDDFADDISLLK 456
DB 468 CALFMLPLCLMWQWRCRLCRLRQHQHDDFADDISLLK 503

RESULT 5
US-09-796-264-3

; Sequence 3, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09796,264
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Pro-memapsin 2
; OTHER INFORMATION: Amino Acids 1-15 are vector-derived residues
; OTHER INFORMATION: Amino Acids 16-64 are a putative pro peptide
; OTHER INFORMATION: Amino Acids 1-13 are the T7 promoter
; OTHER INFORMATION: Amino Acids 16-456 are Pro-memapsin 2-T1
; OTHER INFORMATION: Amino Acids 16-421 are Promemapsin 2-T2
US-09-796-264-3

Query Match 100.0%; Score 2419; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.4e-224;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETDEEPEEPGRGSGYVEMVDNLKSGOGYVYVMTVGPQTNLNVLVDGTSSNFAVGAAP 60
DB 48 ETDEEPEEPGRGSGYVEMVDNLKSGOGYVYVMTVGPQTNLNVLVDGTSSNFAVGAAP 107
QY 61 HPFLHRYQRLSTYRDLRGVYVYPTQGWEGELGTDLVSPHGPNTVTRANIAAITE 120
DB 108 HPFLHRYQRLSTYRDLRGVYVYPTQGWEGELGTDLVSPHGPNTVTRANIAAITE 167
QY 121 SKKFFNGSNWEGILGLAYAEIARPDSDLPEFFDSLVKQTHVPLNLSLQLCGAGFPLNQS 180
DB 168 SKKFFNGSNWEGILGLAYAEIARPDSDLPEFFDSLVKQTHVPLNLSLQLCGAGFPLNQS 227
QY 181 EVLASVGGSMIIGDHSYTGSLWYTPIRREWYVEIIVRVEINGODLKMDCKEYNDK 240
DB 228 EVLASVGGSMIIGDHSYTGSLWYTPIRREWYVEIIVRVEINGODLKMDCKEYNDK 287
QY 241 SIIVDSGTTNLRPKKVFEEAAVKSIAAASSTKFPDGFVLGEQLVCVQAGTTPNNIPFVIS 300
DB 288 SIIVDSGTTNLRPKKVFEEAAVKSIAAASSTKFPDGFVLGEQLVCVQAGTTPNNIPFVIS 347
QY 301 LYLMGEVTNOSFRITILPQQYLRPVEDVATSDDDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 348 LYLMGEVTNOSFRITILPQQYLRPVEDVATSDDDCYKFAISQSSTGTVMGAVIMEGFYV 407
QY 361 FDRARRKIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTTAYVMAAI 420
DB 408 FDRARRKIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTTAYVMAAI 467
QY 421 CALFMPLPLCLMVCWRCRLCRLRQOHHDDFADDISLLK 456
DB 468 CALFMPLPLCLMVCWRCRLCRLRQOHHDDFADDISLLK 503

RESULT 6
US-09-845-226-3
; Sequence 3, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Pro-memapsin 2
; OTHER INFORMATION: Amino Acids 1-15 are vector-derived residues
; OTHER INFORMATION: Amino Acids 16-64 are a putative pro peptide
; OTHER INFORMATION: Amino Acids 1-13 are the T7 promoter
; OTHER INFORMATION: Amino Acids 16-456 are Pro-memapsin 2-T1
; OTHER INFORMATION: Amino Acids 16-421 are Promemapsin 2-T2
US-09-845-226-3

Query Match 100.0%; Score 2419; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.4e-224;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETDEEPEEPGRGSGYVEMVDNLKSGOGYVYVMTVGPQTNLNVLVDGTSSNFAVGAAP 60
DB 48 ETDEEPEEPGRGSGYVEMVDNLKSGOGYVYVMTVGPQTNLNVLVDGTSSNFAVGAAP 107
QY 61 HPFLHRYQRLSTYRDLRGVYVYPTQGWEGELGTDLVSPHGPNTVTRANIAAITE 120
DB 108 HPFLHRYQRLSTYRDLRGVYVYPTQGWEGELGTDLVSPHGPNTVTRANIAAITE 167
QY 121 SKKFFNGSNWEGILGLAYAEIARPDSDLPEFFDSLVKQTHVPLNLSLQLCGAGFPLNQS 180
DB 168 SKKFFNGSNWEGILGLAYAEIARPDSDLPEFFDSLVKQTHVPLNLSLQLCGAGFPLNQS 227
QY 181 EVLASVGGSMIIGDHSYTGSLWYTPIRREWYVEIIVRVEINGODLKMDCKEYNDK 240
DB 228 EVLASVGGSMIIGDHSYTGSLWYTPIRREWYVEIIVRVEINGODLKMDCKEYNDK 287
QY 241 SIIVDSGTTNLRPKKVFEEAAVKSIAAASSTKFPDGFVLGEQLVCVQAGTTPNNIPFVIS 300
DB 288 SIIVDSGTTNLRPKKVFEEAAVKSIAAASSTKFPDGFVLGEQLVCVQAGTTPNNIPFVIS 347
QY 301 LYLMGEVTNOSFRITILPQQYLRPVEDVATSDDDCYKFAISQSSTGTVMGAVIMEGFYV 360
DB 348 LYLMGEVTNOSFRITILPQQYLRPVEDVATSDDDCYKFAISQSSTGTVMGAVIMEGFYV 407
QY 361 FDRARRKIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTTAYVMAAI 420
DB 408 FDRARRKIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTTAYVMAAI 467
QY 421 CALFMPLPLCLMVCWRCRLCRLRQOHHDDFADDISLLK 456
DB 468 CALFMPLPLCLMVCWRCRLCRLRQOHHDDFADDISLLK 503

RESULT 7
US-09-794-927-4
: Sequence 4, Application US/09794927
: Patent No. US20010016324A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: USES
: FILE REFERENCE: 28341/6280FG
: CURRENT APPLICATION NUMBER: US/09/794, 927
: PRIOR FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416, 901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155, 493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404, 133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101, 594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 501
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-794-927-4

Query Match 99.8%; Score 2414; DB 10; Length 501;
Best Local Similarity 99.8%; Pred. No. 7.le-224;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ETDEEPEPCRRGSRFVEMVDNLKSGQGYVVENTVCSPPOTLNILVDTGSSNFAVCAAP 60
Db 46 ETDEEPEPCRRGSRFVEMVDNLKSGQGYVVENTVCSPPOTLNILVDTGSSNFAVCAAP 105
Qy 61 HPFLHRYQRLSSTYRDLRKGYVVPYTOGKWEGLGTLVSIPIHGPNTVVRANIAAITE 120
Db 106 HPFLHRYQRLSSTYRDLRKGYVVPYTOGKWEGLGTLVSIPIHGPNTVVRANIAAITE 165
Qy 121 SDKFFINGSNWEGTLGLAYAEIARPDSDLPPFDLSLVKQTHVPNLFSLHLCGAGFPLNQS 180
Db 166 SDKFFINGSNWEGTLGLAYAEIARPDSDLPPFDLSLVKQTHVPNLFSLHLCGAGFPLNQS 225
Qy 181 EVLASVGGSMIIGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGODLKMDCKEYNYDK 240
Db 226 EVLASVGGSMIIGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGODLKMDCKEYNYDK 285
Qy 241 SIVDSGTNLRPKKVEAAVKSIKAASSTKFPDGFWMGEQLVCMQAGTTPWNIFPVIS 300
Db 286 SIVDSGTNLRPKKVEAAVKSIKAASSTKFPDGFWMGEQLVCMQAGTTPWNIFPVIS 345
Qy 301 LYLGMVETNQSFRITILPQOYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGYV 360
Db 346 LYLGMVETNQSFRITILPQOYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGYV 405
Qy 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465
Qy 421 CALFMLPLCLMVCMQWRCRLRQHQHDDFADDISLLK 456
Db 466 CALFMLPLCLMVCMQWRCRLRQHQHDDFADDISLLK 501

RESULT 8

US-09-795-847-4
: Sequence 4, Application US/09795847
: Patent No. US20010018208A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: USES
: FILE REFERENCE: 28341/6280DE
: CURRENT APPLICATION NUMBER: US/09/795, 847
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 09/416, 901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155, 493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404, 133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101, 594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 501
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-795-847-4

Query Match 99.8%; Score 2414; DB 10; Length 501;
Best Local Similarity 99.8%; Pred. No. 7.le-224;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ETDEEPEPCRRGSRFVEMVDNLKSGQGYVVENTVCSPPOTLNILVDTGSSNFAVGAAP 60
Db 46 ETDEEPEPCRRGSRFVEMVDNLKSGQGYVVENTVCSPPOTLNILVDTGSSNFAVGAAP 105
Qy 61 HPFLHRYQRLSSTYRDLRKGYVVPYTOGKWEGLGTLVSIPIHGPNTVVRANIAAITE 120
Db 106 HPFLHRYQRLSSTYRDLRKGYVVPYTOGKWEGLGTLVSIPIHGPNTVVRANIAAITE 165
Qy 121 SDKFFINGSNWEGTLGLAYAEIARPDSDLPPFDLSLVKQTHVPNLFSLHLCGAGFPLNQS 180
Db 166 SDKFFINGSNWEGTLGLAYAEIARPDSDLPPFDLSLVKQTHVPNLFSLHLCGAGFPLNQS 225
Qy 181 EVLASVGGSMIIGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGODLKMDCKEYNYDK 240
Db 226 EVLASVGGSMIIGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGODLKMDCKEYNYDK 285
Qy 241 SIVDSGTNLRPKKVEAAVKSIKAASSTKFPDGFWMGEQLVCMQAGTTPWNIFPVIS 300
Db 286 SIVDSGTNLRPKKVEAAVKSIKAASSTKFPDGFWMGEQLVCMQAGTTPWNIFPVIS 345
Qy 301 LYLGMVETNQSFRITILPQOYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGYV 360
Db 346 LYLGMVETNQSFRITILPQOYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGYV 405
Qy 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465
Qy 421 CALFMLPLCLMVCMQWRCRLRQHQHDDFADDISLLK 456
Db 466 CALFMLPLCLMVCMQWRCRLRQHQHDDFADDISLLK 501

RESULT 9
US-09-794-743-4
: Sequence 4, Application US/09794743

APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
FILE REFERENCE: 28341/6280H1
CURRENT APPLICATION NUMBER: US/09/794,925
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
US-09-794-925-4

Query Match 99.8%; Score 2414; DB 10; Length 501;
Best Local Similarity 99.8%; Pred. No. 7.le-224;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ETDEEPEEPPGRRGGSFVEMVNDLGRKSGQGYVYVMTGSPQTLNLIIVDTGSSNFAVGAAP 60
Db 46 ETDEEPEEPPGRRGGSFVEMVNDLGRKSGQGYVYVMTGSPQTLNLIIVDTGSSNFAVGAAP 105

Qy 61 HPFLHRYQRLSTYRDLRKGYVYVPTQGWEGELGTDLVSIHPGPNVTVRANTAATE 120
Db 106 HPFLHRYQRLSTYRDLRKGYVYVPTQGWEGELGTDLVSIHPGPNVTVRANTAATE 165

Qy 121 SDKFFINGSNWEGTLGLAYAEIARPDSDLPPFDLSLVKQTHVNPVLSLQCGAGFPLNOS 180
Db 166 SDKFFINGSNWEGTLGLAYAEIARPDSDLPPFDLSLVKQTHVNPVLSLQCGAGFPLNOS 225

Qy 181 EVLASVGSMTIGGDHSLVTSGLWYTPIRREWYEVYIIVRVEINGQDLKMDCKEYNDK 240
Db 226 EVLASVGSMTIGGDHSLVTSGLWYTPIRREWYEVYIIVRVEINGQDLKMDCKEYNDK 285

Qy 241 SIVDSGTTNLRPKKVEAAVKSIAASSTKFPDGFGLGEQLVCHQAGTTPNIFPVIS 300
Db 286 SIVDSGTTNLRPKKVEAAVKSIAASSTKFPDGFGLGEQLVCHQAGTTPNIFPVIS 345

Qy 301 LYLMEVTNQSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
Db 346 LYLMEVTNQSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 405

Qy 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPPVTLDMEDCGYNIPTQDDESTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFRTAAVEGPPVTLDMEDCGYNIPTQDDESTLMTIAYVMAAI 465

Qy 421 CALFMLPLCLMVQWRCRLCRLQHQHDDFADDISLLK 456
Db 466 CALFMLPLCLMVQWRCRLCRLQHQHDDFADDISLLK 501

RESULT 12
US-09-681-442-4
Sequence 4, Application US/09681442
Patent No. US20020081634A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang

TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
FILE REFERENCE: 28341/6280FG
CURRENT APPLICATION NUMBER: US/09/681,442
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
US-09-681-442-4

Query Match 99.8%; Score 2414; DB 10; Length 501;
Best Local Similarity 99.8%; Pred. No. 7.le-224;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ETDEEPEEPPGRRGGSFVEMVNDLGRKSGQGYVYVMTGSPQTLNLIIVDTGSSNFAVGAAP 60
Db 46 ETDEEPEEPPGRRGGSFVEMVNDLGRKSGQGYVYVMTGSPQTLNLIIVDTGSSNFAVGAAP 105

Qy 61 HPFLHRYQRLSTYRDLRKGYVYVPTQGWEGELGTDLVSIHPGPNVTVRANTAATE 120
Db 106 HPFLHRYQRLSTYRDLRKGYVYVPTQGWEGELGTDLVSIHPGPNVTVRANTAATE 165

Qy 121 SDKFFINGSNWEGTLGLAYAEIARPDSDLPPFDLSLVKQTHVNPVLSLQCGAGFPLNOS 180
Db 166 SDKFFINGSNWEGTLGLAYAEIARPDSDLPPFDLSLVKQTHVNPVLSLQCGAGFPLNOS 225

Qy 181 EVLASVGSMTIGGDHSLVTSGLWYTPIRREWYEVYIIVRVEINGQDLKMDCKEYNDK 240
Db 226 EVLASVGSMTIGGDHSLVTSGLWYTPIRREWYEVYIIVRVEINGQDLKMDCKEYNDK 285

Qy 241 SIVDSGTTNLRPKKVEAAVKSIAASSTKFPDGFGLGEQLVCHQAGTTPNIFPVIS 300
Db 286 SIVDSGTTNLRPKKVEAAVKSIAASSTKFPDGFGLGEQLVCHQAGTTPNIFPVIS 345

Qy 301 LYLMEVTNQSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 360
Db 346 LYLMEVTNQSFRITILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYV 405

Qy 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPPVTLDMEDCGYNIPTQDDESTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFRTAAVEGPPVTLDMEDCGYNIPTQDDESTLMTIAYVMAAI 465

Qy 421 CALFMLPLCLMVQWRCRLCRLQHQHDDFADDISLLK 456
Db 466 CALFMLPLCLMVQWRCRLCRLQHQHDDFADDISLLK 501

RESULT 13
US-09-969-671A-2
Sequence 2, Application US/09969671A
Publication No. US20030036112A1
GENERAL INFORMATION:
APPLICANT: CHAPMAN, CONRAD G.
APPLICANT: MURPHY, KAY
APPLICANT: POWELL, DAVID J.
APPLICANT: SMITH, TRUDI S.
TITLE OF INVENTION: ASP2
FILE REFERENCE: GH-70368-DI
CURRENT APPLICATION NUMBER: US/09/969,671A
CURRENT FILING DATE: 2001-10-03

; PRIOR APPLICATION NUMBER: UK 9701684.4
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 09/009,191
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 09/694,200
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-671A-2

Query Match 99.8%; Score 2413; DB 9; Length 501;
Best Local Similarity 99.8%; Pred. No. 8.9e-224;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ETDEEPEPGRGSGFVEMVDNLGRKSGGQYVYEMTVGSPQTLNLLVDTGSSNFAYGAAP 60
Db 46 ETDEEPEPGRGSGFVEMVDNLGRKSGGQYVYEMTVGSPQTLNLLVDTGSSNFAYGAAP 105

Qy 61 HPFLHRYQROLSSYRDLRGVYVYTGQKWEGLGTDLSIPHGPNTVVRANIAAITE 120
Db 106 HPFLHRYQROLSSYRDLRGVYVYTGQKWEGLGTDLSIPHGPNTVVRANIAAITE 165

Qy 121 SDKFFINGSNNEGILGLAYAEIARPDSDLPEFFDSLVKQTHVPLNLSLQCGAGFPLNOS 180
Db 166 SDKFFINGSNNEGILGLAYAEIARPDSDLPEFFDSLVKQTHVPLNLSLQCGAGFPLNOS 225

Qy 181 EVLASVSGSMIIGGDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNDK 240
Db 226 EVLASVSGSMIIGGDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNDK 285

Qy 241 SIVDSGTTNLRPKVFAAANKSIKAASSTKFPDGFGLGQVLCVQAGTTPNIPFVVS 300
Db 286 SIVDSGTTNLRPKVFAAANKSIKAASSTKFPDGFGLGQVLCVQAGTTPNIPFVVS 345

Qy 301 LYLMEVNTQSFRTILPQQYLPRVEDVATSDDCYKFAISOSSTGTVMGAVIMEGFYVV 360
Db 346 LYLMEVNTQSFRTILPQQYLPRVEDVATSDDCYKFAISOSSTGTVMGAVIMEGFYVV 405

Qy 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465

Qy 421 CALFMLPLCLMVQWRCRLRCLRQHQHDDFADDISLLK 456
Db 466 CALFMLPLCLMVQWRCRLRCLRQHQHDDFADDISLLK 501

RESULT 14
US-09-794-927-8
; Sequence 8, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-794-927-8

Query Match 98.8%; Score 2390; DB 10; Length 501;
Best Local Similarity 98.2%; Pred. No. 1.4e-221;
Matches 448; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ETDEEPEPGRGSGFVEMVDNLGRKSGGQYVYEMTVGSPQTLNLLVDTGSSNFAYGAAP 60
Db 46 ETDEEPEPGRGSGFVEMVDNLGRKSGGQYVYEMTVGSPQTLNLLVDTGSSNFAYGAAP 105

Qy 61 HPFLHRYQROLSSYRDLRGVYVYTGQKWEGLGTDLSIPHGPNTVVRANIAAITE 120
Db 106 HPFLHRYQROLSSYRDLRGVYVYTGQKWEGLGTDLSIPHGPNTVVRANIAAITE 165

Qy 121 SDKFFINGSNNEGILGLAYAEIARPDSDLPEFFDSLVKQTHVPLNLSLQCGAGFPLNOS 180
Db 166 SDKFFINGSNNEGILGLAYAEIARPDSDLPEFFDSLVKQTHVPLNLSLQCGAGFPLNOS 225

Qy 181 EVLASVSGSMIIGGDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNDK 240
Db 226 EVLASVSGSMIIGGDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNDK 285

Qy 241 SIVDSGTTNLRPKVFAAANKSIKAASSTKFPDGFGLGQVLCVQAGTTPNIPFVVS 300
Db 286 SIVDSGTTNLRPKVFAAANKSIKAASSTKFPDGFGLGQVLCVQAGTTPNIPFVVS 345

Qy 301 LYLMEVNTQSFRTILPQQYLPRVEDVATSDDCYKFAISOSSTGTVMGAVIMEGFYVV 360
Db 346 LYLMEVNTQSFRTILPQQYLPRVEDVATSDDCYKFAISOSSTGTVMGAVIMEGFYVV 405

Qy 361 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
Db 406 FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465

Qy 421 CALFMLPLCLMVQWRCRLRCLRQHQHDDFADDISLLK 456
Db 466 CALFMLPLCLMVQWRCRLRCLRQHQHDDFADDISLLK 501

RESULT 15
US-09-795-847-8
; Sequence 8, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23

Search completed: March 4, 2003, 10:08:31
Job time : 18 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: March 4, 2003, 10:00:56 : Search time 21 seconds
(without alignments)
2087.490 Million cell updates/sec

Title: US-09-723-722A-43

Perfect score: 2419

Sequence: 1 ETDEPEPEPGRGSGFVEMVD.....CLRLRQHQHDFADDISLLK 456

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2419	100.0	501	2 A59090	aspartic proteinas
2	308	12.7	384	2 JC7574	pepsinogen A - Afr
3	308	12.7	385	2 JC7575	pepsinogen A - bul
4	306	12.6	387	2 JC7573	pepsin (EC 3.4.23.
5	303	12.5	383	2 JC7573	pepsinogen C - Afr
6	302.5	12.5	388	1 S19682	pepsin A (EC 3.4.2
7	301	12.4	382	1 PECH	pepsin A (EC 3.4.2
8	299.5	12.4	396	2 A34401	cathepsin E (EC 3.
9	298.5	12.3	383	2 A41443	pepsin (EC 3.4.23.
10	298.5	12.3	384	2 A39314	gastricsin (EC 3.4
11	296	12.2	387	2 C38302	pepsin (EC 3.4.23.
12	296	12.2	391	2 A43356	cathepsin E (EC 3.
13	295.5	12.2	412	1 KHHUD	cathepsin D (EC 3.
14	295	12.2	387	2 C38302	pepsin (EC 3.4.23.
15	289.5	12.0	388	1 S19684	pepsin A (EC 3.4.2
16	287.5	11.9	444	2 T24204	hypothetical prote
17	287	11.9	407	1 KHRFD	cathepsin D (EC 3.
18	286	11.8	387	2 E38302	pepsin (EC 3.4.23.
19	285.5	11.8	398	2 S66465	cathepsin E (EC 3.
20	285	11.8	398	2 I51185	cathepsin D (EC 3.
21	283.5	11.7	388	1 PEMAQ	pepsin A (EC 3.4.2
22	282.5	11.7	388	1 PEHU	pepsin A (EC 3.4.2
23	281.5	11.6	381	1 CMSHB	chymosin (EC 3.4.2
24	281.5	11.6	388	1 PEMAQJ	pepsin A (EC 3.4.2
25	281.5	11.6	388	2 A30142	pepsin A (EC 3.4.2
26	279.5	11.6	388	2 B30142	pepsin A (EC 3.4.2
27	279.5	11.6	410	1 KMSD	cathepsin D (EC 3.
28	278.5	11.5	386	1 PEPG	pepsin A (EC 3.4.2
29	278	11.5	387	2 JC7245	pepsinogen A - com

ALIGNMENTS

RESULT 1

A59090

aspartic proteinase (EC 3.4.23.-) BACE precursor - human
N;Alternate names: beta-secretase; beta-site APP cleaving enzyme
C;Species: Homo sapiens (man)

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-May-2000
C;Accession: A59090
R;Vassar, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Denis, P.; Teplio
M.A.; Biere, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Treanor, J.; Ro
Science 286, 735-741, 1999

A;Title: beta-Secretase cleavage of Alzheimer's amyloid precursor protein by the tran
A;Reference number: A59090; MUID:20002972; PMID:10531052
A;Note: submitted to GenBank, September 1999
A;Accession: A59090
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-501 <VAS>
A;Cross-references: GB:AF190725; NID:g6118538; PIDN:AAF04142.1; PID:g6118539
C;Genetics:
A;Gene: BACE
C;Superfamily: beta-secretase
C;Keywords: Alzheimer's disease; aspartic proteinase; brain; glycoprotein; hydrolase;
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-45/Domain: propeptide #status predicted <PRO>
F;46-501/Product: acid proteinase BACE #status predicted <MAT>
F;461-477/Domain: transmembrane #status predicted <TRN>
F;93,289/Active site: Asp #status predicted
F;153,172,223,354/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;330-380/Disulfide bonds: #status predicted

Query Match 100.0%; Score 2419; DB 2; Length 501;
Best Local Similarity 100.0%; Pred. No. 3.8e-192;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ETDEPEPEPGRGSGFVEMVDNLKSGQGYVEMTVGSPPTNLIVDTGSSNFVAGAAP	60
Db	46	ETDEPEPEPGRGSGFVEMVDNLKSGQGYVEMTVGSPPTNLIVDTGSSNFVAGAAP	105
Qy	61	HPFHRYRQRLSTYRDLRKGYVYVYTGKWEGLGDLVSIPIHGNVTVRANIAATE	120
Db	106	HPFHRYRQRLSTYRDLRKGYVYVYTGKWEGLGDLVSIPIHGNVTVRANIAATE	165
Qy	121	SDRFFINGSNWEGILGLAYAEIARPDPSLEFFDSLVRKQTHVPNLFSLQLCAGFPLNQS	180
Db	166	SDKEFFINGSNWEGILGLAYAEIARPDPSLEFFDSLVRKQTHVPNLFSLQLCAGFPLNQS	225
Qy	181	EVLASVGSMTIGIDHSLYTGTSLWYTPIRREWYVEYIIVRVEINGDLKMDCKEYNDK	240
Db	226	EVLASVGSMTIGIDHSLYTGTSLWYTPIRREWYVEYIIVRVEINGDLKMDCKEYNDK	285
Qy	241	SYVDSGTNLRLPKKVFEEAAVKSIKAASSTKFFDGFGLGQVLCVQAGTTPWNIFFVIS	300

chymosin (EC 3.4.2
cathepsin E (EC 3.
pepsin C (EC 3.4.2
chymosin (EC 3.4.2
gastricsin (EC 3.4
pepsin (EC 3.4.23.
aspartic proteinas
cathepsin D (EC 3.
prochymosin - comm
candidapepsin (EC
saccharopepsin (EC
aspartic proteinas
pepsinogen C - com
gastricsin (EC 3.4
aspartic proteinas
gastricsin (EC 3.4

Qy	421	CALFMLPLCLMVCQWRCRLCRLRQOHHDDFADDISLLK	4566
Db	466	CALFMLPLCLMVCQWRCRLCRLRQOHHDDFADDISLLK	5011

```

D6 QY 322 LRPVED-VATSDQDC---YKEAFLSQSSGTG--VMGAVIMEGIVYVYVFDRAKRGFA 371
286 ANIQYITIGANQJUSNGQTV---INCNNLSNMPYVVF-----INGVOY 322
D6 327 PUPASAYVROSOOSCTSGFGAMNLPTSSGDLWLIGDVFIRSYVYVFDRAANNVAVA 382

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RESULT 4
B38302
pepsin (BC 3.4.23.-) II-1 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Jun-1991 #sequence_revision 20-Sep-1991
C:Accession: B38302
C:Kageyama, M.; Tanabe, K.; Kikuchi, O.

```

[illegible]

Db 135 TYTGSMTCILGYDVTVKV---GNIEDTNOIFGLSKTEPGITFLV--APPDGLGLAYPSI 189
QY 143 ARPDDSLFPFDSLVKQTHV-PNLFSLQLCGAGFPLNQSEVLASVGSMTIGGIDHSLYT 201
Db 190 SASDAT--PVFDNMNEGLVSEDLFSVYLSNG-----EKGSMVWFGGIDSSYYT 237
QY 202 GSLWTPPIKREWYEVIIIVRVEINGODLKM--DCKEYNYDKSIVDSGTTNLRPKKVFPA 259
Db 238 GSLNWPVSHGYWQITMDSITINGETIACADSC-----QAVVDGTGTSLLAGPTSAISK 291
QY 260 AVKSKAASSTKFPDGFNGLGQLV-CWQAGTTPWNIFFVLSILMGEVNTSFRITILP 318
Db 292 IQSYTICASKNL-----LGENIITSCSAIDSLPDIVF-----TINN 325
QY 319 QOYLPRVED-VATSDDC---YKFAISOSSTGT--VMGAVIMEGFVYVDFDRARKRIGFAV 372
Db 326 VOYPLPASAYILKEDDCLSLGDFGDMMLDTSYCELWILGVOFTROYTTFVDRANNQVGLAA 385
QY 373 SA 374
Db 386 AA 387
RESULT 5
JC7573
pepsinogen C - African clawed frog
N:Alternate names: progastricin
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
C:Accession: JC7573; PC7118
R:Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasu, S.
J. Biochem. 129, 147-153, 2001
A:Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens
A:Reference number: JC7573; MUID:21064922; PMID:11134969
A:Contents: Stomach
A:Accession: JC7573
A:Molecule type: mRNA
A:Residues: 1-383 <IKU>
A:CROSS-references: DDBJ:AB045379
A:Accession: PC7118
A:Molecule type: protein
A:Residues: 17-68 <IK2>
C:Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like a
C:Genetics:
A:Gene: PgC
C:Superfamily: pepsin
C:Keywords: stomach; zymogen
Query Match 12.5%; Score 303; DB 2; Length 383;
Best Local Similarity 27.4%; Pred. No. 3.4e-17;
Matches 104; Conservative 57; Mismatches 122; Indels 96; Gaps 17;
QY 30 YVEMTVGSPPTNLTLVDTGSSNFAVGA-----APHPFLHRYQRLSSTYRDLRK 81
Db 67 YXGETSIGTPPNFLVLTGSSNLWVASTYCSQACTNHPL----FNPSQSSTYSNQ 122
QY 82 GVVPVPTQCKWCELTGLVSLPHGPNVTVRANIAAITESDKFFINGSN----WEGILG 136
Db 123 QFSLQVGTGSLGILGYDVTI---ONVALSQEFGSLSETP----GTNPFVAQFQILG 175
QY 137 LAYAEIARPDSDSLEPPFDSLVKQTHVPNLFSLQLCGAGFPNQNSEVLASVGSMTIGGID 196
Db 176 LAYPSIA--VGGATTVMQGMQO---NLLNQPI--FGFYLSQS--SQNGGEVAFGGVD 225
QY 197 HSLYTGSLWYTPPIRREWYEVIIIVRVEINGOD---LKMDCKEYNYDKSIVDSGTTNLRPL 253
Db 226 QNYVTGQIYVTPVTSYTWQIGIQGFSINGQATGWCSSQGC-----QAVVDGTGTSLLTAP 279
QY 254 KKVFEAAVKSIAKASSTKFPDGFNGLGQLVCHQAGTTPWNI--FPVISLYLNG----- 305
Db 280 QSVFSLIQSIGAQDQN-----GOYVWCS-----NQNLPTISFTTISGFSFPLP 325
QY 306 ---EVTNQS-----FRITILPQOYLPRPVEDVATSDDCYKFAISQSSTGTVMGAVIME 355

Db 326 PSAYVLQSSGYCTIGIMPTLYLPSONQPL-----WTLGDFVFLR 364
QY 356 GEYVVFDRARKRIGFAVSA 374
Db 365 EYISVYDLGNNOVGFAATA 383
RESULT 6
S19682
pepsin A (EC 3.4.23.1) 4 precursor - Japanese macaque
N:Alternate names: pepsinogen A isozyme 4
C:Species: Macaca fuscata (Japanese macaque)
C:Date: 22-Nov-1993 #sequence_revision 19-Oct-1995 #text_change 18-Jun-1999
C:Accession: S19682; S16065
R:Kageyama, T.; Tanabe, K.; Koiwai, O.
Eur. J. Biochem. 202, 205-215, 1991
A:Title: Development-dependent expression of isozymogens of monkey pepsinogens and st
A:Reference number: S19681; MUID:92037645; PMID:1935977
A:Accession: S19682
A:Molecule type: mRNA
A:Residues: 1-388 <KAG>
A:CROSS-references: EMBL:X59753; NID:g38070; PIDN:CAA42425.1; PID:g38071
A:Note: parts of sequence, including amino ends of pepsinogen and activation intermed
C:Comment: This is a minor component of pepsin at all post-partum stages.
C:Superfamily: pepsin
C:Comment: Although two-step activation is observed, activation is predominantly a o
C:Keywords: aspartic proteinase; gastric juice; hydrolase; phosphoprotein; protein di
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-388/Product: pepsinogen A 4 #status experimental <PPT>
F:16-62/Domain: activation peptide #status experimental <APT>
F:63-388/Product: pepsin A 4 #status experimental <ENZ>
F:38-39/cleavage site: Leu-Lys (pepsin) #status experimental
F:62-63/cleavage site: Leu-Ile (pepsin) #status experimental
F:94,277/Active site: Asp #status predicted
F:107-112,268-272,311-344/Disulfide bonds: #status predicted
F:130/Binding site: phosphate (Ser) (covalent) #status predicted
Query Match 12.5%; Score 302.5; DB 1; Length 388;
Best Local Similarity 27.6%; Pred. No. 3.8e-17;
Matches 107; Conservative 64; Mismatches 133; Indels 83; Gaps 17;
QY 3 DEEPEEPGRKGSFEMVDNLGRKSGQGYVEMTVGSPPTNLTLVDTGSSNFAVGAAPHP 62
Db 64 DEQPLE-----NYLDV-----EYFGTIGTGTAAQNFVTVFDTGSSNLWV---PSV 105
QY 63 FL-----HRYQRLSSTYRDLRKGVVYPTQGWEGELGTDLVSIHPGNVTVRANI 115
Db 106 YCYSLACMDHNLFPQDSSYRATSKVTSITYGTGSMTGILGYDVTVKV---GGISDTNQI 162
QY 116 AAITESDK-PFINGSNWEGTLGAYAEIARPDSDSLEPPFDSLVKQTHV-PNLFSLQLCGA 173
Db 163 FGUSETEPGFFLFPDGLGLAYPSIS---SSGATPVFDNIWNQRLVSDLSFVLSAD 220
QY 174 GFPNLQSEVLASVGSMTIGGIDHSLYTGSLWYTPPIRREWYEVIIIVRVEINGODL--KM 231
Db 221 ---DQS-----GSVVFGGIDSSYTGSLNWPVSVVEGYWQISVDSITMCKGTACAK 270
QY 232 DCKEYNYDKSIVDSGTTNLRPKKVFPAVAAVKSIAKASSTKFPDGFNGLGQLV-CWQAGT 290
Db 271 GC-----QAVVDGTGTSLLTGTPTSPIANIQSDIGASENSD-----GEMVYSCSAISS 316
QY 291 TPNWIFVLSILMGEVNTSFRITILPQOY-LRPVEDVATSDDCYK-----FAISQSS 344
Db 317 LPDIVF-----TINGVOYPLPPSAYILQSOGSCSTSGFGQMDVPTFESG 358
QY 345 TGTVMGAVIMEGFVYVDFDRARKRIGFA 371
Db 359 ELWILGDFVIRQYTFVDRANNQVGLA 385
RESULT 7
PECH

pepsin A (EC 3.4.23.1) precursor - chicken
N:Alternate names: pepsinogen A
C:Species: Gallus gallus (chicken)
C:Date: 18-Apr-1984 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: J03070; A00984
R:Sakamoto, N.; Saiga, H.; Yasugi, S.
Biochem. Biophys. Res. Commun. 250, 420-424, 1998
A:Title: Analysis of temporal expression pattern and cis-regulatory sequences of chicken
A:Reference number: JE0370; MUID:98440813; PMID:9753645
A:Accession: JE0370
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-382 <SAK>
A:Cross-references: GB:AB025281; NID:g4589837; PIDN:BAA76891.1; PID:g4589838
R:Baudys, M.; Kostka, V.
Eur. J. Biochem. 136, 89-99, 1983
A:Title: Covalent structure of chicken pepsinogen.
A:Reference number: A00984; MUID:84004412; PMID:6617663
A:Accession: A00984
A:Molecule type: protein
A:Residues: 16-87, 'S', 89-382 <BAU>
C:Superfamily: pepsin
C:Keywords: aspartic proteinase; gastric juice; glycoprotein; hydrolase; protein digestion
F:16-57/Domain: activation peptide #status experimental <APP>
F:58-382/Product: pepsin A #status predicted <MAT>
F:92,275/Active site: Asp #status predicted
F:105-110,266-270,305-338/Disulfide bonds: #status experimental
F:128/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 12.4%; Score 301; DB 1; Length 382;
Best Local Similarity 24.0%; Pred. No. 5e-17;
Matches 88; Conservative 68; Mismatches 126; Indels 84; Gaps 13;
QY 30 YVEMTVGSPQTLNLIIVDTGSSNFAVGAAPHPFL-----HRYVQRLSSYRDLRKG 82
DB 74 YGTISIGTQQDFTVIFDTGSSMLV---PSIYCKSSACSNHKKRDPKSSYVSTNET 130
QY 83 VYVYTGQKWEGLGTDLVSIHPGNVTVRANIAITESDK-FFINGSNWEGILGLAYAE 141
DB 131 VYIAYTGSGMGIIGYDTAV---SSIDVQVQIFGLSETEPGSFYFYCNFDGILGLAFPS 187
QY 142 IARPDLSLEFPFSLVQKTHV-PNLFSLQLCGAGPLNQLVSGVSGMIIGIDHSLY 200
DB 188 IS--SSGATPVFNMMSQHLVAQDLFVLSKDG-----ETGSEVLFGGIDPNYT 235
QY 201 TGLSLWTPIRREYVYVLIIVRVEINGDOLK--MDCKEYNVDKSIDVSGTTLNRLPKKVEE 258
DB 236 TKGIYVWPLSAEYVWQTMMDRVTVGNKYVACFFTC-----QAIVDTGTSLLVMPQAYN 289
QY 259 AAVKSIKAASSTE-----KFPDGFNLGELQVLCVQAGTPWNIPFVSIYLMGEVTNQS 311
DB 290 RIKDLGVSSDGEISCDISKLPD-----VTFHINGHA--- 322
QY 312 FRITILPQQLRVEDVATSDCCYKFAISOSTGT-----VMGAVINEGFVYVDFRAR 365
DB 323 -----FTLPASAYVLNEDGSCMLGFENMGTPTELGEQWILGDVFIREFYVIFDRAN 373
QY 366 KRIGFA 371
DB 374 NKVGLS 379
RESULT 8
A34401
C:Species: Homo sapiens (man)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Jun-1999
C:Accession: A42038; A34401; S35663; S34467; A34643
R:Azuma, T.; Liu, W.; Vander Laan, D.J.; Bowcock, A.M.; Taggart, R.T.
J. Biol. Chem. 267, 1609-1614, 1992
A:Title: Human gastric cathepsin E gene. Multiple transcripts result from alternative pro
A:Reference number: A42038; MUID:92112877; PMID:1370478
A:Accession: A42038

A:Molecule type: DNA
A:Residues: 1-396 <AZU>
A:Cross-references: GB:M82847; NID:g181203; PIDN:AAA52300.1; PID:g18120
A:Note: sequence extracted from NCBI backbone (NCBIN:75963, NCBIN:75966, NCBIN:759
J. Azuma, T.; Pals, G.; Mohandas, T.K.; Couvreur, J.M.; Taggart, R.T.
J. Biol. Chem. 264, 16748-16753, 1989
A:Title: Human gastric cathepsin E. Predicted sequence localization to chromosome
A:Reference number: A34401; MUID:89380302; PMID:2674141
A:Accession: A34401
A:Molecule type: mRNA
A:Residues: 1-396 <AZ2>
A:Cross-references: GB:J05036; NID:g181193; PIDN:AAA52130.1; PID:g181194
R:Takeda-Ezaki, M.; Yamamoto, K.
Arch. Biochem. Biophys. 304, 352-358, 1993
A:Title: Isolation and biochemical characterization of procathepsin E from human e
A:Reference number: S35663; MUID:93349047; PMID:8346912
A:Accession: S35663
A:Status: preliminary
A:Molecule type: protein
A:Residues: 20-38; 54-76 <TAK>
R: Hill, J.; Montgomery, D.S.; Kay, J.
FEBS Lett. 326, 101-104, 1993
A:Title: Human cathepsin E produced in E. coli.
A:Reference number: S34467; MUID:93314762; PMID:8325357
A:Accession: S34467
A:Status: preliminary
A:Molecule type: protein
A:Residues: 57-60; 62-81 <HIL>
R: Athauda, S.B.P.; Matsuzaki, O.; Kageyama, T.; Takahashi, K.
Biochem. Biophys. Res. Commun. 168, 878-885, 1990
A:Title: Structural evidence for two isozymic forms and the carbohydrate attachmen
A:Reference number: A34643; MUID:90241267; PMID:2334440
A:Accession: A34643
A:Status: preliminary
A:Molecule type: protein
A:Residues: 54-58, 'XX', 62-64, 'M', 66-89, 'X', 91-95 <ATH>
A:Accession: B34643
A:Status: preliminary
A:Molecule type: protein
A:Residues: 54-59, 'X', 61-68 <AT2>
C:Genetics:
A:Gene: GDB:CTSE
A:Cross-references: GDB:119821; OMIM:116890
A:Map position: 1q31-1q31
C:Superfamily: pepsin
C:Keywords: aspartic proteinase; blocked amino end; hydrolase; zymogen
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-53/Domain: activation peptide #status predicted <PRO>
F:54-396/Product: cathepsin E #status predicted <MAT>
F:18/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidone
F:96,281/Active site: Asp #status predicted
Query Match 12.4%; Score 299.5; DB 2; Length 396;
Best Local Similarity 25.9%; Pred. No. 7e-17;
Matches 100; Conservative 65; Mismatches 148; Indels 73; Gaps 16;
QY 3 DEEPEEPRGRGSFVEMVDNLKRGKSGQGVVEMTPPOTLNLIVDTGSSNFAVGA---- 58
DB 63 DQSAKEP-----LNYLD-----MEVFGTISIGSPQNFVIFDTGSSNLWVPSVYCT 110
QY 59 APHPFLHRYVQRLSSYRDLRKGVYVPTQGWEGELGTDLVSIHPGNVTVRANIAAI 118
DB 111 SPACKTHSRFPQSSTSYSPQCQSFSIQVGTGSLSLIGADQVSV-EGLTVVGQDFGRSV 169
QY 119 TESDKPFINGSNWEGILGLAYAEIARPDLSLEPFFDLSLVKQTHVNLFLQLCGAGFLN 178
DB 170 TEPQGTQFVD-AEFDGILGLGYPSLA--VGGVTPVFEDNMAQ----NLVDLPMFVSVMSSN 222
QY 179 QSEVLASVGSMTIIGGIDHSLYTGLSWTPIRREYVYVLIIVRVEINGDOLKMPCKEYNY 238
DB 223 PE---CGAGSELIFGGYDHSFSGSLNWPVTVKQAYWQIALDNIQVGG--TVMFCSE--G 275
QY 239 DKSIVDSGTTNLRPLPKVFEAAVKSIIKAASSTSEKFPDGFNLGELQVLCVQAGTTPWNIPV 298

[illegible]

F;91-160,110-117,286-290,329-366/Disulfide bonds: #status experimental
F;97,295/Active site: Asp #status experimental
F;134,263/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 12.2%; Score 295.5; DB 1; Length 412;
Best Local Similarity 28.3%; Pred. No. 1.6e-16;
Matches 105; Conservative 58; Mismatches 146; Indels 59; Gaps 15;

QY 30 YVEMTVGSPPTLNILVDGTSSNFVGAAPHPEL-----HRYYORQLSSTYRDLRKG 83
DB 79 YGEIGTGPQCFVTVDFDTGSSNLWVPSHCKLDTACWIHHKYNKSDKSTYVKNKTSF 138
QY 84 YVPYTOGKWEGLTDLVSIIP-----HGNVTVVRANTAAITESDKFFINGSNWEG 134
DB 139 DIHYGSGSLGYLSQDTSVSPQSSASSASALGGVKVQVFEATKQPGITFAAKFDGI 198
QY 135 LGLAYAEIARPDSDSLEPFDFSLVKQTHV-PNLFSQLCGAGFPLNQSEVLASVGGSMIG 193
DB 199 LGMAYPRIS--VNVLPVFNLMQOKLVQDNIFSYL-----SRDPDAQPGGELMLG 248
QY 194 GIDHSLVTGSLWVTPIRREWYEVIIIVRVEI-NGODLKMCKEYNYDKSIVDSGTTNLR 252
DB 249 GTSDSKYKGSLSYLNVTWKAYQVHLDQVEVASGLTL---CKE--GCEAIVDTGTSUMVG 303
QY 253 PKKVFEAAVKSIIKAASSTKPPDGFGLGEQLV-CWQAGTTPWNIFPVISLYLMGEVFNQS 311
DB 304 PVDEVRELQKAIGAVPLIQ-----GEYMIPEKYST-----LPAITLKLGG---KG 346
QY 312 FRITLPQOYLRPVEDVATSDCCYKFAISO-----SSTGTVMGAVIMEGFYVDFDRAR 366
DB 347 YKLS--PEDYTLKVSQAGKTL--CLSGFMGMIPPPSGPLWILGDVFIGRYTYVDFDRNN 402
QY 367 RIGFAVSA 374
DB 403 RVGFAEAA 410

RESULT 14
D38302
pepsin (EC 3.4.23.-) II-4 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Jun-1991 #sequence_revision 20-Sep-1991 #text_change 23-Feb-1997
C:Accession: D38302
R:Kageyama, T.; Tanabe, K.; Koiwai, O.
J. Biol. Chem. 265, 17031-17038, 1990
A:Title: Structure and development of rabbit pepsinogens. Stage-specific zymogens, nucle
A:Reference number: A38302; MUID:91009127; PMID:2129536
A:Accession: D38302
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-387 <RAG>
A:Cross-references: GB:M59235; GB:J05638
A:Superfamily: pepsin
C:Keywords: aspartic proteinase; hydrolase; phosphoprotein; protein digestion

Query Match 12.2%; Score 295; DB 2; Length 387;
Best Local Similarity 26.1%; Pred. No. 1.6e-16;
Matches 97; Conservative 65; Mismatches 123; Indels 86; Gaps 14;

QY 30 YVEMTVGSPPTLNILVDGTSSNFVGAAPHPEL-----LHRYORQLSSTYRDLRKG 82
DB 75 YFGTISGTTPQDPTVIFDTGSSNLWV---PSTYCSSLACALHRRFPNDSSTYQGTSET 131
QY 83 YVYPYTOGKWEGLTDLVSIIPGPNVTVRANTAAITESDKFF-----INGSNWE 132
DB 132 LSITYTGTSGMTGILGYDTV-----KVGSIETNQIFGLSKTEPLGTLFLFAPFD 179
QY 133 GILGLAYAEIARPDSDSLEPFDFSLVKQTHV-PNLFSQLCGAGFPLNQSEVLASVGGSMI 191
DB 180 GILGLAYPSISSDAT--PVFDNWNNEGLVSQDLFSVYLSDD-----EKGLSLV 227
QY 192 IGGIDHSLVTGSLWVTPIRREWYEVIIIVRVEINGODLKM--DCKEYNYDKSIVDSGTTN 249
||||| ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

Db 228 FGGIDSSYYTGSLNMWVPVSEGYWQITMDSVSYNGETIACADSC-----QAIVDTGTSL 281
QY 250 LRLPKKVFEEAAVKSIIKAASSTKPPDGFGLGEQLV-CWQAGTTPWNIFPVISLYLMGEVT 308
DB 282 LTGP-----TSAISNIQSYIGASK-----NLLGENVISCAISDLSLDPIVF----- 321
QY 309 NQSFRIITLPQOYLRPVEDVATSDCCYKFAISOSSSTGT-----VMGAVIMEGFYVVPD 362
DB 322 -----TINGIQYPLPASAYILKEDDCTSGLEGMNVDTYTGELWILGDVFIQYFTVFD 375
QY 363 RARKRIGFAVS 373
DB 376 RANNOGLAAA 386

RESULT 15
S19684
pepsin A (EC 3.4.23.1) 2/3 precursor - Japanese macaque
N:Alternate names: pepsinogen A isozyme 2/3
C:Species: Macaca fuscata (Japanese macaque)
C:Date: 22-Nov-1993 #sequence_revision 19-Oct-1995 #text_change 18-Jun-1999
C:Accession: S19684; S16064
R:Kageyama, T.; Tanabe, K.; Koiwai, O.
Eur. J. Biochem. 202, 205-215, 1991
A:Title: Development-dependent expression of isozymogens of monkey pepsinogens and st
A:Reference number: S19681; MUID:92037645; PMID:1935977
A:Accession: S19684
A:Molecule type: mRNA
A:Residues: 1-388 <RAG>
A:Cross-references: EMBL:X59755; NID:g38068; PIDN:CAAA2427.1; PID:g38069
A:Note: parts of sequence, including amino ends of pepsinogen and activation intermed
C:Comment: It could not be determined if this sequence represents isozyme 2 or 3, whi
in by 4 months of age.
C:Comment: Although two-step activation is observed, activation is predominantly a o
C:Superfamily: pepsin
C:Keywords: aspartic proteinase; gastric juice; hydrolase; phosphoprotein; protein di
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-388/Product: pepsinogen A 2/3 #status experimental <PPT>
F;16-62/Domain: activation peptide #status experimental <APT>
F;63-388/Product: pepsin A 2/3 #status experimental <ENZ>
F;40-61/Cleavage site: Asp-Phe (pepsin) #status experimental
F;62-63/Cleavage site: Leu-Ile (pepsin) #status experimental
F;94,277/Active site: Asp #status predicted
F;107-112,268-272,311-344/Disulfide bonds: #status predicted
F;130/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 12.0%; Score 289.5; DB 1; Length 388;
Best Local Similarity 27.0%; Pred. No. 4.5e-16;
Matches 103; Conservative 66; Mismatches 141; Indels 71; Gaps 16;

QY 3 DEPEEPGRGGSFVEMVDNLRKSGQGYVYVEMTVGSPPTLNILVDGTSSNFVGAAPH 62
DB 64 DEQPLE-----NYLDM-----EYFGTIGITGPAQDFTVIFDTGSSNLWVSPSYCS 108
QY 63 FL-----HRYYORQLSSTYRDLRKGYYVYPYTGKWEGLTDLVSIIPGPNVTVRANTA 118
DB 109 SLACTNNRNPQDSSTYQSTSGTVSITYGTGSMTGILGYDTVQV---GGISDNTQIFGL 165
QY 119 TESDK--FFINGSNWEGILGLAYAEIARPDSDSLEPFDFSLVKQTHV-PNLFSQLCGAGFP 176
DB 166 SETEPGFLYAPDPDGLILGLAYPSIS---SSGATPVFDNWNNEGLVSQDLFSVYLSAD--- 220
QY 177 LNQSEVLASVGGSMIIGIDHSLVTGSLWVTPIRREWYEVIIIVRVEINGODLKMCKEY 236
DB 221 -DOS-----GSSVIFGGIDSSYYTGSNLWVPSVEGTWQISVDSITMNGEAI--CAE- 270
QY 237 NYKSVSDSGTTLNLRPKKVFEEAAVKSIIKAASSTKPPDGFGLGEQLV-CWQAGTTPWNI 295
DB 271 -GCOAIVDTGTSLLTGTSPITANTQSDIGASENSD-----GEMVVSICSAISLPIV 321
QY 296 FPIVSLYLMGEVNTNQSFRITILPQOYLRPVEDVATSDCCYK-----FAISQSTGTVMG 350
DB 322 F-----TINGIOYVPVPSAY-----ILQSQSCISGFGMDVPTESGELWILG 364

QY 351 AVINEGYYVFDRAKKGFA 371
| : : ||||| : : |
Db 365 DVFIQYFTVFDRAKKGFA 385

Search completed: March 4, 2003, 10:01:28
Job time : 23 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run On: March 4, 2003, 10:00:56 ; Search time 14 seconds
(without alignments)
1350.943 Million cell updates/sec

Title: US-09-723-722A-43

Perfect score: 2419

Sequence: 1 ETDEPEPGRGSGFVEMVD.....CLRLRQHQHDFADDSLK 456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2419	100.0	501	1 BACE_HUMAN	P56817 homo sapien
2	2392	98.9	501	1 BACE_RAT	P56819 rattus norv
3	2390	98.8	501	1 BACE_MOUSE	P56818 mus musculus
4	1171.5	48.4	518	1 BAE2_HUMAN	Q9Y520 homo sapien
5	327	13.5	324	1 PEP1_GADMO	P56272 gadus morhu
6	314.5	13.0	390	1 CATD_BOVIN	P80209 bos taurus
7	306	12.6	387	1 PEP1_RABIT	P28712 oryctolagus
8	302.5	12.5	388	1 PEP4_MACFU	P27678 macaca fusc
9	302	12.5	367	1 PEP4_CHICK	P00793 gallus gall
10	299.5	12.4	396	1 PEP4_HUMAN	P14091 homo sapien
11	298.5	12.3	383	1 PEP4_CHICK	P16476 gallus gall
12	296	12.2	387	1 PEP2_RABIT	P27821 oryctolagus
13	296	12.2	391	1 CATE_CAVPO	P25796 cavia porce
14	295.5	12.2	412	1 CATD_HUMAN	P07339 homo sapien
15	295	12.2	387	1 PEP4_RABIT	P28713 oryctolagus
16	289.5	12.0	388	1 PEP2_MACFU	P27677 macaca fusc
17	287	11.9	407	1 CATD_RAT	P24268 rattus norv
18	286	11.8	387	1 PEP3_RABIT	P27822 oryctolagus
19	285.5	11.8	398	1 CATE_RAT	P16228 rattus norv
20	285	11.7	398	1 CATD_CHICK	Q05744 gallus gall
21	283.5	11.7	388	1 PEP4_MACMU	P11489 macaca mula
22	282.5	11.7	388	1 PEP4_HUMAN	P00790 homo sapien
23	281.5	11.6	381	1 CHYM_SHEEP	P18276 ovis aries
24	281.5	11.6	388	1 PEP1_MACFU	P03954 macaca fusc
25	279.5	11.6	410	1 CATD_MOUSE	P18242 mus musculus
26	278.5	11.5	386	1 PEP4_PIG	P00791 sus scrofa
27	278	11.5	387	1 PEP4_CALJA	Q9N2d4 callithrix
28	277.5	11.5	396	1 CATE_RABIT	P43159 oryctolagus
29	277.5	11.5	397	1 CATE_MOUSE	P70269 mus musculus
30	276.5	11.4	419	1 CATV_CANAL	P10977 candida alb
31	273.5	11.3	381	1 CHYM_BOVIN	P00794 bos taurus
32	273	11.3	388	1 PEPF_RABIT	P27823 oryctolagus
33	270.5	11.2	377	1 PEPF_MACFU	P03955 macaca fusc

RESULT 1

ID	NAME	STANDARD	PRT:	501 AA
AC	P56817: Q9JUT5; Q9BYC1: Q9BYB9;			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Beta-secretase precursor (EC 3.4.23.-) (Beta-site APP cleaving enzyme)			
DE	(Beta-site amyloid precursor protein cleaving enzyme) (Aspartyl			
DE	protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2)			
DE	(Memapsin-2).			
GN	BACE OR BACE1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM A).			
RC	TISSUE=Brain;			
RX	MEDLINE=20002972; PubMed=10531052;			
RA	Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,			
RA	Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,			
RA	Fisher S., Fuller J., Edenson S., Lille J., Jarosinski M.A.,			
RA	Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,			
RA	Treanor J., Rogers G., Citron M.;			
RT	"Beta-secretase cleavage of Alzheimer's amyloid precursor protein by			
RL	the transmembrane aspartic protease BACE.";			
RL	Science 286:735-741(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND			
RP	CHARACTERIZATION.			
RC	TISSUE=Brain;			
RX	MEDLINE=20051717; PubMed=10591214;			
RA	Sinha S., Anderson J.P., Barbour R., Basi G.S., Caccavello R.,			
RA	Davis D., Doan M., Dovey H.F., Frigon N., Hong J., Jacobson-Croak K.,			
RA	Jewett N., Keim P., Knops J., Lieberburg I., Power W., Tan H.,			
RA	Tatsuno G., Tung J., Schenk D., Seubert P., Suomensari S.M., Wang S.,			
RA	Walker D., Zhao J., McConlogue L., Varghese J.;			
RT	"Purification and cloning of amyloid precursor protein beta-secretase			
RT	from human brain.";			
RL	Nature 402:537-540(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM A).			
RX	MEDLINE=20051717; PubMed=10591213;			
RA	Van R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,			
RA	Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,			
RA	Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.E.;			
RT	"Membrane-anchored aspartyl protease with Alzheimer's disease beta-			
RT	secretase activity.";			
RL	Nature 402:533-537(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM A).			
RX	MEDLINE=20120043; PubMed=10656250;			
RA	Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,			
RA	Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,			
RA	Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;			

Q28057 bos taurus
Q9n2d2 callithrix
Q9mzs8 ovis aries
P07267 saccharomyc
Q01294 neurospora
Q9n2d3 callithrix
Q64411 cavia porce
Q03168 aedes aegypt
P20142 homo sapien
Q28389 equus caball
P00795 sus scrofa
P42211 oryza sativ

ALIGNMENTS

"Identification of a novel aspartic proteinase (Asp 2) as beta-secretase.";
Mol. Cell. Neurosci. 14:419-427(1999).
[5]
SEQUENCE FROM N.A. (ISOFORM B).
TISSUE=Brain, and pancreas;
RA Michael B., De Pietri Tonelli D., Zaccchetti D., Keller P.;
"New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from human brain and pancreas.";
Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A. (ISOFORM C).
TISSUE=Pancreas;
RA Zaccchetti D., De Pietri Tonelli D., Schnurbus R.;
"New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from human pancreas.";
Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
[7]
SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
TISSUE=Brain;
RA Tanahashi H., Tabira T.;
"Three novel alternatively spliced isoforms of the human beta-site amyloid precursor protein cleaving enzyme (BACE) and their effect on amyloid beta-peptide production.";
Neurosci. Lett. 307:9-12(2001).
[8]
SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
MEDLINE=20144050; PubMed=10677483;
RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
"Human aspartic protease mepsin 2 cleaves the beta-secretase site of beta-amyloid precursor protein.";
Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
[9]
DISULFIDE BONDS.
MEDLINE=21950860; PubMed=11953458;
RA Fischer F., Molinari M., Bodendorf U., Paganetti P.;
"The disulfide bonds in the catalytic domain of BACE are critical but not essential for amyloid precursor protein processing activity.";
J. Neurochem. 80:1079-1088(2002).
CC -!- FUNCTION: RESPONSIBLE FOR THE PROTEOLYTIC PROCESSING OF THE AMYLOID PRECURSOR PROTEIN (APP). CLEAVES AT THE AMINO TERMINUS OF THE A-BETA PEPTIDE SEQUENCE, BETWEEN RESIDUES 671 AND 672 OF APP, LEADS TO THE GENERATION AND EXTRACELLULAR RELEASE OF BETA-CLEAVED SOLUBLE APP, AND A CORRESPONDING CELL-ASSOCIATED CARBOXY-TERMINAL FRAGMENT WHICH IS LATER RELEASED BY GAMMA-SECRETASE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 4 isoforms; A/BACE-1A/BAC-501 (shown here), B/BACE-1B/BACE-I-476; C/BACE-1C/BACE-I-457 and D/BACE-1D/BACE-I-432; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

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EMBL AF190725; AAF04142.1; -
EMBL AF201468; AAF18982.1; -
EMBL AF200343; AAF17079.1; -
EMBL AF204943; AAF26367.1; -
EMBL AF338816; AAK38374.1; -
EMBL AF338817; AAK38375.1; -
EMBL AB050436; BAB40931.1; -
EMBL AB050437; BAB40932.1; -
EMBL AB050438; BAB40933.1; -
EMBL AF200193; AAF13715.1; -
HSP: P32329; LYPS.
MEROPS; A01.004; -.

DR Genew: HGNC:933; BACE.
DR MIM: 604252; -
DR InterPro: IPR001461; AspproteaseA1.
DR InterPro: IPR001969; Aspprotease_site.
DR Pfam: PF00026; asp; 1.
DR PRINTS: PR00792; PEPsin.
DR PROSITE: PS00141; ASP_PROTEASE; 1.
KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW Signal; Alternative splicing.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 45
FT CHAIN 46 501 BETA-SECRETASE.
FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 458 478 POTENTIAL.
FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 289 289 BY SIMILARITY.
FT DISULFID 216 420
FT DISULFID 278 443
FT DISULFID 330 380
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 146 189 MISSING (IN ISOFORM C AND ISOFORM D).
FT VARSPIC 190 214 MISSING (IN ISOFORM B AND ISOFORM D).
SQ SEQUENCE 501 AA; 55763 MW; 377CE4C824ACEF05 CRC64;

Query Match 100.0%; Score 2419; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 2.5e-193;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETDEEPEEPCRRGSGFVEMVDNLRGKSGGYYVEMTVGSPPTNLILVDTGSSNFAVGAAP 60
DB 46 ETDEEPEEPCRRGSGFVEMVDNLRGKSGGYYVEMTVGSPPTNLILVDTGSSNFAVGAAP 105

QY 61 HPFLHRYQRLSSTYRDLRGVYVYPTGKWEGLGTDLVSIPIHGPNTVVRANIAAITE 120
DB 106 HPFLHRYQRLSSTYRDLRGVYVYPTGKWEGLGTDLVSIPIHGPNTVVRANIAAITE 165

QY 121 SDRFFINGSNWEGTILGLAYAEIARPDSDLPEFFDSLVKOTHPNLSLQLCGAGFPLNOS 180
DB 166 SDRFFINGSNWEGTILGLAYAEIARPDSDLPEFFDSLVKOTHPNLSLQLCGAGFPLNOS 225

QY 181 EVLASVGSMTIGGIDHSYLTGSLWYTPIRREMYEVIIVRVEINGDLKMDCKEYNYDK 240
DB 226 EVLASVGSMTIGGIDHSYLTGSLWYTPIRREMYEVIIVRVEINGDLKMDCKEYNYDK 285

QY 241 SIVDSGTTNLRPKKVFEEAAVKSIAASSTKFPDGFGLGQLVGVQAGTTPWNIPFVIS 300
DB 286 SIVDSGTTNLRPKKVFEEAAVKSIAASSTKFPDGFGLGQLVGVQAGTTPWNIPFVIS 345

QY 301 LYLMGEVTNOSFRITILPQOYLRPVEDVATSDCCYKFAISQSSTGTVMGAVIMEGFVYV 360
DB 346 LYLMGEVTNOSFRITILPQOYLRPVEDVATSDCCYKFAISQSSTGTVMGAVIMEGFVYV 405

QY 361 FDRARRKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420
DB 406 FDRARRKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465

QY 421 CALFMPLCLCMVCOMRCLRLRQOHHDDFADDISLLK 456
DB 466 CALFMPLCLCMVCOMRCLRLRQOHHDDFADDISLLK 501

RESULT 2
BACE_RAT
ID BACE_RAT STANDARD: PRT: 501 AA.
AC P56819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-secretase precursor (EC 3.4.23.-) (beta-site APP cleaving enzyme)

CC FRAGMENT WHICH IS LATER RELEASE BY GAMMA-SECRETASE (BY
CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: BRAIN.

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

CC -----
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CC -----

DR EMBL: AF190726; AAF04143.2; -

DR EMBL: AF200346; AAF17082.1; -

DR HSSP: P56272; 1AM5.

DR MEROPS: A01.004; -

DR MGD: MGI:1346542; Bace.

DR InterPro: IPR001461; AspproteaseA1.

DR Pfam: PF00026; asp; 1

DR PRINTS: PR00792; PEPsin.

DR PROSITE: PS00141; ASP-PROTEASE; 1.

KW Hydrolase; Aspartyl protease; Glycoprotein; zymogen; Transmembrane;

KW Signal.

FT SIGNAL 1 21 POTENTIAL.

FT PROPEP 22 45 POTENTIAL.

FT CHAIN 46 501 BETA-SECRETASE.

FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 458 478 POTENTIAL.

FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).

FT ACT_SITE 93 93 BY SIMILARITY.

FT DISULFID 216 420 BY SIMILARITY.

FT DISULFID 278 443 BY SIMILARITY.

FT DISULFID 330 380 BY SIMILARITY.

FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 501 AA; 55747 MW; C085A013145E474E CRC64;

Query Match 98.8%; Score 2390; DB 1; Length 501;

Best Local Similarity 98.2%; Pred. No. 6.4e-191;

Matches 448; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 ETDEEPEPGRGSEFVENVDNLRGSGGQYGVYVMTVGSPPQTLNVLVDTCSSNFVAGAAP 60

DB 46 ETDEESEPGRGSEFVENVDNLRGSGGQYGVYVMTVGSPPQTLNVLVDTCSSNFVAGAAP 105

QY 61 HPFLHRYQQLSRYRDLRGVYVYTOGKWEGELGTLVSTPHGPNVTVRANIAATTE 120

DB 106 HPFLHRYQQLSRYRDLRGVYVYTOGKWEGELGTLVSTPHGPNVTVRANIAATTE 165

QY 121 SDRKFFINGSNWEGLGLAYAEIARDDSLPEPFDLSLVKQTHVNLFLSLQCGAGFPLNQS 180

DB 166 SDRKFFINGSNWEGLGLAYAEIARDDSLPEPFDLSLVKQTHVNLFLSLQCGAGFPLNQT 225

QY 181 EVLASVGSMIIGIDISLHYTGLSWYTPIRREWYVEIIVRVEINGDLKMDCKEYNDK 240

DB 226 EALASVGSMIIGIDISLHYTGLSWYTPIRREWYVEIIVRVEINGDLKMDCKEYNDK 285

QY 241 SIYDSGTTNLRPKKVFEEAAVKSIAAASSTKEFPDGFVLGEQLVGVCAWGTTPWNIFPVIS 300

DB 286 SIYDSGTTNLRPKKVFEEAAVKSIAAASSTKEFPDGFVLGEQLVGVCAWGTTPWNIFPVIS 345

QY 301 LYLMGEVTNOSFRITILPQQYLRPVEDVATSDDCYKFAISQSSTGTVMGAVIMEGFYV 360

DB 346 LYLMGEVTNOSFRITILPQQYLRPVEDVATSDDCYKFAISQSSTGTVMGAVIMEGFYV 405

QY 361 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420

DB 106 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 420

DB 406 FDRARKRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQTDSTLMTIAYVMAAI 465

QY 421 CALFMLPLCLMVQWCRCLRCLRQHQHDDFADDISLLK 456

DB 466 CALFMLPLCLMVQWCRCLRCLRQHQHDDFADDISLLK 501

RESULT 4

BAE2_HUMAN

ID BAE2_HUMAN STANDARD; PRT; 518 AA.

AC Q9Y5Z0; Q9UJT6;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Beta secretase 2 precursor (EC 3.4.23.-) (Beta-site APP-cleaving

DE enzyme 2) (Aspartyl protease 1) (Asp 1) (ASPI) (Membrane-associated

DE aspartic protease 1) (Memapsin-1).

GN BACE2 OR ASP21.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20057170; PubMed=10591213;

RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,

RA Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,

RA Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.E.;

RT "Membrane-anchored aspartyl protease with Alzheimer's disease

RT beta-secretase activity.";

RL Nature 402:533-537(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Bone marrow.

RA Xin H., Stephens J.C., Duan X., Harrowe G., Kim E., Grieshammer U.,

RA Glese K.;

RT "Identification of a novel aspartic-like protease differentially

RT expressed in human breast cancer cell lines.";

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Accarino M.P., Fumagalli P., Ottolenghi S., Taramelli R.;

RT "Cloning of a gene from chromosome 21 Down region encoding a potential

RT transmembrane aspartyl protease.";

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Solans A., Estivill X., de la Luna S.;

RT "Cloning of a novel mammalian aspartyl protease.";

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=20120043; PubMed=10656250;

RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,

RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,

RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;

RT "Identification of a novel aspartic protease (Asp 2) as

RT beta-secretase.";

RL Mol. Cell. Neurosci. 14:419-427(1999).

RN [6]

RP SEQUENCE FROM N.A.

RX MEDLINE=20144060; PubMed=10677483;

RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;

RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of

RT beta-amyloid precursor protein.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).

RN [7]

RP SEQUENCE FROM N.A.

RX MEDLINE=20289799; PubMed=10830953;

RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,

RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,

RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,

RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,

QY 191 EGGIDHSYTGSLWYTPPIRREWEYEVIIVRVEINGQDLKMD-CKEYNDKSIIVDSGTTN 249
 Db 167 LGGVNSHYTSGIHLIPVTAKEYQWQVALDGIIVNGQTAACECC-----QAIVDTGTSK 219
 QY 250 ERLPKVFEAAVSIKAASTKEKPDGWLGBQLWCWQAGTTPWNPFPVLSLYLMGEVTN 309
 Db 220 EVAPVSALANIMKDIGASEN-----QGEEMGN---CASVQSLPDITF-----TI 260
 QY 310 @SPRITLPOQLRPVEDVATSDQDCYKFAISQSSTGT-----VMGAVIMEGFYVVF 361
 Db 261 NGVKQLPPSAYIEGDAQFCTS-----GLGSSGVPNSNTSELWIFGVFLRNYYTII 311
 QY 362 DRARKRIGFAVSA 374
 Db 312 DRNNKVGFAVSA 324

RESULT 6
 CATD_BOVIN
 ID CATD_BOVIN STANDARD; PRT; 390 AA.
 AC P80209: Q9T527;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cathepsin D precursor (EC 3.4.23.5).
 GN CTSB
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-48.
 RC TISSUE=Milk;
 RX MEDLINE=93202276; PubMed=8454061;
 RA Larsen L.B., Boisen A., Petersen T.E.;
 RT "Procathepsin D cannot autoactivate to cathepsin D at acid pH.";
 RL FEBS Lett. 319:54-58(1993).
 RN [2]
 RP SEQUENCE OF 45-390, AND X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
 RC TISSUE=Liver;
 RX MEDLINE=93223670; PubMed=8467789;
 RA Metcalf P., Fusek M.;
 RT "Two crystal structures for cathepsin D: the lysosomal targeting
 signal and active site";
 RL EMBO J. 12:1293-1302(1993).
 CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.
 CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
 CC that of pepsin A. Does not cleave the 4-Gln-I-His-5 bond in B
 CC chain of insulin.
 CC -!- SUBUNIT: CONSISTS OF A LIGHT CHAIN AND A HEAVY CHAIN.
 CC -!- SUBCELLULAR LOCATION: Lysosomal.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 DR PIR: S32383; S32383.
 DR PIR: S37419; S37419.
 DR HSSP: P07339; ILYB.
 DR MEROPS: A01.009; -.
 DR InterPro: IPR001461; Aspartyl protease.
 DR Pfam: PF00026; asp; 1.
 DR PROSITE: PS00192; PEPSIN.
 DR PROSITE: PS00141; ASP_PROTEASE; 2.
 KW Hydrolyase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen.
 FT PROPEP 1 44
 FT CHAIN 45 390
 FT ACT_SITE 77 77
 FT ACT_SITE 273 273
 FT DISULFID 71 140
 FT DISULFID 90 97
 FT DISULFID 264 268
 FT DISULFID 307 344
 FT CARBOHYD 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT

FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 390 AA; 42488 MW; 5B38AA1C33C48D35 CRC64;
 Query Match 13.0%; Score 314.5; DB 1; Length 390;
 Best Local Similarity 28.0%; Pred. No. 1.2e-18;
 Matches 113; Conservative 72; Mismatches 128; Indels 91; Gaps 21;
 QY 8 EPG-RRGSFVEMVNLGRKSGQGYVEMTVGSPPTQLNLILVDTGSSNFAVGAARHPPFL-- 64
 Db 39 EPAVRGPIPELLKNYMDAQ---YYGEIGITPPQCGTVVFDGSAANLWVPSIHCKLLDI 95
 QY 65 ----HRYYQRLSSTYRDLRKGVY--VPYTOGKWEGLCTDLVSIPIHCNP-----VTVR 112
 Db 96 ACWTHRKYNDSKSTY--VKNGTTFDIHYGSGLSGLYSDTVSVPCNPSSSSPGGVTVQ 153
 QY 113 ANI--AAITSDKFFINGSNWEGILGLAYAEIARPPDSLEPFDSLVKQTHV--PNLFSIQ 169
 Db 154 RQTFGEAIKQGVVFI-AAKFDGILGMAYPRIS--VNNVLPVFDNLMOOKLVKDNVFS-- 208
 QY 170 LCGAGFPLNOSVLAASVGSMTIGGIDHSYTGSLWYTPPIRREWEYEVIIVRVEINGODL 229
 Db 209 -----PFLNR-DPKAQPCCGELMLGGTDSKYRGSLMFHNVTROYWQHMDOLDV-GSSL 261
 QY 230 KMDCKEYNDKSIIVDSGTTNLRPKKVFEEAAVKSAASSTKPEPDGFWLGEQLV-CWQA 288
 Db 262 TV-CK--GCCEAIVDTGTSLIVGPVEEVRELQKACAVPLIQ-----GEYWIPECKV 310
 QY 289 GTTPWNIPFVLSLYLMGEVNTQSFRTITLPOQLRPVEDVATSDQDCYKFAISQSSTGT- 347
 Db 311 SS-----LPEVTVKLGG-----KDYALSPED-YALKVSOAETVTC 344
 QY 348 -----VMGAVIMEGFYVVFDRARKRIGFAVSA 374
 Db 345 LSGFMGMNDIPPPGGLWLIGDVFICRYTYVFDQNRVGLAEAA 388

RESULT 7
 PEPL_RABIT
 ID PEPL_RABIT STANDARD; PRT; 387 AA.
 AC P28712;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Pepsin II-1 precursor (EC 3.4.23.1) (Pepsin A).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91009127; PubMed=2129536;
 RA Kageyama T., Tanabe K., Koiwai O.;
 RT "Structure and development of rabbit pepsinogens. Stage-specific
 RT zymogens, nucleotide sequences of cDNAs, molecular evolution, and
 RT gene expression during development";
 RL J. Biol. Chem. 265:17031-17038(1990).
 CC -!- FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; ALTHOUGH BONDS
 CC INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERRED, MANY OTHERS ARE
 CC ALSO CLEAVED TO SOME EXTENT.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: hydrophobic, preferably
 CC aromatic, residues in P1 and P1' positions. Cleaves 1-Phe-I-Val-2,
 CC 4-Gln-I-His-5, 13-Glu-I-Ala-14, 14-Ala-I-Leu-15, 15-Leu-I-Tyr-16,
 CC 16-Tyr-I-Leu-17, 23-Gly-I-Phe-24, 24-Phe-I-Phe-25 and 25-Phe-I-
 CC Tyr-26 bonds in the B chain of insulin.
 CC -!- DEVELOPMENTAL STAGE: PEPSINOGENS IN GROUP I, II, AND III WHERE
 CC THE PREDOMINANT ZYMOGENS AT LATE POSTNATAL STAGE.
 CC -!- MISCELLANEOUS: THE EXPRESSION OF PEPSINOGEN GENES IS REGULATED BY
 CC HORMONES AND RELATED SUBSTANCES.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 DR PIR: B38302; B38302.
 DR HSSP: P00791; IPSA.
 DR MEROPS: A01.001; -.
 DR InterPro: IPR001461; AsparticaseA1.


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DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp. 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Digestion; Zymogen; Signal;
KW Phosphorylation; Multigene family.
FT SIGNAL 1 15
FT PROPEP 16 59
FT CHAIN 60 387
FT MOD_RES 129 129
FT ACT_SITE 93 93
FT ACT_SITE 276 276
FT DISULFID 106 111
FT DISULFID 267 271
FT DISULFID 310 343
SQ SEQUENCE 387 AA; 42070 MW; A6EC48F715541A48 CRC64;

Query Match 12.6%; Score 306; DB 1; Length 387;
Best Local Similarity 27.1%; Pred. No. 6.3e-18;
Matches 98; Conservative 67; Mismatches 131; Indels 66; Gaps 15;

QY 30 YVEMTVGSPPTNLILVDTCSSNFVAG---AAPHPLHRYVQORQLSSYRDLRKGVYV 85
DB 75 YFGTISTGTPPEPTVIFDTGSSNLWPFSTYCSLACFLHKKRPNDDSTFQATSETLSI 134
QY 86 PYTGKWEGLGTLDSIPHGPNNVTVRANIAAITEPD---KFFTINGSNWEGILGAYAEI 142
DB 135 TYTGSGMTGILGYTVK---GNIEDTNOIFGLSKTEPGITFLV--APFDGILGLAYPSI 189
QY 143 ARPDSDLEPFDSLVKQTHV--PNLFSIOLCGAGPELNQSEVLASVGSGMIIGDHSLYT 201
DB 190 SASDAT--PVFDNMNEGLVSEDLFSVYLSNG-----BKGSVMVFGGIDSSVYT 237
QY 202 GSWLYTPIREWYEVILVIRVEINGQDLKM--DCKEYNDKSIYDSGTTNLRPKKVFEEA 259
DB 238 GSNLWVPVSHGYWQITMDSTINGETIACADSC-----QAVVDGTGSLLAGPTSISK 291
QY 260 AVKSAKASSTKEKPPDGFWMGLQV--CWQACTTPWNIPFVLSYLMGEVTVNQSPRITLP 318
DB 292 IQSYIGASKNL-----LGENIISCAIDSLPDIVF-----FINN 325
QY 319 QOYLRPVED-VATSDQDC---YKFAISOSSTGT---VMGAVIMEGFYVVDRAKRIGFAV 372
DB 326 VQYPLPASAVILKDDCLSGFGMNLDTSYGELWILGDVEIRQYFVFDRAANNQVGLAA 385
QY 373 SA 374.
DB 386 AA 387

RESULT 8
PEP4_MACFU STANDARD; PRT; 388 AA.
AC P27678;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pepsin A-4 precursor (EC 3.4.23.1) (Pepsin I/II).
GN PGA.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 16-70.
RC TISSUE=Gastric mucosa;
RX MEDLINE=92037645; PubMed=1935977;
RA Kageyama T., Tanabe K., Koizumi O.;
RT "Development-dependent expression of isozymogens of monkey
RL pepsinogens and structural differences between them.";
RL Eur. J. Biochem. 202:205-215(1991).
CC -!- FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; ALTHOUGH BONDS
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INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERRED, MANY OTHERS ARE
ALSO CLEAVED TO SOME EXTENT.
-!- CATALYTIC ACTIVITY: Preferential cleavage: hydrophobic, preferably
aromatic, residues in P1 and P1' positions. Cleaves 1-Phe-I-Val-2,
4-Gln-I-His-5, 13-Glu-I-Ala-14, 14-Ala-I-Leu-15, 15-Leu-I-Tyr-16,
16-Tyr-I-Leu-17, 23-Gly-I-Phe-24, 24-Phe-I-Phe-25 and 25-Phe-I-
Tyr-26 bonds in the B chain of insulin.
-!- MISCELLANEOUS: THE EXPRESSION OF PEPsin GENES IS REGULATED BY
HORMONES AND RELATED SUBSTANCES.
-!- MISCELLANEOUS: EACH PEPsin IS CONVERTED TO CORRESPONDING
PEPsin AT PH 2.0 IN PART AS A RESULT OF THE RELEASE OF A 47 AA
ACTIVATION SEGMENT AND IN PART AS A RESULT OF STEPWISE PROTEOLYTIC
CLEAVAGE VIA AN INTERMEDIATE FORM(S).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
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CC -----
DR EMBL; X59753; CAA42425.1; -
DR PIR; S16065; S16065.
DR PIR; S19682; S19682.
DR HSP; P00790; IPSN.
DR MEROPS; A01.001; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR InterPro; IPR001791; Laminin_G.
DR Pfam; PF00026; asp. 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Digestion; Zymogen; Multigene family;
KW Signal; Glycoprotein.
FT SIGNAL 1 15
FT PROPEP 16 38
FT PROPEP 39 62
FT CHAIN 63 388
FT ACT_SITE 94 94
FT ACT_SITE 277 277
FT DISULFID 107 112
FT DISULFID 268 272
FT DISULFID 311 344
FT CARBOHYD 88
SQ SEQUENCE 388 AA; 41955 MW; A2923AB1F7FCDEB9 CRC64;

Query Match 12.5%; Score 302.5; DB 1; Length 388;
Best Local Similarity 27.6%; Pred. No. 1.2e-17;
Matches 107; Conservative 64; Mismatches 133; Indels 83; Gaps 17;

QY 3 DEEPPEPGRGSRFVEMVDNLKRGSGQGYVEMTVGSPPTNLILVDTCSSNFVAGAAHP 62
DB 64 DEQPLE-----NYLDV-----EYFGTIGTGAQNETVVDTCSSNLWV---PSV 105
QY 63 FL-----HRYVQORQLSSTYRDLRKGVYVPTGKWEGLGTLDSVIPHGPNNVTVRANI 115
DB 106 YCYSLACMDHNLFPQDSSTYRATSKVTSITYTGSMTGILGYDFVKV---GGISDTNQI 162
QY 116 AAITESDK--FFINGSNWEGLGAYAEIARPDSDLEPFDSILVKQTHV--PNLFSIOLCGA 173
DB 163 FGLSETPEGFLYFAPFDGILGLAYPSIS--SSGATPVFDNINWQRLVSQDLFSVYLSAD 220
QY 174 GFPLNQSEVLASVGSGMIIGDHSLYTGSWLYTPIREWYEVILVIRVEINGQDL--KM 231
DB 221 ----DQS-----GSVIFGGIDSSYTGSLNWWPVSVEGYWQISVDSITMNGKTIACAK 270
QY 232 DCKEYNDKSIYDSGTTNLRPKKVFEEA VKSAKSTEFPPDGFWMGLQV--CWQACT 290
DB 271 GC-----QAVVDGTGSLTGTSPFIANIQSDIGASENSD-----GEMVVSATISS 316
QY 291 TPWNIFPVISLYLMGEVTVNQSPRITLPQOY--LRPVEDVATSDQDCYK-----FAISQSS 344
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Db 317 LPDIVF-----TINGVOYPLPPSAVILQSGSCTSGFOGMDVPTESG 358
QY 345 TGTVMGAVMEGFYVVFDRKRIGFA 371
Db 359 ELWILGDVFIROYFTVFDNRANNOVGLA 385

RESULT 9
PEPA_CHICK
ID PEPA_CHICK STANDARD: PRT: 367 AA.
AC P00793;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pepsin A precursor (EC 3.4.23.1).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=84004412; PubMed=6617663;
RA Baudys M., Kostka V.;
RT "Covalent structure of chicken pepsinogen.";
RL Eur. J. Biochem. 136:89-99(1983).
CC -1- FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY. ALTHOUGH BONDS
CC INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERRED, MANY OTHERS ARE
CC ALSO CLEAVED TO SOME EXTENT.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: hydrophobic, preferably
CC aromatic, residues in p1 and p1' positions. Cleaves 1-Phe-|-Val-2,
CC 4-Gln-|-His-5, 13-Glu-|-Ala-14, 14-Ala-|-Leu-15, 15-Leu-|-Tyr-16,
CC 16-Tyr-|-Leu-17, 23-Gly-|-Phe-24, 24-Phe-|-Phe-25 and 25-Phe-|-
CC Tyr-26 bonds in the B chain of insulin.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR PIR; A00984; PECH.
DR HSSP; P00794; 4CMS.
DR MEROPS; A01.0PM; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW hydrolase; Aspartyl protease; Digestion; Zymogen; Glycoprotein.
FT PROPEP 1 42 ACTIVATION PEPTIDE.
FT CHAIN 43 367 PEPsin A.
FT ACT_SITE 77 77
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .).
FT DISULFID 90 95
FT DISULFID 251 255
FT DISULFID 290 323
SQ SEQUENCE 367 AA; 40431 MW; 0C547E7FD8F5B341 CRC64;

Query Match 12.5%; Score 302; DB 1; Length 367;
Best Local Similarity 24.0%; Pred. No. 1.3e-17;
Matches 88; Conservative 69; Mismatches 125; Indels 84; Gaps 13;

QY 30 YVEMTVGSPQTNILVDVTGSSNFAVGAHPFL-----HRYQRLSSSTYRDLRKG 82
Db 59 YGPISTGTPOQDFSVIFDTGSSNLWV---PSIYCKSSACSNNHKRFPDPSKSTYVSTNET 115
QY 83 VYVPTGCKWEGELGTLVLSIPHPNVTVRANIAATESDK-FFINGSNNEGILGLAYAE 141
Db 116 VYIAYGTGSMGILGYDTAVV---SSIDVQNIQIFGUSEPFGFFYYCNDGILGLAPPS 172
QY 142 IARPDSDLEPFDSLKVQTHV--PNLFSLOLCGAGFLPNQSEVLASVGGSMIIGIDHSLY 200
Db 173 IS--SSGATPVFDNMMSQHLVAQDLFSVYLSKDG-----ETSGFVLFGGIDPNYT 220
QY 201 TGSWYTPIREWYEVIIIVRVEINGQDLK--MDCKEYNVDKSLVDSGTTNLRPLPKVFE 258
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Db 221 TKGIYVWPLSAETYYQWITMDRVTVGNGKYVACFFTC-----QAIVDTGTSLLVMPQGVAYN 274
QY 259 AAVKSIIKAASSTE-----KPPDGEWLGEQLVCWQACTTPWNIFPVLISLYLMGEVTNQS 311
Db 275 RIIRKDLGVSSDGEISCDISKLPD-----VTFHINGHA----- 307
QY 312 FRITILPOOYLPRPVEDVATSQDDCYKFAISQSSSTGT-----VMGAVIMEGFYVVFDRAR 365
Db 308 -----FTLPASAYVLNEDGSCMLGFENMGTPTELGOWILGDVFIREFYVVFDRAN 358
QY 366 KRIGFA 371
Db 359 NKVGLS 364

RESULT 10
CATE_HUMAN
ID CATE_HUMAN STANDARD: PRT: 396 AA.
AC P14091;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cathepsin E precursor (EC 3.4.23.34).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89380302; PubMed=2674141;
RA Azuma T., Pals G., Mohandas T.K., Couvreur J.M., Taggart R.T.;
RT "Human gastric cathepsin E. Predicted sequence, localization to
RT chromosome 1, and sequence homology with other aspartic
RT proteinases.";
RL J. Biol. Chem. 264:16748-16753(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112877; PubMed=1370478;
RA Azuma T., Liu W.G., Vander Laan D.J., Bowcock A.M., Taggart R.T.;
RT "Human gastric cathepsin E gene. Multiple transcripts result from
RT alternative polyadenylation of the primary transcripts of a single
RT gene locus at 1q31-q32.";
RL J. Biol. Chem. 267:1609-1614(1992).
RN [3]
RP SEQUENCE FROM N.A.
RA Tatnell P.J., Kay J.;
RT "Human procathepsin E.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 54-68; 77-95; 141-155; 275-285 AND 389-396.
RX MEDLINE=90241267; PubMed=2334440;
RA Ahnada S.B.P., Matsuzaki O., Kageyama T., Takahashi K.;
RT "Structural evidence for two isozyme forms and the carbohydrate
RT attachment site of human gastric cathepsin E.";
RL Biochem. Biophys. Res. Commun. 168:878-885(1990).
CC -1- FUNCTION: DUE OF ITS INTRACELLULAR LOCATION AND DISTRIBUTION IN
CC LYMPHOID ASSOCIATED TISSUE, IT MAY HAVE A ROLE IN IMMUNE FUNCTION.
CC -1- CATALYTIC ACTIVITY: Similar to cathepsin D, but slightly broader
CC specificity.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
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CC or send an email to license@isb-sib.ch).
CC EMBL; M84424; AAA52300.1; -.
DR EMBL; M84413; AAA52300.1; JOINED.
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DR EMBL; M84417; AAA52300.1; JOINED.
DR EMBL; M84418; AAA52300.1; JOINED.
DR EMBL; M84419; AAA52300.1; JOINED.
DR EMBL; M84420; AAA52300.1; JOINED.
DR EMBL; M84421; AAA52300.1; JOINED.
DR EMBL; M84422; AAA52300.1; JOINED.
DR EMBL; J05036; AAA52130.1; -.
DR EMBL; AJ250717; CAB82850.1; -.
DR PIR; A34401; A34401.
DR PIR; A34643; A34643.
DR PIR; A42038; A42038.
DR HSP; P00794; 4CMS.
DR MEROPS; A01.010; -.
DR Genew; HGNC:2530; CTSE.
DR MIM; 116890; -.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 17
FT PROPEP 18 53 ACTIVATION PEPTIDE.
FT CHAIN 54 396 CATHEPSIN E.
FT MOD_RES 18 18 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 96 96 BY SIMILARITY.
FT ACT_SITE 281 281 BY SIMILARITY.
FT DISULFID 60 60 INTERCHAIN (PROBABLE).
FT DISULFID 109 114 BY SIMILARITY.
FT DISULFID 272 276 BY SIMILARITY.
FT DISULFID 314 351 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .).
FT CARBOHYD 220 220 O-LINKED (POTENTIAL).
FT CARBOHYD 333 333 O-LINKED (POTENTIAL).
SQ SEQUENCE 396 AA; 4793 MW; 40B643C5FB01521E CRC64;

Query Match 12.4%; Score 299.5; DB 1; Length 396;
Best Local Similarity 25.9%; Pred. No. 2.2e-17;
Matches 100; Conservative 65; Mismatches 148; Indels 73; Gaps 16;

QY 3 DEEPEPGRGSGFVEMVDNLGRSGQGYVEMTVGSPQTLNILLVDTGSSNFAVGA---- 58
DQ 63 DOSAKEP-----LNYLD-----MEYFGTISGSPQNTVFDTGSSNLWPSVYCT 110
QY 59 APHFLHRYQRLSSYRDLKGVVYPTQGWKEGELGTLVSIHPGPNVTVRANIAAI 118
DQ 111 SPACKTHSRFQSPSSSYSPQGSFQYGTGSLGIIGADQVSV-EGLTVVGQGFGEV 169
QY 119 TESDKFFINGSNNRIGILGLAYAEIARPDSDSLEPPFDSLVKQTHVPNLFSLQCGAGPPLN 178
DQ 170 TEPQTEVD-AEFDGILGLGVPSLA--VGGVTPVFDNMAQ-----NLVDLPMSVYKSN 222
QY 179 QSEVLASVGSMTIGGDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNY 238
DQ 223 PE---GGAGSELIFGGYDHFSGSLNWPVTKQYQIALDNIQVGQ--TVMFCSE--G 275
QY 239 DKSIVDSGTTNLRPLKPKVFAAANKSIRKASSTERKFPDGEVLGEQLVCWQAGTTPWNPFPV 298
DQ 276 QCAIVDTGTSLSITGSPDKIKQLQNAICAP-----VGEYAVE-----CANLNWPD 322
QY 299 ISLYLMGEVNTQSPRITILPQQYLRPVEDVATSDODCKYKFAISQSSSTG----- 346
DQ 323 VTFTING-----VPYTLSPATY--TLLDVFDGMQFC-----SSGFGQLDHPAGP 366
QY 347 -TVMGVIMGFIYVVFDRARKRIGFA 371
DQ 367 LWILGDVFIQFYSVFDRGNRRVGLA 392

RESULT 11
PEPE_CHICK
ID PEPE_CHICK STANDARD; PRT; 383 AA.
AC P16476;
```

```
Db 295 AVGANQNT-----YGEYSV-----NCSHILAMPDVVFVIGGI----- 326
QY 319 QOYLRPVEDVA---TSDDCYKFAISQSSTGTGVMGAVTMEGEGVVVDFDRKRIGFA 371
Db 327 -QY--PVPALAYTEQNGOGTCKMSSFSQSSADLWILGDVFRVYYSIFDRANRRVGLA 380

RESULT 12
PEP2_RABIT
ID PEP2_RABIT STANDARD; PRT; 387 AA.
AC P27821;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pepsin II-2/3 precursor (EC 3.4.23.1) (Pepsin A).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91009127; PubMed=2129536;
RA Kageyama T., Tanabe K., Koiwai O.;
RT "Structure and development of rabbit pepsinogens. Stage-specific
RT zymogens, nucleotide sequences of cDNAs, molecular evolution, and
RT gene expression during development."
RL J. Biol. Chem. 265:17031-17038(1990).
CC -!- FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; ALTHOUGH BONDS
CC INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERRED, MANY OTHERS ARE
CC ALSO CLEAVED TO SOME EXTENT.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: hydrophobic, preferably
CC aromatic, residues in p1 and p1' positions. Cleaves 1-Phe-I-Val-2,
CC 4-Gln-I-His-5, 13-Glu-I-Ala-14, 14-Ala-I-Leu-15, 15-Leu-I-Tyr-16,
CC 16-Tyr-I-Leu-17, 23-Gly-I-Phe-24, 24-Phe-I-Phe-25 and 25-Phe-I-
CC Tyr-26 bonds in the B chain of insulin.
CC -!- DEVELOPMENTAL STAGE: PEPSINOGENS IN GROUP I, II, AND III WHERE
CC THE PREDOMINANT ZYMOGENS AT LATE POSTNATAL STAGE.
CC -!- MISCELLANEOUS: THE EXPRESSION OF PEPSINOGEN GENES IS REGULATED BY
CC HORMONES AND RELATED SUBSTANCES.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M59235; AAA85369.1;
DR PIR; C38302; C38302.
DR HSP; P00790; IPSN.
DR MEROPS; A01.001;
DR InterPro; IPR001461; AsparticaseA1.
DR InterPro; IPR001969; Asparticase_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Digestion; Zymogen; Signal;
KW Phosphorylation; Multigene family.
FT SIGNAL 1 15
FT PROPEP 16 59 ACTIVATION PEPTIDE.
FT CHAIN 60 387 PEPSIN II-2/3.
FT MOD_RES 129 129 PHOSPHORYLATION (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 276 276 BY SIMILARITY.
FT DISULFID 106 111 BY SIMILARITY.
FT DISULFID 267 271 BY SIMILARITY.
FT DISULFID 310 343 BY SIMILARITY.
SQ SEQUENCE 387 AA; 42100 MW; 66FC331A3DC75891 CRC64;
```

Query Match

12.2%; Score 296; DB 1; Length 387;

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Best Local Similarity 26.9%; Pred. No. 4.2e-17;
Matches 97; Conservative 63; Mismatches 135; Indels 66; Gaps 13;

QY 30 YVVENTGSPQTLNILDVTGSSNFAVGAAPHPF-----LHRYQROLSTSYRDLKKG 82
Db 75 YFGTISGTTPQDFTVIFDTGSSNLWV---PSTYCSLACALHKKRFPEDSSTYOGTSET 131
QY 83 VYVPYTOGKEGELCTDLVSIPIHGPNNVTVRANIAATESDKFFINGSNWEGTGLAYAEI 142
Db 132 LSIYTGSGMTGILGYDVKVGSIEDTNQIFGLSKTEPSLTFLF--APFDGILGLAYPSI 189
QY 143 ARPDLSLEPFDDSLVKQTHV-PNLFSLQLCGAGFPLNQSVLASVGGSMIIGGDHSLYT 201
Db 190 SSSDAT--PVFDNMNNEGLVSQDLFSVYLSSDD-----EKGLSLVMFGGIDSSVYT 237
QY 202 GSLWYTPIRREWYEVIIIVRVEINQODLKM--DCKEYNYDKSIVDSGTTNLRPKKVEA 259
Db 238 GSLNMVPSYEGYQWITMDSVINGETIACADSC-----QAVDTGTSLLTGP---TS 287
QY 260 AVKSIKAASSTKFPDGFGLGQVLV-CWQAGTTPWNIPFVVISLYLMGEVTVNQSPRITILP 318
Db 288 AISNIQSYIGASK-----NLNGENVISCSAIDSLDIVF-----TING 325
QY 319 QOYLRPVEDVATSDDCYKFAISQSSTGT-----VMGAVTMEGEGVVVDFDRKRIGFAV 372
Db 326 IQYPLPASAYILKEDDDCTSGLEGMNVDTYTGELWILGDVFIQYFTVDFRANNGQLAA 385
QY 373 S 373
Db 386 A 386

RESULT 13
CATE_CAVPO STANDARD; PRT; 391 AA.
ID CATE_CAVPO
AC P25796;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cathepsin E precursor (EC 3.4.23.34).
GN CTSE.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=92355614; PubMed=1644829;
RA Kageyama T., Ichinose M., Tsukada S., Miki K., Kurokawa K., Koiwai O.,
RA Tanji M., Yakabe E., Athauda S.B., Takahashi K.;
RA "Gastric procathepsin E and progastricsin from guinea pig.
RT Purification, molecular cloning of cDNAs, and characterization of
RT enzymatic properties, with special reference to procathepsin E.";
RL J. Biol. Chem. 267:16450-16459(1992).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Gastric mucosa;
RX MEDLINE=96073637; PubMed=8540321;
RA Kageyama T., Ichinose M., Miki K., Moriyama A., Yonezawa S.,
RA Tanji M., Athauda S.B., Takahashi K.;
RA "Isolation, characterization, and structure of procathepsin E and
RT cathepsin E from the gastric mucosa of guinea pig.";
RL Adv. Exp. Med. Biol. 362:211-221(1995).
CC -!- FUNCTION: DUE TO ITS INTRACELLULAR LOCATION AND DISTRIBUTION IN
CC LYMPHOID ASSOCIATED TISSUE, IT MAY HAVE A ROLE IN IMMUNE FUNCTION.
CC -!- CATALYTIC ACTIVITY: Similar to cathepsin D, but slightly broader
CC specificity.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
```


Query Match	12.2%;	Score 295.5;	DB 1;	Length 412;
Best Local Similarity	28.5%;	Pred. No. 5.1e-17;		
Matches 105;	Conservative 58;	Mismatches 146;	Indels 59;	Gaps
Qy	30	YVEMTVGSPPTNLILVDTGSSNFAVGAAPHPEL-----HRYYORQLSSTYRDLRKGV	83	
Db	79	YVGEIGTTPPQCFTVFDTGSSNLWVPSIHCLLDIACWIIHKYNSDKSSTYVKNGTSF	138	
Qy	84	YVPYTOGWEGELCTDLVIP-----HGPNTVTRANIAAITESDKFFINGSNWEG	134	
Db	139	DIHYGSGSLGYSQDTSVSPQCSASSASALGGVYKVERQVEGATKQPGITFIAAKFDGI	198	
Qy	135	LGLAYAEIARPDSDLEPPFDLSLVKQTHV-PNLFSQLCGAGFPLNQSEVLASVGGSMITG	193	
Db	199	LGMAYPRIIS--VNNVLVPFDNLMOOKLVDQNIIFSFL-----SRPDAPQPGELMLG	248	
Qy	194	GIDISLYTGSLSWYTPIRREWYEVVIVRVEI-NQODLKMDCKEYNYDKSIVDSGTTNLR	252	
Db	249	GTDSKYYKGSLSYLVNTRKAYWQVHLDQVEVASGLTL---CKE--GCEAIVDTGTSMLVG	303	
Qy	253	PKKVFEAAVKSIKAASSTKEKFPDGFWLGEOLV-CWQAGTTTPWNTFPVLSLYLMGEVTNOS	311	
Db	304	PVDEVRELQKALGAPLQI-----GEYMIPEKVKST-----LPATILKLG-----KG	346	
Qy	312	FRITILPQOYLRPVEDVATSQDDCYKPAISO-----SSTGTGMGAVIMEGFYVVFDRARK	366	
Db	347	YKLS--PEDYTLLKVSQAGKTL--CLSGFMCMDDIPPPSGPLWILGDFVFIGRYTVTFDRDNN	402	

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QY 367 RIGFAVSA 374
ID PEP4_RABIT
Db 403 RVGFAEA 410
PRT; 387 AA.
STANDARD;
AC P28713;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pepsin II-4 precursor (EC 3.4.23.1) (Pepsin A).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91009127; PubMed=2129536;
RA Kageyama T., Tanabe K., Koiwai O.;
RT "Structure and development of rabbit pepsinogens. Stage-specific
RT zymogens, nucleotide sequences of cDNAs, molecular evolution, and
RT gene expression during development.";
RL J. Biol. Chem. 265:17031-17038(1990).
CC -!- FUNCTION: SHOWS PARTICULARLY BROAD SPECIFICITY; ALTHOUGH BONDS
CC INVOLVING PHENYLALANINE AND LEUCINE ARE PREFERRED, MANY OTHERS ARE
CC ALSO CLEAVED TO SOME EXTENT.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: hydrophobic, preferably
CC aromatic, residues in p1 and p1' positions. Cleaves 1-phe-1'-Val-2,
CC 4-Gln-1'-His-5, 13-Glu-1'-Ala-14, 14-Ala-1'-Leu-15, 15-Leu-1'-Tyr-16,
CC 16-Tyr-1'-Leu-17, 23-Gly-1'-Phe-24, 24-Phe-1'-Phe-25 and 25-Phe-1'-
CC Tyr-26 bonds in the B chain of insulin.
CC -!- DEVELOPMENTAL STAGE: PEPINOGENS IN GROUP I, II, AND III WHERE
CC THE PREDOMINANT ZYMOGENS AT LATE POSTNATAL STAGE.
CC -!- MISCELLANEOUS: THE EXPRESSION OF PEPINOGEN GENES IS REGULATED BY
CC HORMONES AND RELATED SUBSTANCES.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR PIR: D38302; D38302.
DR HSP: P00790; LPSN.
DR MEROPS: A01.001; -.
DR InterPro: IPR001461; AsparticaseA1.
DR InterPro: IPR001969; Asparticase_site.
DR Pfam: PF00026; asp; 1.
DR PRINTS: PR00792; PEPsin.
DR PROSITE: PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Digestion; Zymogen; Signal;
KW Phosphorylation; Multigene family.
FT SIGNAL 1 15
FT PROPEP 16 59 ACTIVATION PEPTIDE.
FT CHAIN 60 387 PEPsin II-4.
FT MOD_RES 129 129 PHOSPHORYLATION (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 276 276 BY SIMILARITY.
FT DISULFID 106 111 BY SIMILARITY.
FT DISULFID 267 271 BY SIMILARITY.
FT DISULFID 310 343 BY SIMILARITY.
SQ SEQUENCE 387 AA; 42052 MW; 21ADD07782A89585 CRC64;
```

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Query Match 12.2%; Score 295; DB 1; Length 387;
Best Local Similarity 26.1%; Pred. No. 5.1e-17;
Matches 97; Conservative 65; Mismatches 123; Indels 86; Gaps 14;

QY 30 YVEMTVGSPPTQTLNLTVDGSSNFAVGAAPHF-----LHRYQRLSSTYRDLKRG 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 YFTGISGTPQDFTVIFDTGSSNLWV---PSTYCSLACALHKRPEDSSTYQGTSET 131
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 83 VVVPYTGKWEGLGTDLYSIPHPNVTVRANIAATESDKPF-----INGSNWE 132
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 132 LSITVTGSMTGILGYDVT-----KVGSTEDTNQIFGLSKTEPGLTFLEAPFD 179
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 133 GILGLAYAEIARPDSDLEFPFDSLVKQTHV-PNLFSLQLCGAGFPLNQSEVLASVGSMI 191
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: March 4, 2003, 10:02:13
Job time : 17 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: March 4, 2003, 10:00:57 ; Search time 36 seconds
(without alignments)
2609.930 Million cell updates/sec

Title: US-09-723-722a-43

Perfect score: 2419

Sequence: 1 ETDEPEEPGRGSEFVEMVD.....CLRLRQHQDDFADDSILK 456

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2419	100.0	532	4 Q9ULS1	Q9ULS1 homo sapien
2	2264.5	93.6	476	4 Q9BYC1	Q9BYC1 homo sapien
3	2161	89.3	457	4 Q9BYC0	Q9BYC0 homo sapien
4	2016.5	83.4	432	4 Q9BYB9	Q9BYB9 homo sapien
5	1407	58.2	266	11 Q9CUU5	Q9CUU5 mus musculus
6	1160.5	48.0	439	4 Q9H2V8	Q9H2V8 homo sapien
7	1146.5	47.4	514	11 Q9JL18	Q9JL18 mus musculus
8	972.5	40.2	468	4 Q9NZL2	Q9NZL2 homo sapien
9	967.5	40.0	396	4 Q9NZL1	Q9NZL1 homo sapien
10	712.5	29.5	213	4 Q9P0D2	Q9P0D2 homo sapien
11	596.5	24.7	255	11 Q9RLP7	Q9RLP7 mus musculus
12	359.5	14.9	244	5 Q8WQY9	Q8WQY9 aphrocallis
13	332.5	13.7	391	5 Q9VKP6	Q9VKP6 drosophila
14	332	13.2	354	5 Q9GYX7	Q9GYX7 boophilus m
15	312.5	12.9	386	6 Q9BGU5	Q9BGU5 bos taurus
16	308	12.7	384	13 Q9DEC2	Q9DEC2 xenopus lae

17	308	12.7	385	13 Q9DEC4	Q9DEC4 rana catesb
18	305	12.6	386	6 Q9GMV7	Q9GMV7 rhinolophus
19	305	12.6	387	6 Q9GMV8	Q9GMV8 sorex unqui
20	304.5	12.6	372	5 Q9VLK3	Q9VLK3 drosophila
21	304.5	12.6	387	13 Q9DDV5	Q9DDV5 salvelinus
22	304	12.6	387	6 Q9GMV9	Q9GMV9 suncus muri
23	303.5	12.5	383	13 Q9DEC5	Q9DEC5 salvelinus
24	303	12.5	383	13 Q9DEC3	Q9DEC3 xenopus lae
25	302.5	12.5	376	13 Q9PUR8	Q9PUR8 pseudopleur
26	301	12.4	382	13 Q9PRG9	Q9PRG9 gallus gall
27	301	12.4	423	5 Q9VRP7	Q9VRP7 drosophila
28	298.5	12.3	384	13 Q91322	Q91322 rana catesb
29	295.5	12.2	386	6 Q9GMV6	Q9GMV6 canis fami
30	294	12.2	396	13 Q93428	Q93428 chionodraco
31	290.5	12.0	381	6 Q9GK11	Q9GK11 camelus dro
32	288	11.9	399	13 Q93458	Q93458 podarcis si
33	287.5	11.9	444	5 Q21966	Q21966 caenorhabdi
34	284	11.7	398	13 P87370	P87370 oncorhynch
35	284	11.7	427	5 P91802	P91802 schistosoma
36	281	11.6	378	13 Q9PUR9	Q9PUR9 pseudopleur
37	280	11.6	390	6 Q8S041	Q8S041 canis fami
38	279.5	11.6	390	6 Q9GK10	Q9GK10 camelus dro
39	278	11.5	370	6 Q9FTW1	Q9FTW1 bos taurus
40	278	11.5	399	13 Q9DD89	Q9DD89 brachydania
41	278	11.5	422	5 Q96906	Q96906 onchocerca
42	277.5	11.5	380	6 Q28950	Q28950 sus scrofa
43	277	11.5	446	5 Q9N9H3	Q9N9H3 necator ame
44	276	11.4	389	13 Q9PWK1	Q9PWK1 gallus gall
45	276	11.4	389	13 Q9W643	Q9W643 gallus gall

ALIGNMENTS

RESULT 1

Q9ULS1
ID Q9ULS1 PRELIMINARY; PRT; 532 AA.
AC Q9ULS1;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-OCT-2001 (TREMREL. 18, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE KIAA1149 protein (fragment).
GN KIAA1149.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirose M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
RL DNA Res. 6:329-336(1999).
DR EMBL; AB032975; BAA86463.2;
DR HSSP; P56272; 1AM5;
DR MEROPS; A01.004;
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 532 AA; 58720 MW; 98B135D0D5FBD2E8 CRC64;

Query Match 100.0%; Score 2419; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.7e-192;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY i ETDEPEEPGRGSEFVEMVDNLKSGQGYVEMTVGSPQTLNLVDVTGSSNFAVGAAP 60
|||||
Db 77 ETDEPEEPGRGSEFVEMVDNLKSGQGYVEMTVGSPQTLNLVDVTGSSNFAVGAAP 136

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QY 61 HPFLHRYQRLSTYRDLRKGVVYPYTGKWEGLGTDLVSIHPGPNVTVRANIAAITE 120
|||||
Db 137 HPFLHRYQRLSTYRDLRKGVVYPYTGKWEGLGTDLVSIHPGPNVTVRANIAAITE 196
|||||
QY 121 SKKFFINGSNWEGILGLAYABIAIARPDSDLPPFDLSLVKQTHVFNLFSLQLCGAGFPLNQS 180
|||||
Db 197 SKKFFINGSNWEGILGLAYABIAIARPDSDLPPFDLSLVKQTHVFNLFSLQLCGAGFPLNQS 256
|||||
QY 181 EVLASVGSMTIGIDHSLYTGLSWYTPIRREWYEVIIIVRVEINGODLKMCKEYNDK 240
|||||
Db 257 EVLASVGSMTIGIDHSLYTGLSWYTPIRREWYEVIIIVRVEINGODLKMCKEYNDK 316
|||||
QY 241 SIIVDSGTTNLRPKKVFEEAAVKSIAAASSTKFPDGFGLGEQLVCHVQAGTTPWNIPFV 300
|||||
Db 317 SIIVDSGTTNLRPKKVFEEAAVKSIAAASSTKFPDGFGLGEQLVCHVQAGTTPWNIPFV 376
|||||
QY 301 LYLMGEVNTGSRITILPQQYLRLPVEDVATSDDCYKFAISQSSSTGTVMGAVIMEGFYV 360
|||||
Db 377 LYLMGEVNTGSRITILPQQYLRLPVEDVATSDDCYKFAISQSSSTGTVMGAVIMEGFYV 436
|||||
QY 361 FDRARRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQDDESTLMTIAYVMAAI 420
|||||
Db 437 FDRARRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQDDESTLMTIAYVMAAI 496
|||||
QY 421 CALFMLPLCLMVCOMVCLRLCRLRQHQHDDFADDISLLK 456
|||||
Db 497 CALFMLPLCLMVCOMVCLRLCRLRQHQHDDFADDISLLK 532
|||||
```

RESULT 2

```
Q9BYC1
ID Q9BYC1 PRELIMINARY; PRT; 476 AA;
AC Q9BYC1;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Beta-site APP cleaving enzyme I-476.
GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=21408467; PubMed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
RT cleaving enzyme (BACE) and their effect on amyloid beta-peptide
RT production.";
RL Neurosci. Lett. 307:9-12(2001).
DR HSSP; P32329; IYPS.
DR EMBL; AB050436; BAB40931.1; -.
DR HSSP; P32329; IYPS.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; ppsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN.1.
SQ SEQUENCE 476 AA; 52907 MW; 6C8C87F8A953AF66 CRC64;
```

Query Match 93.6%; Score 2264.5; DB 4; Length 476;
Best Local Similarity 94.5%; Pred. No. 9,9e-180;
Matches 431; Conservative 0; Mismatches 0; Indels 25; Gaps 1;

```
QY 1 ETDEEPEEPGRGSGFVEMVDNLRKSGGQYVYEMTVGSPPTNLINLVDGTSSNFAVGAAP 60
|||||
Db 46 ETDEEPEEPGRGSGFVEMVDNLRKSGGQYVYEMTVGSPPTNLINLVDGTSSNFAVGAAP 105
|||||
QY 61 HPFLHRYQRLSTYRDLRKGVVYPYTGKWEGLGTDLVSIHPGPNVTVRANIAAITE 120
|||||
Db 106 HPFLHRYQRLSTYRDLRKGVVYPYTGKWEGLGTDLVSIHPGPNVTVRANIAAITE 165
|||||
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```
QY 121 SKKFFINGSNWEGILGLAYABIAIARPDSDLPPFDLSLVKQTHVFNLFSLQLCGAGFPLNQS 180
|||||
Db 166 SKKFFINGSNWEGILGLAYABIAIARPDSDLPPFDLSLVKQTHVFNLFSLQLCGAGFPLNQS 200
|||||
QY 181 EVLASVGSMTIGIDHSLYTGLSWYTPIRREWYEVIIIVRVEINGODLKMCKEYNDK 240
|||||
Db 201 EVLASVGSMTIGIDHSLYTGLSWYTPIRREWYEVIIIVRVEINGODLKMCKEYNDK 260
|||||
QY 241 SIIVDSGTTNLRPKKVFEEAAVKSIAAASSTKFPDGFGLGEQLVCHVQAGTTPWNIPFV 300
|||||
Db 261 SIIVDSGTTNLRPKKVFEEAAVKSIAAASSTKFPDGFGLGEQLVCHVQAGTTPWNIPFV 320
|||||
QY 301 LYLMGEVNTGSRITILPQQYLRLPVEDVATSDDCYKFAISQSSSTGTVMGAVIMEGFYV 360
|||||
Db 321 LYLMGEVNTGSRITILPQQYLRLPVEDVATSDDCYKFAISQSSSTGTVMGAVIMEGFYV 380
|||||
QY 361 FDRARRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQDDESTLMTIAYVMAAI 420
|||||
Db 381 FDRARRIGFAVSACHVHDEFTAAVEGPFVTLDMEDCGYNIPQDDESTLMTIAYVMAAI 440
|||||
QY 421 CALFMLPLCLMVCOMVCLRLCRLRQHQHDDFADDISLLK 456
|||||
Db 441 CALFMLPLCLMVCOMVCLRLCRLRQHQHDDFADDISLLK 476
|||||
```

RESULT 3

```
Q9BYC0
ID Q9BYC0 PRELIMINARY; PRT; 457 AA.
AC Q9BYC0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Beta-site APP cleaving enzyme I-457 (Beta-site APP cleaving enzyme
DE type C).
GN BACE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=21408467; PubMed=11516562;
RA Tanahashi H., Tabira T.;
RT "Three novel alternatively spliced isoforms of the human beta-site APP
RT cleaving enzyme (BACE) and their effect on amyloid beta-peptide
RT production.";
RL Neurosci. Lett. 307:9-12(2001).
DR HSSP; P32329; IYPS.
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; ppsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN.1.
SQ SEQUENCE 457 AA; 51068 MW; C794C9A9E85FE7A2 CRC64;
```

Query Match 89.3%; Score 2161; DB 4; Length 457;
Best Local Similarity 90.4%; Pred. No. 3,7e-171;
Matches 412; Conservative 0; Mismatches 0; Indels 44; Gaps 1;

```
QY 1 ETDEEPEEPGRGSGFVEMVDNLRKSGGQYVYEMTVGSPPTNLINLVDGTSSNFAVGAAP 60
|||||
Db 46 ETDEEPEEPGRGSGFVEMVDNLRKSGGQYVYEMTVGSPPTNLINLVDGTSSNFAVGAAP 105
|||||
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QY 191 IIGGIDSLYTGSLWYTPIRREWEYEVIIIVRVEINGODLMDCKEYNDKSIYVDSGTTNL 250
DB 1 IIGGIDSLYTGSLWYTPIRREWEYEVIIIVRVEINGODLMDCKEYNDKSIYVDSGTTNL 60
QY 251 RLPKKVFEEAAVKSIIKAASSTKFPDGFGLGOLVCWQAGCTTWNIFPVISLYLMGEVTNQ 310
DB 61 RLPKKVFEEAAVKSIIKAASSTKFPDGFGLGOLVCWQAGCTTWNIFPVISLYLMGEVTNQ 120
QY 311 SFRITILPOQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARRIGF 370
DB 121 SFRITILPOQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARRIGF 180
QY 371 AVSACHVHDEFRTAAVCGPFTVLDMECGYNIPOQDESLMTIAYVMAAICALFMLPLCL 430
DB 181 AVSACHVHDEFRTAAVCGPFTVLDMECGYNIPOQDESLMTIAYVMAAICALFMLPLCL 240
QY 431 MVCWRCLRLCRQHQHDDFADDISLLK 456
DB 241 MVCWRCLRLCRQHQHDDFADDISLLK 266

RESULT 6
Q9H2V8 PRELIMINARY; PRT; 439 AA.
AC Q9H2V8:
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDAL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PHEOCHROMOCYTOMA;
RA Li Y., Huang Q., Peng, Y., Song H., Yu Y., Xu S., Ren S., Chen Z.,
RA Han Z.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF212252; AAG41783.1; -
DR HSP; P00797; 2REN.
DR InterPro: IPR001461; AspproteaseA1.
DR InterPro: IPR001969; Aspprotease_site.
DR Pfam: PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 439 AA; 48275 MW; 02EC0E050F11602 CRC64;

Query Match 48.0%; Score 1160.5; DB 4; Length 439;
Best Local Similarity 50.1%; Pred. No. 5e-88;
Matches 220; Conservative 78; Mismatches 134; Indels 7; Gaps 4;

QY 18 MVDNLRGKSGGYVEMTVGSPPTLTNLTVDGSSNFAYCAAPHPLHRYRQLSSTYR 77
DB 1 MVDNLRGDSRGYYLEMLIGTPPKQLQILVDTGSSNFAYCAACTPHSYIDYFDRSSTYR 60
QY 78 DLKRGYVVPYTGQWEGELGTLVSIPIHGNVTVRANIAAITESDKFFI 137
DB 61 SKGFDVTVKVTGQSWTGFVGDVLTIPKGFNTSFLVNIATIFESNFPLPKWNGILGL 120
QY 138 AYAEIARPDLSLEPFFDSLVKQTHVPLNLSLQCCAGPFLNOSSEVLASVGGSMIGIDH 197
DB 121 AVATLAKPSSLETFDFSLVTKQANIPNVFSMQMCGAGLPVAGS---GTNGSGSLVGGIEP 177
QY 198 SLYTGSWYTPIRREWEYEVIIIVRVEINGODLMDCKEYNDKSIYVDSGTTNLRPLKVF 257
DB 178 SLYKGIWYTPKEEYQIETLKEIGQSINLDCREYNADKAIYVDSGTTNLRPLKVF 237
QY 258 EAAVKSIIKAASSTKFPDGFGLGOLVCWQAGCTTWNIFPVISLYLMGEVTNQSFRTIL 317
DB 238 DAVVAVARASLIPEFSDGFTGWSQLACNTSETPWSYPPKISLYLRDENSRSRFRITIL 297
QY 318 PQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARRIGFAVSACHV 377
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DB 298 PQYIQPMMGAGLNY-ECYREGISPTNALVIGATVMEGFYVIFDRQKRVGFAPSAACAE 356
QY 378 HDEFRTAAVCGPFTVLDMECGYNIPOQDESLMTIAYVMAAICALFMLPLCLMVCOWR 436
DB 357 IAGAAVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCGAIIIVLIVLLLPFR 416
QY 437 CLRLCRQHQHDDFADDISLL 455
DB 417 QCR--RPRDPEVNDSESL 433

RESULT 7
Q9JL18 PRELIMINARY; PRT; 514 AA.
AC Q9JL18:
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Aspartyl protease 1.
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi D.K., Sugano S., Sakaki Y.;
RT "Molecular characterization of the mouse Aspl gene, a homolog of the
RT human ASPL (Down Syndrome Region aspartyl protease).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216310; AAF36599.1; -
DR HSP; P32329; IYPS.
DR MEROPS; A01.041; -
DR MGD; MGI:1860440; Bace2.
DR InterPro: IPR001461; AspproteaseA1.
DR InterPro: IPR001969; Aspprotease_site.
DR Pfam: PF00026; asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 514 AA; 55799 MW; A70725F2C1DF5B47 CRC64;

Query Match 47.4%; Score 1146.5; DB 11; Length 514;
Best Local Similarity 50.7%; Pred. No. 9.3e-87;
Matches 216; Conservative 75; Mismatches 130; Indels 5; Gaps 3;

QY 8 EPCR-RGSFVEMVDNLRGKSGGYVEMTVGSPPTLTNLTVDGSSNFAYCAAPHPLH 66
DB 65 EPVRATANFLAMVDNLRGDSRGYYLEMLIGTPPKQVQILVDTGSSNFAYGAPHSYIDT 124
QY 67 YYQRQSLSTYRDLRKGVVVPYTGQWEGELGTLVSIPIHGNVTVRANIAAITESDKFFI 126
DB 125 YFDESSTYHSKGFVTVKVTGQSWTGFVGDVLTIPKGFNSFLVNIATIFESNFPL 184
QY 127 NGNWEIGILGAYAEIARPDLSLEPFFDSLVKQTHVPLNLSLQCCAGPFLNOSSEVLASV 186
DB 185 PGIKWNGILGAYAAALAKPSSLETFDFSLVQAQAKIPDIFSMQMGAGLPVAGS---CTN 241
QY 187 GGSMLIGIDHSLVTSGLWYTPIRREWEYEVIIIVRVEINGODLMDCKEYNDKSIYVDSG 246
DB 242 GGSVLGGIGLPSLVKGIWYTPKEEYQIETLKEIGQSINLDCREYNADKAIYVDSG 301
QY 247 TTLNLRPKKVFEEAAVKSIIKAASSTKFPDGFGLGOLVCWQAGCTTWNIFPVISLYLMGE 306
DB 302 TTLNLRPKQVDAVVAEAVARTSLIPEFSDGFTWGAOLACNTSETPWAYFPKISLYLWDE 361
QY 307 VTNQSFRITILPOQYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARR 366
DB 362 NASRSFRITILPOLYIQPMMGAGLNY-ECYREGISPTNALVIGATVMEGFYVVFDRARR 420
QY 367 RIGFAVSACHVHDEFRTAAVCGPFTVLDMECGYNIPOQDESLMTIAYVMAAICALFML 426
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Db 421 RVGFAVSPCAIEGTTVTSEISGPFSTEDIASNCVPAQALNEPILIVSVALMSVCGAILL 480
QY 427 PCLLMV 432
Db 481 VLILL 486

RESULT 8
Q9NZL2 PRELIMINARY; PRT; 468 AA.
AC Q9NZL2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A., Estivill X., de La Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT Alzheimer's amyloid precursor protein beta-secretase.";
RL Cytochrome. Cell Genet. 89:177-184(2000).
DR EMBL: AF188276; AAF35835.1;
DR HSP: P00797; 2REN.
DR MEROPS: A01.041;
DR InterPro: IPR001461; AspproteaseA1.
DR InterPro: IPR001969; Aspprotease_site.
DR Pfam: PF00026; asp. 1.
DR PRINTS: PR00792; PEPsin.
DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 468 AA; 50324 MW; 717E0920126A0142 CRC64;

Query Match 40.2%; Score 972.5; DB 4; Length 468;
Best Local Similarity 43.1%; Pred. No. 2.3e-72;
Matches 193; Conservative 74; Mismatches 124; Indels 57; Gaps 5;

QY 9 PGRGSEFVEMVNLKRGSGGYVEMTVPQTNLILVDVTGSSNFVAGAAPHPFLHRY 68
Db 71 PAGAANFLAVMDNLQDSGRGYYLEMIGTPPKQLQLVDVTGSSNFVAGTTPHSYIDTYF 130
QY 69 QRLSTYDLKRGVYVPTQGWEGELGTDLVSIPIHGNVTVRANIAATESDKFFING 128
Db 131 DTERSSTYKSGFDVTVKYTGQSWTGFVGEDLVTPKGFNTSLVNIATIFESNFPLG 190
QY 129 SNNEGILGLAYAEIARDDSLPEFDSLVKQTHVPLNLSLQLCGAGFPLNOSVLSVGG 188
Db 191 IKWNGILGLAYATLAKPSSLETFEFDLSVTOANIPNVFSMQMGAGLPVAGS---GTNGG 247
QY 189 SMITGGIDHSLYTGSLWYTPIRREWYEVIIIVVEINGQDLKMDCKEYNDKSIDVSGTT 248
Db 248 SLVGGIEPSLYKGIWYTPIKEWYQIEILKLEIGGOSLNLDREYNADKAIVDSGTT 307
QY 249 NLRLPKVFAAVKSKAASSTKFFPDGFWLGQVQAGTTPWNIFFVISLYLMGEVT 308
Db 308 LLRLPKVFDVAVVEAVARASLLPEFSDGFWTGSQACWTNSETPWSVFPKISIVLRDENS 367
QY 309 NQSFRTILPQOYLRPVEDVATSDQDCYKFAISQSSTGTVMGAVINEGFFVVFEDARKRI 368
Db 308 LLRLPKVFDVAVVEAVARASLL-----CLKFPGLSQ 393

RESULT 10
Q9P0D2 PRELIMINARY; PRT; 213 AA.
AC Q9P0D2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE HSPC104 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RESULT 9
Q9NZL1 PRELIMINARY; PRT; 396 AA.
AC Q9NZL1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A., Estivill X., de La Luna S.;
RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT Alzheimer's amyloid precursor protein beta-secretase.";
RL Cytochrome. Cell Genet. 89:177-184(2000).
DR EMBL: AF188277; AAF35836.1;
DR HSP: P00797; 2REN.
DR MEROPS: A01.041;
DR InterPro: IPR001461; AspproteaseA1.
DR InterPro: IPR001969; Aspprotease_site.
DR Pfam: PF00026; asp. 1.
DR PRINTS: PR00792; PEPsin.
DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_2.
KW Protease.
SQ SEQUENCE 396 AA; 43013 MW; 5023A7AF391CEAC9 CRC64;

Query Match 40.0%; Score 967.5; DB 4; Length 396;
Best Local Similarity 54.6%; Pred. No. 4.7e-72;
Matches 183; Conservative 54; Mismatches 85; Indels 13; Gaps 4;

QY 9 PGRGSEFVEMVNLKRGSGGYVEMTVPQTNLILVDVTGSSNFVAGAAPHPFLHRY 68
Db 71 PAGAANFLAVMDNLQDSGRGYYLEMIGTPPKQLQLVDVTGSSNFVAGTTPHSYIDTYF 130
QY 69 QRLSTYDLKRGVYVPTQGWEGELGTDLVSIPIHGNVTVRANIAATESDKFFING 128
Db 131 DTERSSTYKSGFDVTVKYTGQSWTGFVGEDLVTPKGFNTSLVNIATIFESNFPLG 190
QY 129 SNNEGILGLAYAEIARDDSLPEFDSLVKQTHVPLNLSLQLCGAGFPLNOSVLSVGG 188
Db 191 IKWNGILGLAYATLAKPSSLETFEFDLSVTOANIPNVFSMQMGAGLPVAGS---GTNGG 247
QY 189 SMITGGIDHSLYTGSLWYTPIRREWYEVIIIVVEINGQDLKMDCKEYNDKSIDVSGTT 248
Db 248 SLVGGIEPSLYKGIWYTPIKEWYQIEILKLEIGGOSLNLDREYNADKAIVDSGTT 307
QY 249 NLRLPKVFAAVKSKAASSTKFFPDGFWLGQVQAGTTPWNIFFVISLYLMGEVT 308
Db 308 LLRLPKVFDVAVVEAVARASLLPEFSDGFWTGSQACWTNSETPWSVFPKISIVLRDENS 367
QY 309 NQSFRTILPQOYLRPVEDVATSDQDCYKFAISQS 342
Db 368 SRSFRITILPKQ-LRVLQ-----CLKFPGLSQ 393

RESULT 10
Q9P0D2 PRELIMINARY; PRT; 213 AA.
AC Q9P0D2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE HSPC104 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORD BLOOD;
RA Zhang Q.H., Ye M., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
  Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human partial CDS cloned from cd34+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161367; AAF28927.1; -.
DR InterPro: IPR001461; AspproteaseA1.
DR Pfam: PF00026; asp; 1.
FT NON_TER 1 1
SQ SEQUENCE 213 AA; 24338 MW; EC9D3FA31CFA835C CRC64;

  Query Match      29.5%; Score 712.5; DB 4; Length 213;
  Best Local Similarity 83.5%; Pred. No. 2.9e-51;
  Matches 137; Conservative 4; Mismatches 12; Indels 11; Gaps 1;

QY 193 GGIDHSLYTGSWMYTPIRREWYEVIIVRVEINGQDLKMDCKEYNDKSIIVDSGTTNLR 252
  |||||
Db 1 GGIDHSLYTGSWMYTPIRREWYEVIIVRVEINGQDLKMDCKEYNDKSIIVDSGTTNLR 60

QY 253 PKVFEAAVKSIRAASTKRPDPGFGLCEQLVCWQAGTTPWNIFFVISLYLMEVNTNQS 312
  |||||
Db 61 PKVFEAAVKSIRAASTKRPDPGFGLCEQLVCWQAGTTPWNIFFVISLYLMEVNTNQS 120

QY 313 RITILPQOYLPRVEDVATSDQDCYKFAISQSSTGTVMGAVIMEG 356
  |||||
Db 121 RITILPQOYLPR-----WKMPRPKTTVTVCHLTIVNG 153

RESULT 11
QYR1P7
ID Q9R1P7 PRELIMINARY; PRT; 255 AA.
AC Q9R1P7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Aspartyl protease (Fragment).
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Accarino M., Fumagalli P., Taramelli R., Ottolenghi S.;
RT "Cloning of a gene from chromosome 21 Down Region encoding a potential
  transmembrane protease.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF051150; AAD45964.1; -.
DR MEROPS: A01.041; -.
DR MGD: MGI:1860440; Bace2.
DR InterPro: IPR001461; AspproteaseA1.
DR InterPro: IPR001969; Aspprotease_site.
DR PRINTS: PRO0792; PEPsin.
DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_1.
KW Protease.
FT NON_TER 1 1
SQ SEQUENCE 255 AA; 28685 MW; 53DE317815996D63 CRC64;

  Query Match      47.7%; Score 596.5; DB 11; Length 255;
  Best Local Similarity 47.8%; Pred. No. 1.7e-41;
  Matches 109; Conservative 44; Mismatches 74; Indels 1; Gaps 1;

QY 205 WYTPIRREWYEVIIVRVEINGQDLKMDCKEYNDKSIIVDSGTTNLRPKKVEAAVKSI 264
  |||||
Db 1 WYTPIRREWYEQIEILKLEIGGNLNDCKREYNADKAIIVDSGTTNLRPKKVEAAVVEAV 60

QY 265 KAASSTKFPDGFGLVCWQAGTTPWNIFFVISLYLMEVNTNQSFRITILPQOYLPR 324
  |||||
Db 61 ARTSLIPESDGFWTGAQLACWTNSETPWAYEPKISIVLRDENASRSFRITILPQYIQP 120

QY 325 VEDVATSDQDCYKFAISQSSTGTVMGAVIMEGFFVYVDFRARKRIGFAVSACHVDEPRTA 384
  :|||
Db 121 MCGAGFNY-ECYRFGISSSTNALVIGATVMEGFFVYVDFRARRVGVFAVSCAEIEGTIVS 179

QY 385 AVGGPFTVLMDEDCGYNIPQDTESLMTIAYVMAATCALFMLPLCLMV 432
  :|||
Db 180 EISGPFSTEDIASNCVPAQALNEPLTWISYALMSVCGAILLVILL 227

RESULT 12
Q8WQY9
ID Q8WQY9 PRELIMINARY; PRT; 244 AA.
AC Q8WQY9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Aspartate protease (Fragment).
GN APP.
OS Aphrocallistes vastus.
OC Eukaryota; Metazoa; Porifera; Hexactinellida; Hexasterophora;
OC Lyssacinosida; Rossellidae; Aphrocallistes.
OX NCBI_TaxID=83887;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller W.E.G., Mueller I.M., Grebenjuk V.A.;
RT "Unmetazoan: Origin and evolution of the common ancestor of Metazoa.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ304863; CAC83293.1; -.
DR InterPro: IPR001461; AspproteaseA1.
DR InterPro: IPR001969; Aspprotease_site.
DR Pfam: PF00026; asp; 1.
DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_1.
DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
KW Protease.
FT NON_TER 244 244
SQ SEQUENCE 244 AA; 26366 MW; 6536902661E0B4C7 CRC64;

  Query Match      14.9%; Score 359.5; DB 5; Length 244;
  Best Local Similarity 36.0%; Pred. No. 7.9e-22;
  Matches 81; Conservative 41; Mismatches 90; Indels 13; Gaps 6;

QY 19 VDNLRKSGGGYVYVMTVGSPPQTLLNLTGSSNFAGVAAPHPFHRY--YORQLSSTY 76
  |::|
Db 22 VYQLQGQESGYLVSNLGTTPQEFKVLVDGSSNFAVAAGFGYIQDYPRFDKSLSKTF 81

QY 77 RDLRKGVYVYPTOCKWEGELGTDLVS----IPHGPNVTVRANIAAI-TESDKPFINGSNW 131
  ||::|
Db 82 RDINSEVGKVIIDGWSGRVGEDYFAFASDVTTNASKSVKVVYSLIESVSEGFETSGGW 141

QY 132 EGILGLAYAFIARPDSDLPEPFDSILVKOTHPNLFSLQLCGAGFPPLNQSE-VLASVCGSM 190
  |||||
Db 142 VGLTGMGYAVLAKPDSSITPVMSLSVSGVTSDKFGLQLCQ---PLSNSRELNVQNGKM 198

QY 191 IIGGDHSLYTGSS--LWYTPIRREWYEVIIVRVEINGQDLKMDCK 233
  :|||
Db 199 SLGSARPLPSNSDVFRYVAITEESFYEVILTNIKVGSTSLDLP 243

RESULT 13
Q9VKP6
ID Q9VKP6 PRELIMINARY; PRT; 391 AA.
AC Q9VKP6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG17134 protein (RE02351p).
GN CG17134.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
```

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RN RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananietides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy J., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacieb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNOWN AS THE
CC EUKARYOTIC ASPARTYL PROTEASES FAMILY.
DR EMBL: AE003630; AAF53016.1; -.
DR EMBL: AY070911; AAL48533.1; -.
DR HSSP: P00794; 4CMS.
DR FlyBase: FBgn0032304; CG17134.
DR InterPro: IPR001461; AspproteaseA1.
DR InPar: IPR001969; Aspprotease_site.
DR Pfam: PF00026; asp.1.
DR PRINTS: PR00792; PEPSIN.
DR PROSITE: PS00141; ASP_PROTEASE; 2.
KW Aspartyl protease; Hydrolase.
SQ SEQUENCE 391 AA; 42016 MW; 99A18E7131025E1B CRC64;

Query Match 13.7%; Score 332.5; DB 5; Length 391;
Best Local Similarity 29.1%; Pred. No. 2.6e-19;
Matches 105; Conservative 61; Mismatches 146; Indels 49; Gaps 13;

QY 20 DNLGRSGGGYVEMTVGSPPTQNLILVDTGSSNFAVGAAPHF-----LHRYQRQLS 73
Db 66 ENLHSMNNNEYGVIAIGTPEQRNLFDTGSANLWPSACSPASNTACQRHNKYDSSAS 125

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QY 74 STYDLRKGVVVPYTOGKWEGLGTLVLSIPHGNVTVRANIAAITESDKFFINGSNWEG 133
Db 126 STYVANGEEFAIEYGTGSLSGFLSNDIVTIA-GISIQNTFGEALSPEGTFVD-APFAG 183
QY 134 ILGLAVAEIARPDSDLPPFDLSLVKQHPVN-LFSLQLCGAGPLNLOSEVLASVGSMMI 192
Db 184 ILGLAFSAIA--VDGVTTPFDNMTISQGLDEPVTISFYLKRQG-----TAVRGELIL 233
QY 193 GGDHSLYTSGLWYTPIRREWYVEIIVRVEINGODLKMCKEYNYDKSIVDSGTTNLR 252
Db 234 GGDSSLYRSLTVVPVSPAYWQFKVNTIKTNGTLTCNGC-----OAIADTGTSLIAV 287
QY 253 PKVFFAAVKSIAKASSTEREPDGFGLGQLV-CWQAGTTPWNIPFPVISLYLMGEVNTQS 311
Db 288 PLAYRKINQLGATDND-----GEAFVRCGRVSS-----LPKVNINIGTV---- 329
QY 312 FRITLPQOYLRPVEDVATSDQCYK-FAISQSTGTVMGAVINEGVYVDFDRARKRIGF 370
Db 330 --FTLAPRDYI--VKVTPQNGQTYCMSAFTYMEGLSFLWILGDFVFGKTYTFDKNERIGF 385
QY 371 A 371
Db 386 A 386

RESULT 14
Q9GYX7 PRELIMINARY; PRT; 354 AA.
ID Q9GYX7 PRELIMINARY; PRT; 354 AA.
AC Q9GYX7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heme-binding aspartic proteinase (Fragment).
OS Boophilus microplus (cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PORTO ALEGRE; TISSUE=OVARY;
RA Sorgine M.H.F., Logullo C., Zingali R.B., Paiva-Silva G.O.,
RA Juliano L., Oliveira P.L.;
RT "A heme-binding aspartic proteinase from the eggs of the hard tick
RT Boophilus microplus."
RL J. Biol. Chem. 0:0-0(2000).
DR EMBL: AF286865; AAG00993.1; -.
DR HSSP: P00797; 2REN.
DR MEROPS: A01.054; -.
DR InterPro: IPR001461; AspproteaseA1.
DR Pfam: PF00026; asp.1.
DR PRINTS: PR00792; PEPSIN.
DR NON_TER 1
FT SEQUENCE 354 AA; 38512 MW; B50D7C638CF27091 CRC64;

Query Match 13.7%; Score 332; DB 5; Length 354;
Best Local Similarity 26.2%; Pred. No. 2.6e-19;
Matches 101; Conservative 74; Mismatches 135; Indels 76; Gaps 15;

QY 19 VDNLRGK-----SGQGYVEMTVGSPPTQNLILVDTGSSNFAVGAAPHFPL- 64
Db 13 VTEIRGALGDPPIILNTYNNMQFYGIITGTPQSFKLMDTGSSNFWYI---PSIN 67
QY 65 -----HRYQRQLSSYRDLRGVYVPYTOGKWEGLGTLVLSIPHGNVTVRANI 115
Db 68 CDOSMACRDHAKYDSSKSTFTSGRYIRIRYSGVGVVGRITSIDNVGV--GPATVYQYKF 125
QY 116 AAITESDKFFINGSNWEGILGLAVAEIARPDSDLPEPFDLSLVKQHPVN-LFSLQLCGAG 174
Db 126 AEMDHSCKLFRNAKYDGLGAPPSISQ--NNOLPLFDAMVKGVVQAVFSLYL--SK 181
QY 175 FPLNQSEVLASVGSMMIIGGIDHSLYTSGLWYTPIRREWYVEIIVRVEINGODLKM-DC 233

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Db 182 QPSEQN-----GGEIYFGGINAQRYTGAIHVVPVSQAHHQVVMNDINVQGTTLVCVGGC 235
QY 234 KEYNDSKISVDSGTTLNLRPKKVFEEAAVKSIAKASSTEFPPDGFELGQVLVCWQAGTTPW 293
Db 236 -----PTVDSGTSFLSGP-----SADVETLNRVIGATKTAAGY-----FEVNCATI 277
QY 294 NIFPVISLYLME---VTNQSFRTILPQOYLRPVEDVATSDQDCYKFAISQSSTGT--- 347
Db 278 SSLPPTIFNLNGKSFPLQGEAVTIRI-----PLTTGGQCFTRISESADASGTNLW 327
QY 348 VMGAVIMEGFYVDFDRARKRIGFAVS 373
Db 328 ILGAVETQTYTYTVEDRAQNRVGFATA 353

RESULT 15

Q9BGU5 PRELIMINARY; PRT; 386 AA.
AC Q9BGU5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cathepsin D (Fragment).
GN CAT-D.
OS Bos taurus (Bovine).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Higuchi M., Miyashita N., Nagamine Y., Awata T.;
RT "Complementary DNA sequence of bovine cathepsin D.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDAJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNOWN AS THE
CC EUKARYOTIC ASPARTYL PROTEASES FAMILY.
DR EMBL; AB055312; BAB21620.1; -
DR HSSP; P07339; 1LYB.
DR MEROPS; A01.009; -
DR InterPro; IPR001461; AspproteaseA1.
DR InterPro; IPR001969; Aspprotease_site.
DR Pfam; PF00026; asp.1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Aspartyl protease; Hydrolase.
FT NON_TER 1
SQ SEQUENCE 386 AA; 41965 MW; 33BF00B080585490D CRC64;

Query Match 12.98; Score 312.5; DB 6; Length 386;
Best Local Similarity 28.0%; Pred. NO. 1.3e-17;
Matches 113; Conservative 69; Mismatches 131; Indels 91; Gaps 20;

QY 8 EPG-RGSGFVEMVDNLRKSGQGYVEMTVGSPPTLNILVDTGSSNFAYGAAPHPEL-- 64
Db 35 EPAVRQGPPELLKNYMDAQ---YGEIGTGPPOCFVTFVDFGSLANLWPSIHCULKLDI 91
QY 65 ----HRYYQRLSSTRDLRRGVY--VPYTGKWEGLGTLVLSIPHGN-----VTVR 112
Db 92 ACWTHRKYNDSKSTY--VKNGTTFDIHYGSGSLGSLQDTSVPCNPSSSPGGVTQ 149
QY 113 ANT--AAITSDKFFINGNWEGLGLAYAEIARDDSLPFDLSLVKQTHV-PNLFSLQ 169
Db 150 RQTFGEAIKQPGVVFI-AAKFGGLGMAYPRIS--VNNVLPVFDNLMMQKLVOKNVFS-- 204
QY 170 LCGAGPLNQSEVLASVGGSMILGIDHSLSYTLPTIRREWYVEIIVRVEINGDL 229
Db 205 -----FFLNR-DPKAQGGELMLGTDTSKYRGSLMFHNVTRQAYWQHMDQLDV-GSSL 257
QY 230 KMDCKEYNIDKISVDGTTNLRPKKVFEEAAVKSIAKASSTEFPPDGFELGQVLVCWQAG 289
Db 258 TV-CK--GGCEAIVDTGTSLVGVPVEEVRLEQKAI-----G 290
QY 290 TTPWNIFPVISLYLMGEVNTNOSFRITILPQQYLR-PVEDVATSQDDCYKFAISOSSTGT- 347

Db 291 AVP-----LIQGEYMIPECVSSLPQVTVKLGKDYAXSPED-YALKVSOAGTTCVC 340
QY 348 -----VMGAVIMEGFYVDFDRARKRIGFAVS 374
Db 341 LSGFMGMDIPPPGGLWILGDVFIGRYTYTVFDRDQNRVGLAEAA 384
Search completed: March 4, 2003, 10:04:29
Job time : 40 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2003, 13:38:25 ; Search time 4002 Seconds
(without alignments)
17074.810 Million cell updates/sec

Title: US-09-723-722A-44
Perfect score: 2348
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
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- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
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- 33: em_htg_mus:*
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- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2342.8	99.8	2526	9	AF190725	AF190725 Homo sapi
2	2341.2	99.7	5878	9	AF201468	AF201468 Homo sapi
3	2331.8	99.3	5814	9	AB032975	AB032975 Homo sapi
4	2181.2	92.9	5757	6	AX364933	AX364933 Sequence
5	2041.4	86.9	2070	9	AF200343	AF200343 Homo sapi
6	2039.8	86.9	2070	6	AX105385	AX105385 Sequence
7	2039.8	86.9	2070	6	AX378015	AX378015 Sequence
8	2024	86.2	2541	6	AR178469	AR178469 Sequence
9	2024	86.2	2541	6	AX002655	AX002655 Sequence
10	2024	86.2	2541	6	E50816	E50816 Aspartate p
11	2004	85.3	3252	6	AX062111	AX062111 Sequence
12	2004	85.3	3252	6	AX063201	AX063201 Sequence
13	2004	85.3	3252	6	AX472368	AX472368 Sequence
14	2004	85.3	3252	9	AF200193	AF200193 Homo sapi
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25	1506	64.1	1506	9	AF204943	AF204943 Homo sapi
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27	1355.8	57.7	1362	6	AX105411	AX105411 Sequence
28	1355.8	57.7	1380	6	AX105413	AX105413 Sequence
29	1344.4	57.3	1431	9	AF338816	AF338816 Homo sapi
30	1298	55.3	1506	6	AR202196	AR202196 Sequence
31	1293.8	55.1	1341	6	AX105403	AX105403 Sequence
32	1293.8	55.1	1380	6	AX105405	AX105405 Sequence
33	1270.4	54.1	1302	6	AX105407	AX105407 Sequence
34	1266	53.9	1408	9	AB050437	AB050437 Homo sapi
35	1230.4	52.4	1374	9	AF338817	AF338817 Homo sapi
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37	1197.4	51.0	1305	6	AX105434	AX105434 Sequence
38	1180	50.3	1278	6	AX105409	AX105409 Sequence
39	1116	47.5	1333	9	AB050438	AB050438 Homo sapi
40	990	42.2	1114	9	AF161367	AF161367 Homo sapi
C 41	781.2	33.3	134278	9	AP001822	AP001822 Homo sapi
C 42	781.2	33.3	199892	2	AC020997	AC020997 Homo sapi
C 43	779.6	33.2	98305	2	AP000685	AP000685 Homo sapi
C 44	779.6	33.2	149843	9	AP000892	AP000892 Homo sapi
C 45	779.6	33.2	162610	2	AP000761	AP000761 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds.
ACCESSION AF190725
VERSION AF190725.1 GI:6118538
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2526)
AUTHORS Vassar,R., Bennett,B.D., Babu-Khan,S., Kahn,S., Mendiaz,E.A., Denis,P., Teplow,D.B., Ross,S., Amarante,P., Loeloff,R., Luo,Y.,

AF190725 2526 bp mRNA linear PRI 26-OCT-1999
Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds.

Fisher, S., Fuller, J., Edenson, S., Lile, J., Jarosinski, M.A.,
Biere, A.L., Curran, E., Burgess, T., Louis, J.C., Collins, F.,
Treanor, J., Rogers, G., and Citron, M.
Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
the transmembrane aspartic protease BACE

Science 286 (5440), 735-741 (1999)

JOURNAL MEDLINE 20002972

PUBMED 10531052

REFERENCE 2 (bases 1 to 2526)

Bennett, B.D., Vassar, R., and Citron, M.

Direct Submission

Submitted (29-SEP-1999) Neuroscience, Amgen Inc., One Amgen Center

Dr., Thousand Oaks, CA 91320-1799, USA

Location/Qualifiers

1. .2526

/organism="Homo sapiens"

/db_xref="taxon:9606"

1. .2526

/gene="BACE"

454. .1959

/gene="BACE"

/codon_start=1

/product="beta-site APP cleaving enzyme"

/protein_id="AA04142.1"

/db_xref="GI:6118539"

/translation="MAQALPWLMLMAGVLPAGHTQHGIRLPLRSLGLGAPLGLRLP

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AAITPESKFFNGSNWGLGLAYABIAIPDDSLPEPFDLSLVKQTHVPLNLSLQCGA

GFPLNQSLVASGSMITGGIDHSITGLTPIIRREMYEVLIVREINGDQLKM

DKREYNVDKSIDVSTGNLRLPKKFEAAVSIKASSTSEKFPDGLWGLQVCMQAG

TTNPWIFPISLYLMGEVNTNQSFRIITLPQYLRPVEDVATSDQDCYKFAISQSTGT

VMGAVIMEGFYVDFRARKRIGFAVMSCHVRCWRLCLRLRQHQHDFADDISLLK"

DESTLMTAYVMAALCALFMLPLCLMVCQWRCLRLRQHQHDFADDISLLK"

BASE COUNT 534 a 781 c 715 g 496 t

ORIGIN

Query Match 99.8%; Score 2342.8; DB 9; Length 2526;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2344; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATGCCGCGCCCTCACAGCCCGCGGAGCCGCGGAGCCGCTGCCAGGCTGCGCGCG 60

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Sinha, S., Anderson, J.P., Barbour, R., Basi, G.S., Caccavello, R.,
Davis, D., Doan, M., Dovey, H.F., Frigon, N., Hong, J.,
Jacobson-Croak, K., Jewett, N., Keim, P., Knops, J., Lieberburg, I.,
Power, M., Tan, H., Tatsuno, G., Tung, J., Schenk, D., Seubert, P.,
Suomensaari, S., Wang, S., Walker, D., Zhao, J., McConlogue, L. and
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John, V.
Purification and cloning of amyloid precursor protein
beta-secretase from human brain
Nature 402 (6761), 537-540 (1999)
200517171
PUBMED 10591214
REFERENCE 2 (bases 1 to 5878)
AUTHORS Basi, G.S., Power, M.D., Wang, S., Tatsuno, G., Frigon, N., Doan, M.,
Hong, G., Keim, P., Anderson, J., Sinha, S. and McConlogue, L.M.
Direct Submission
Submitted (03-NOV-1999) Gene Expression Group, Elan
Pharmaceuticals, Inc., 800 Gateway Blvd., S. San Francisco, CA
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TITLE Characterization of cDNA clones selected by the Genemark analysis
from size-fractionated cDNA libraries from human brain
JOURNAL DNA Res. 6 (5), 329-336 (1999)
MEDLINE 20039618
REFERENCE 2 (bases 1 to 5814)
AUTHORS Ohara, O., Nagase, T. and Kikuno, R.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdmainfo@kazusa.or.jp)
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RESULT 4
AX364933
LOCUS AX364933
DEFINITION Sequence 84 from Patent WO0206315.
ACCESSION AX364933
VERSION AX364933.1 GI:18696823
KEYWORDS linear PAT 15-FEB-2002

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SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Mintz, L., Freilich, S. and Bernstein, J.  
TITLE Novel nucleic acid and amino acid sequences  
JOURNAL Patent: WO 0206315-A 84 24-JAN-2002;  
Compugen Ltd. (IL)  
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AF200343 Homo sapiens chromosome 11 aspartyl protease 2 mRNA, complete cds.
LOCUS AF200343
DEFINITION AF200343
ACCESSION AF200343
VERSION AF200343.1 GI:6561813
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ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2070)
AUTHORS Yan, R., Blenkowski, M.J., Shuck, M.E., Miao, H., Tory, M.C.,
Pauley, A.M., Brashier, J.R., Stratman, N.C., Mathews, W.R., Buhl, A.E.,
Carter, D.B., Tomasselli, A.G., Parodi, L.A., Heinrikson, R.L. and
Gurney, M.E.
Membbrane-anchored aspartyl protease with Alzheimer's disease
beta-secretase activity
Nature 402 (6761), 533-537 (1999)
JOURNAL MEDLINE 20057170
PUBMED 10591213
REFERENCE 2 (bases 1 to 2070)
AUTHORS Blenkowski, M.J., Shuck, M.E., Slightom, J.L. and Drong, R.F.
TITLE Direct Submission
JOURNAL Submitted (29-Oct-1999) Genomics Research, Pharmacias&Upjohn, 301
Henrietta, Kalamazoo, MI 49007, USA
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DEFINITION Sequence 3 from Patent WO0123533.
ACCESSION AX105385
VERSION AX105385.1 GI:13921511
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2070)
AUTHORS Gurney,M. and Bienkowski,M.J.
TITLE Alzheimer's disease secretase, app substrates therefor, and uses therefor
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AX378015
LOCUS AX378015 2070 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 1 from Patent WO0206306.
ACCESSION AX378015
VERSION AX378015.1 GI:19574050
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Yan, R., Tomasselli, A.G., Gurney, M.E., Emmons, T.L., Bienkowski, M.J.
and Heinrikson, R.L.
TITLE Substrates and assays for g(b)-secretase activity
JOURNAL Patent: WO 0206306-A 1 24-JAN-2002;
PHARMACIA & UPJOHN COMPANY (US)
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Db 2041 AATT 2044

RESULT 9
LOCUS AX002655
DEFINITION Sequence 1 from Patent EP085444.
ACCESSION AX002655
VERSION AX002655.1 GI:7242133
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2541)
AUTHORS Murphy,K. and Chapman,C.G.
TITLE Aspartic proteinase 2 (ASP2)
JOURNAL Patent: Ep 085444-A 1 29-JUL-1998;
SMITHKLINE BEECHAM PLC (GB); SMITHKLINE BEECHAM CORP (US)
FEATURES
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BASE COUNT 598 a 673 c 675 g 579 t 16 others
ORIGIN

Query Match 86.2%; Score 2024; DB 6; Length 2541;
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RESULT 10
E50816
LOCUS Aspartate proteinase ASP2. 2541 bp DNA linear PAT 18-JUN-2001
DEFINITION Aspartate proteinase ASP2.
ACCESSION E50816
VERSION E50816.1 GI:13023199
KEYWORDS JP 2000060579-A/1.
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 2541)
AUTHORS David,J.P., Conrad,G.C., Kay,M. and Trudy,S.S.
TITLE Aspartate proteinase ASP2
JOURNAL Patent: JP 2000060579-A 1 29-FEB-2000;
SMITHKLINE BEECHAM CORP
COMMENT OS Unidentified
PN JP 2000060579-A/1
PD 29-FEB-2000
PF 03-AUG-1999 JP 1999219665
PI 28-JAN-1997 GB 9701684:4
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PC A61P25/28,A61P35/00,A61P43/00,C07K16/40,C12N1/15,C12N1/19,PC
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Db 2041 AATT 2044

RESULT 11
AX062111

LOCUS AX062111 Sequence 1 from Patent WO0100665.
DEFINITION AX062111

ACCESSION AX062111
VERSION AX062111.1 GI:12540032

KEYWORDS human.
SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

3252 bp DNA linear PAT 24-JAN-2001

REFERENCE 1 (bases 1 to 3252)
AUTHORS Tang, J. J., Hong, L. and Ghosh, A. K.
TITLE Inhibitors of memapsin 2 and use thereof
JOURNAL Patent: WO 0100665-A 1 04-JAN-2001;
Oklahoma Medical Research Foundation (US); THE BOARD OF TRUSTEES
OF THE UNIVERSITY OF ILLINOIS (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 12
LOCUS AX063201 3252 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 1 from Patent WO0100663.
ACCESSION AX063201
VERSION AX063201.1 GI:12541045
KEYWORDS human,
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3252)
AUTHORS Tang,J.J., Lin,X. and Koelsch,G.
TITLE Catalytically active recombinant memapsin and methods of use there
of
JOURNAL Patent: WO 0100663-A 1 04-JAN-2001;
Oklahoma Medical Research Foundation (US)
FEATURES
Location/Qualifiers
Source 1..3252
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BASE COUNT 804 a 863 c 811 g 771 t 3 others
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AX472368 3252 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1 from Patent WO02053594.
ACCESSION AX472368
VERSION AX472368.1 GI:22207364
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
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AUTHORS Ghosh,A.K., Koelsch,G. and Tang,J.J.
TITLE Inhibitors of memapsin 2 and use thereof
JOURNAL Patent: WO 02053594-A 1 11-JUL-2002;
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LOCUS AX105387 1977 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 5 from Patent WO0123533.
ACCESSION AX105387
VERSION AX105387.1 GI:13921512
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1977)
AUTHORS Gurney,N. and Bienkowski,M.J.
TITLE Alzheimer's disease secretase, app substrates therefor, and uses therefor
JOURNAL Patent: WO 0123533-A 5 05-APR-2001;
Pharmacia & Upjohn Company (US)
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Db 1306 GTCATGGCTGCGCTATGGCCCTCTTTCATCTGCCACTCTGCCCTCATGGTGTGTCAGTGG 1365
QY 1746 CGCTGCGCTCGCTGCGCGCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1805
Db 1366 CGCTGCGCTCGCTGCGCGCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1425
QY 1806 AAGTGAGGAGCCCATGGCAGAGATAGAGATTCCCTGGACCACACCTCCGTTGTTCA 1865
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